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**SEQUENCE-DETERMINED DNA FRAGMENTS AND
CORRESPONDING POLYPEPTIDES ENCODED THEREBY**

This application is a continuation-in-part of the following co-pending applications. The entire contents of which are hereby incorporated by reference:

Number	Attorney Docket No.	FILED	Application Number
1	2750-1153P	05-Jan-01	09/754,184
2	2750-1556P	09-Apr-03	10/409,117
3	2750-1434P	04-Apr-01	09/824,790
4	2750-1565P	17-Jun-03	Unknown
5	2750-1383P	29-Dec-00	09/750,044
6	2750-1537P	21-Nov-02	10/300,941
7	2750-1542P	06-Jan-03	10/336,798
8	2750-1536P	07-Nov-02	10/289,416
9	2750-1539P	09-Dec-02	10/314,246
10	2750-1570P	04-Aug-03	Unknown
11	2750-1541P	06-Jan-03	10/336,816
12	2750-1544P	13-Jan-03	10/340,649
13	2750-1545P	13-Jan-03	10/340,584
14	2750-1569P	29-Jul-03	Unknown
15	2750-1567P	15-Jul-03	Unknown
16	2750-1559P	05-May-03	10/428,842
17	2750-1566P	15-Jul-03	Unknown
18	2750-1067P	21-Jul-00	09/620,394
19	2750-1243P	09-Nov-00	09/708,427
20	2750-1572P	15-Aug-03	Unassigned
21	2750-1385P	02-Jan-01	09/750,910
22	2750-1538P	18-Dec-02	60/433,952
23	2750-1560P	08-May-03	Unknown
24	2750-1548P	10-Feb-03	10/360,648
25	2750-1531P	12-Aug-02	10/216,621
26	2750-1564P	16-Jun-03	Unknown

27	2750-1535P	29-Oct-02	10/282,058
28	2750-1551P	03-Mar-03	10/376,785
29	2750-1552P	03-Mar-03	10/376,797
30	2750-0709P	25-Feb-00	09/513,996
31	2750-1481P	24-Aug-01	09/935,625
32	2750-1550P	28-Feb-03	10/375,265
33	2750-1553P	03-Mar-03	10/376,766
34	2750-1033P	12-Oct-00	09/686,093
35	2750-1032P	06-Oct-00	09/680,498
36	2750-1026P	28-Sep-00	09/671,635
37	2750-1024P	22-Sep-00	09/667,517
38	2750-1022P	20-Sep-00	09/665,714
39	2750-0990P	20-Jul-00	09/621,323
40	2750-1000P	04-Aug-00	09/633,191
41	2750-1014P	30-Aug-00	09/651,370
42	2750-1558P	01-May-03	10/426,837
43	2750-1330P	01-Nov-00	09/702,841
44	2750-1309P	25-Oct-00	09/696,751
45	2750-1547P	02-Feb-03	10/356,562
46	2750-1540P	06-Jan-03	10/336,799
47	2750-1546P	21-Jan-03	10/347,322
48	2750-1555P	04-Apr-03	10/406,556
49	2750-1543P	13-Jan-03	10/340,820
50	2750-1568P	18-Jul-03	Unknown

Through the 50 applications listed above, the present application also claims priority to and incorporates by reference the following applications:

Number 2

Application No. 10/409,117 (attorney no. 2750-1556P) is a continuation of Application No. 10/084,376 (attorney no. 2750-1486P) filed February 28, 2002, to which the present application also claims priority to and incorporates by reference. Furthermore, Application No. 10/084,376 is a continuation of Application No. 09/924,701 (attorney no. 2750-1470P) filed August 9, 2001, to which the present application also claims priority to and incorporates by

reference. Moreover, Application No. 09/924,701 claims priority to under 35 USC 119(e) of provisional application no. 60/224,391 (attorney no. 2750-1115P) filed August 9, 2000, to which the present application also claims priority to and incorporates by reference.

Number 3

Application No. 09/824,790 listed above (as item no. 3 – attorney no. 2750-1434P) is a continuation-in-part of the following applications to which the present application also claims priority and incorporates by reference:

Attorney No.	Appln.	Filed
2750-	60/199,12	4/24/2000
2750-0792P	60/194,69	4/5/2000
2750-0802P	60/196,16	4/11/2000
2750-0814P	60/197,39	4/14/2000
2750-0797P	60/195,25	4/7/2000
2750-0784P	60/194,88	4/6/2000
2750-0805P	60/196,48	4/12/2000
2750-0789P	60/194,68	4/5/2000
2750-0785P	60/194,38	4/4/2000
2750-0820P	60/198,40	4/19/2000
2750-0826P	60/198,76	4/21/2000
2750-0823P	60/198,62	4/20/2000
2750-0817P	60/198,26	4/17/2000

Number 4

Application No. 4 listed above (attorney no. 2750-1565P) claims priority under 35 USC §119(e) of provisional application no: 60/389,140 filed June 17, 2002 (attorney no. 2750-1527P) the entire contents of which are also hereby incorporated by reference.

Number 6

Application No. 10/300,941 (attorney no. 2750-1537P) listed above is a continuation-in-part of Application No. 09/617,682 (Attorney No. 2750-1063P) filed on July 19, 2000, Application No. 09/617,681 (Attorney No. 2750-1064P) filed on July 19, 2000, and Application No. 09/688,051 (Attorney No. 2750-1242P) filed on October 13, 2000, the entire contents of all three (3) of these applications are hereby incorporated by reference.

Through the three applications mentioned above, Application No. 10/300,941 also claims priority under 35 USC §119(e) of the following provisional applications, the entire contents of which are hereby incorporated by reference:

Country	Filing Date	Attorney	Appln. No.	Status
United	July 19,	2750-492P	60/144,331	Pending at the time of filing Appln No.
United	July 19,	2750-494P	60/144,333	Pending at the time of filing Appln No.
United	Oct. 13,	2750-0583P	60/159,294	Pending at the time of filing Appln No.

Number 7

Application No. 10/336,798 (attorney no. 2750-1542P) listed above is a continuation of co-pending Application No. 10/136,365, filed on May 2, 2002, the entire contents of which are also hereby incorporated by reference. Through Application No. 10/136,365, this application also claims priority under 35 USC §119(e) and §120 of the following applications, the entire contents of which are hereby incorporated by reference:

Country	File	Attorney No.	Client No.	Application No.
United	12/08/00	2750-1250P	80180.003	09/731,809
which is a conversion of and claims priority to the following provisional applications:				
United	12/08/99	2750-0675P	80180.001	60/169,692
United	12/08/99	2750-0676P	80180.002	60/169,691

Number 8

Application No. 10/289,416 (Attorney No. 2750-1536P) listed above is a continuation of co-pending Application No. 10/103,783 filed on March 25, 2002, the entire contents of which are hereby incorporated by reference. Through application No. 10/103,783, this application also

claims priority under 35 USC §119(e) and §120 of the following applications, the entire contents of which are hereby incorporated by reference:

Country	Filing	Attorney No.	Client No.	Application	Status
United	1/19/01	2750-1387P	80182.003	09/764,425	Pending at the time of filing
					Which claims priority of the provisional applications listed below:
United	1/19/00	2750-0681P	80182.002	60/176,866	Pending at the time of filing
United	1/19/00	2750-0685P	80183.002	60/176,867	Pending at the time of filing
United	1/20/00	2750-0688P	80184.002	60/176,910	Pending at the time of filing
United	1/26/00	2750-0689P	00152.001	60/178,166	Pending at the time of filing
United	1/27/00	2750-0680P	80182.001	60/178,544	Pending at the time of filing
United	1/27/00	2750-0682P	80183.001	60/178,546	Pending at the time of filing
United	1/27/00	2750-0687P	80184.001	60/178,545	Pending at the time of filing

Number 9

Application No. 10/314,246 (attorney no. 2750-1539P) listed above is a continuation of co-pending Application No. 09/570,582 (attorney no. 2750-0873P) filed on May 12, 2000, the entire contents of which are hereby incorporated by reference. Through application No. 09/570,582, this application claims priority under 35 USC §119(e) of the following application, the entire contents of which are hereby incorporated by reference:

Country	Filing	Attorney No.	Application	Status
United	05/14/199	2750-0433P	60/134,221	Pending at the time of filing

Number 10

Application 10 (attorney docket no. 2750-1570P) listed above is a continuation of Application No. 09/649,866 (Attorney No. 2750-1097P), filed on August 23, 2000, the entire contents of which are hereby incorporated by reference. Through application no. 09/649,866, this application also claims priority under 35 USC §119(e) of the following provisional application, the entire contents of which are hereby incorporated by reference:

Country	Filing Date	Attorney No.	Application No.
United States	8/23/1999	2750-0540P	60/149,930

Number 11

Application No. 10/336,816 (attorney no. 2750-1541P) listed above is a continuation of Application No. 10/119,718 filed on April 11, 2002, the entire contents of which are hereby incorporated by reference. Through application no. 10/119,718, this application also claims priority under 35 U.S.C. §120 of the following application, the entire contents of which are hereby incorporated by reference:

Country	File	Attorney No.	Client No.	Appln. No.
United States	08/10/01	2750-1251P	710-0004-55300-US-U-31610.01	09/925,897

Number 12

Application No. 10/340,649 (attorney no. 2750-1544P) listed above is a continuation of Application No. 10/112,879 (attorney no. 2750-1503P) filed on April 2, 2002, the entire contents of which are hereby incorporated by reference. Through application No. 10/112,879 this application also claims priority under 35 USC §119(e) and §120 of the following applications, the entire contents of which are hereby incorporated by reference:

Country	Filing Date	Attorney No.	Application No.	Status
United States	June 16, 2000	2750-0954P	09/594,599	Pending at the time of filing 10/112,879. This application is a continuation of the following provisional application:
United States	June 16, 1999	2750-0461P	60/139,453	Pending at the time of filing 09/594,599

Number 13

Application No. 10/340,584 (attorney no. 2750-1545P) listed above is a continuation of Application No. 10/128,238 (attorney no. 2750-1511P) filed on April 24, 2002, the entire contents of which are also hereby incorporated by reference. Through application No. 10/128,238, the present application also claims priority under 35 USC §120 of the following application, the entire contents of which are hereby incorporated by reference:

Country	Application No.	Filing Date	Attorney No.	Status
United States	09/925,483	8/10/01	2750-1252P	Pending at the time of filing 10/128,238

Number 14

Application 14 (attorney docket no. 2750-1569P) listed above is a continuation-in-part of Application No. 09/637,780 (Attorney No. 2750-1096P), filed on August 11, 2000, the entire contents of which are hereby incorporated by reference. Through application no. 09/637,780, this application also claims priority under 35 USC §119(e) of the following provisional application, the entire contents of which are hereby incorporated by reference:

Country	Filing Date	Attorney No.	Application No.
United States	8/13/1999	2750-0532P	60/148,684

Number 15

Application 15 (attorney docket no. 2750-1567P) listed above is a continuation of Application No. 09/689,980 (Attorney No. 2750-1237P), filed on October 13, 2000, the entire contents of which are hereby incorporated by reference. Through application no. 09/689,980, this application also claims priority under 35 USC §119(e) of the following application, the entire contents of which are hereby incorporated by reference:

Country	Filing Date	Attorney No.	Client No.	Application No.
United States	10/14/1999	2750-0578P	80146.001	60/159,331

Number 16

Application No. 10/428,842 listed above is a continuation of Application No. 09/620,111 (Attorney No. 2750-1070P) filed July 21, 2000, the entire contents of which are hereby incorporated by reference. Application No. 09/620,111 claims priority under 35 USC 119(e) of

provisional Application No. 60/145,089 (Attorney No. 2750-0487P), filed July 22, 1999, the entire contents of which are also hereby incorporated by reference.

Number 17

Application 17 (attorney docket no. 2750-1566P) listed above claims priority under 35 USC §119(e) of provisional application no: 60/395,650 filed July 15, 2002 (att. docket no. 2750-1532P) the entire contents of which are hereby incorporated by reference.

Number 18

Application No. 09/620,394 (attorney no. 2750-1067P) listed above claims priority under 35 USC §119(e), of the following applications, the entire contents of which are hereby incorporated by reference:

Country	Filing Date	Attorney No.	Client No.	Application No.
United States	07/21/99	2750-0483P	80134.001	60/145,088

Number 19

Application No. 09/708,427 (attorney no. 2750-1243P) listed above is a continuation-in-part and claims priority under 35 USC §120 of the following applications, the entire contents of which are hereby incorporated by reference:

Country	Filing Date	Attorney No.	Client No.	Appln No.
United States	1/7/00	2750-0684P	80070.002	09/479,221
United States	4/28/00	2750-0788P	80123.002	09/559,232
United States	6/16/00	2750-0955P	80132.024	09/595,331
United States	7/14/00	2750-1060P	80134.017	09/614,388
United States	7/19/00	2750-1062P	80134.020	09/617,683
United States	7/20/00	2750-1065P	80134.026	09/620,998

Country	Filing Date	Attorney No.	Client No.	Appln No.
United States	7/21/00	2750-1069P	80134.023	09/620,313
United States	7/21/00	2750-1071P	80134.021	09/620,390
United States	7/21/00	2750-1073P	80134.025	09/620,314
United States	8/2/00	2750-1077P	80137.004	09/630,442
United States	8/4/00	2750-1092P	80138.004	09/635,643
United States	8/4/00	2750-1078P	80138.003	09/635,640
United States	8/9/00	2750-1094P	80139.004	09/635,642
United States	8/10/00	2750-1093P	80139.003	09/635,641
United States	8/16/00	2750-1095P	80142.003	09/643,672
United States	8/18/00	2750-1098P	80143.004	09/643,671
United States	8/25/00	2750-1099P	80144.003	09/649,868
United States	8/25/00	2750-1100P	80144.004	09/649,867
United States	10/13/00	2750-1241P	80148.003	09/689,981
United States	10/13/00	2750-1236P	80145.004	09/688,050
United States	10/13/00	2750-1238P	80146.004	09/688,052
United States	10/13/00	2750-1239P	80147.003	09/689,982
United States	10/13/00	2750-1240P	80147.004	09/689,983

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Application No. 09/708,427 also claims priority under 35 USC §119(e) of the following provisional applications, the entire contents of which are hereby incorporated by reference:

Country	Fi	Attorney No.	Client No.	Application No.
United States	11/10/99	2750-0622P	80161.001	60/164,319
United States	11/9/99	2750-0623P	80161.002	60/164,260
United States	11/10/99	2750-0624P	80162.001	60/164,317
United States	11/9/99	2750-0625P	80162.002	60/164,259
United States	11/10/99	2750-0626P	80163.001	60/164,321
United States	11/10/99	2750-0627P	80163.002	60/164,318
United States	11/24/99	2750-0654P	80173.001	60/167,382
United States	11/23/99	2750-0655P	80173.002	60/167,362

Number 20

Application No. 20 (attorney docket no. 2750-1572P) listed above is a continuation of co-pending Application No. 09/689,984 (Attorney No. 2750-1235P), filed on October 13, 2000, the

entire contents of which are hereby incorporated by reference. Through application no. 09/689,984, this application also claims priority under 35 USC §119(e) of the following provisional application, the entire contents of which are hereby incorporated by reference:

Country	Filing Date	Attorney No.	Application No.
United States	10/14/1999	2750-0573P	60/159,330

Number 23

Application 23 (attorney docket no. 2750-1560P) listed above is a continuation of Application No. 10/227,279 (Att. No, 2750-1533P), filed on August 26, 2002, the entire contents of which are hereby incorporated by reference.

Application No. 10/227,279 (Att. No. 2750-1533) is a continuation of Application No. 09/940,245 (Att. No, 2750-1467P), filed on August 24, 2001, the entire contents of which are also hereby incorporated by reference.

Application No. 09/940,245, is a Continuation-In-Part of the following applications to which the present application also claims priority under 35 USC §119(e) and §120, the entire contents of which are hereby incorporated by reference:

Client No.	Attorney No.	Filing Date	Appln. No.	
91000.002	2750-0783P	04/06/2000	09/543,680	which claims priority to
91000.001	2750-0416P	04/06/1999	60/128,234	and
91001.001	2750-0417P	04/08/1999	60/128,714	
80126.002	2750-0852P	05/04/2000	09/566,262	which claims priority to
80126.001	2750-0426P	05/04/1999	60/132,484	
80127.002	2750-0853P	05/05/2000	09/565,309	which claims priority to
80127.001	2750-0427P	05/05/1999	60/132,485	
91002.002	2750-0851P	05/05/2000	09/565,308	which claims priority to
91002.001	2750-0428P	05/06/1999	60/132,487	

Client No.	Attorney No.	Filing Date	Appln. No.	
80129.002	2750-0854P	05/05/2000	09/565,307	which claims priority to
80129.001	2750-0429P	05/06/1999	60/132,486	
80130.002	2750-0855P	05/05/2000	09/565,310	which claims priority to
80130.001	2750-0430P	05/07/1999	60/132,863	
80131.002	2750-0871P	05/11/2000	09/572,408	which claims priority to
80131.001	2750-0431P	05/11/1999	60/134,256	
80117.002	2750-0872P	05/12/2000	09/570,768	and
80116.002	2750-0874P	05/12/2000	09/570,738	which both claim priority to
80116.001	2750-0434P	05/14/1999	60/134,219	and
80117.001	2750-0435P	05/14/1999	60/134,218	
91007.002	2750-0876P	05/18/2000	09/573,655	which claims priority to
91007.001	2750-0436P	05/18/1999	60/134,768	and
91008.001	2750-0437P	05/19/1999	60/134,941	and
91009.001	2750-0438P	05/20/1999	60/135,124	and
91010.001	2750-0439P	05/21/1999	60/135,353	and
91011.001	2750-0440P	05/24/1999	60/135,629	and
91012.001	2750-0441P	05/25/1999	60/136,021	and
91013.001	2750-0442P	05/27/1999	60/136,392	and
91014.001	2750-0444P	05/28/1999	60/136,782	and
91015.001	2750-0445P	06/01/1999	60/137,222	and
91016.001	2750-0446P	06/03/1999	60/137,528	and
91017.001	2750-0447P	06/04/1999	60/137,502	and
91018.001	2750-0449P	06/07/1999	60/137,724	and
91019.001	2750-0450P	06/08/1999	60/138,094	
80132.013	2750-0944P	06/16/2000	09/595,330	which claims priority to
80132.001	2750-0443P	06/18/1999	60/139,458	
80132.014	2750-0945P	06/16/2000	09/595,333	which claims priority to
80132.002	2750-0448P	06/18/1999	60/139,454	
80132.015	2750-0946P	06/16/2000	09/595,328	which claims priority to
80132.003	2750-0451P	06/18/1999	60/139,459	
80132.016	2750-0947P	06/16/2000	09/595,335	which claims priority to

Client No.	Attorney No.	Filing Date	Appln. No	
80132.004	2750-0452P	06/18/1999	60/139,461	
80132.017	2750-0948P	06/16/2000	09/595,329	which claims priority to
80132.005	2750-0453P	06/18/1999	60/139,462	
80132.018	2750-0949P	06/16/2000	09/595,332	which claims priority to
80132.006	2750-0454P	06/18/1999	60/139,457	
80132.019	2750-0950P	06/16/2000	09/594,598	which claims priority to
80132.007	2750-0455P	06/18/1999	60/139,460	
80132.020	2750-0951P	06/16/2000	09/594,595	which claims priority to
80132.008	2750-0456P	06/18/1999	60/139,456	
00033.003	2750-0928P	06/09/2000	09/592,459	which claims priority to
00033.001	2750-0457P	06/10/1999	60/138,540	and
00033.002	2750-0458P	06/10/1999	60/138,847	
80132.021	2750-0952P	06/16/2000	09/594,597	which claims priority to
80132.009	2750-0459P	06/18/1999	60/139,463	
80132.022	2750-0953P	06/16/2000	09/595,298	which claims priority to
80132.010	2750-0460P	06/18/1999	60/139,455	
00034.002	2750-0934P	06/14/2000	09/593,710	which claims priority to
00034.001	2750-0463P	06/14/1999	60/139,119	
00045.002	2750-0975P	06/23/2000	09/602,016	which claims priority to
00045.001	2750-0471P	06/24/1999	60/140,695	
00048.002	2750-0977P	06/29/2000	09/606,181	which claims priority to
00048.001	2750-0473P	06/29/1999	60/140,991	
00050.002	2750-0979P	06/30/2000	09/607,081	which claims priority to
00050.001	2750-0475P	07/01/1999	60/141,842	
00051.002	2750-0980P	06/30/2000	09/610,157	which claims priority to
00051.001	2750-0476P	07/01/1999	60/142,154	
00052.002	2750-0981P	06/30/2000	09/609,198	which claims priority to
00052.001	2750-0477P	07/02/1999	60/142,055	
00053.002	2750-0982P	07/06/2000	09/611,409	which claims priority to

Client No.	Attorney No.	Filing Date	Appln. No	
00053.001	2750-0478P	07/06/1999	60/142,390	
00054.002	2750-0983P	07/07/2000	09/612,645	which claims priority to
00054.001	2750-0479P	07/08/1999	60/142,803	
00058.002	2750-0984P	07/07/2000	09/613,547	which claims priority to
00058.001	2750-0480P	07/09/1999	60/142,920	
80134.016	2750-1068P	07/21/2000	09/620,393	which claims priority to
80134.002	2750-0484P	07/21/1999	60/145,086	
80134.018	2750-1061P	07/14/2000	09/614,450	which claims priority to
80134.004	2750-0486P	07/16/1999	60/144,085	and
80134.014	2750-0496P	07/19/1999	60/144,334	
80135.003	2750-1072P	07/21/2000	09/621,900	which claims priority to
80135.001	2750-0501P	07/23/1999	60/145,224	
80135.004	2750-1066P	07/20/2000	09/620,978	which claims priority to
80135.002	2750-0502P	07/20/1999	60/144,884	
80136.004	2750-1074P	07/27/2000	09/628,984	which claims priority to
80136.001	2750-0507P	07/27/1999	60/145,918	and
80136.003	2750-0519P	08/05/1999	60/147,192	
80136.005	2750-1075P	07/27/2000	09/628,987	which claims priority to
80136.002	2750-0508P	07/27/1999	60/145,919	
80137.003	2750-1076P	08/02/2000	09/628,985	which claims priority to
80137.001	2750-0511P	08/02/1999	60/146,388	

Number 24

Application No. 10/360,648 (attorney no. 2750-1548P) listed above is a continuation of Application No. 10/156,076 (2750-1526P), filed on May 29, 2002, which in turn is a continuation of Application No. 09/940,256 (2750-1483P) filed on August 24, 2001, the entire contents of these applications are hereby incorporated by reference.

Through Application No. 09/940,256, the present application claims priority under 35 USC §119(e), §119(a-d) and §120 of the following applications, the entire contents of which are also

hereby incorporated by reference:

Client No.	Attorney No.	Filing Date	Appln. No
91000.002	2750-0783P	04/06/2000	09/543,680
91000.001	2750-0416P	04/06/1999	60/128,234
91001.001	2750-0417P	04/08/1999	60/128,714
80126.002	2750-0852P	05/04/2000	09/566,262
80126.001	2750-0426P	05/04/1999	60/132,484
80127.002	2750-0853P	05/05/2000	09/565,309
80127.001	2750-0427P	05/05/1999	60/132,485
91002.002	2750-0851P	05/05/2000	09/565,308
91002.001	2750-0428P	05/06/1999	60/132,487
80129.002	2750-0854P	05/05/2000	09/565,307
80129.001	2750-0429P	05/06/1999	60/132,486
80130.002	2750-0855P	05/05/2000	09/565,310
80130.001	2750-0430P	05/07/1999	60/132,863
80131.002	2750-0871P	05/11/2000	09/572,408
80131.001	2750-0431P	05/11/1999	60/134,256
80117.002	2750-0872P	05/12/2000	09/570,768
80116.002	2750-0874P	05/12/2000	09/570,738
80116.001	2750-0434P	05/14/1999	60/134,219
80117.001	2750-0435P	05/14/1999	60/134,218
91007.002	2750-0876P	05/18/2000	09/573,655
91007.001	2750-0436P	05/18/1999	60/134,768
91008.001	2750-0437P	05/19/1999	60/134,941
91009.001	2750-0438P	05/20/1999	60/135,124
91010.001	2750-0439P	05/21/1999	60/135,353
91011.001	2750-0440P	05/24/1999	60/135,629

Client No.	Attorney No.	Filing Date	Appln. No
91012.001	2750-0441P	05/25/1999	60/136,021
91013.001	2750-0442P	05/27/1999	60/136,392
91014.001	2750-0444P	05/28/1999	60/136,782
91015.001	2750-0445P	06/01/1999	60/137,222
91016.001	2750-0446P	06/03/1999	60/137,528
91017.001	2750-0447P	06/04/1999	60/137,502
91018.001	2750-0449P	06/07/1999	60/137,724
91019.001	2750-0450P	06/08/1999	60/138,094
80132.013	2750-0944P	06/16/2000	09/595,330
80132.001	2750-0443P	06/18/1999	60/139,458
80132.014	2750-0945P	06/16/2000	09/595,333
80132.002	2750-0448P	06/18/1999	60/139,454
80132.015	2750-0946P	06/16/2000	09/595,328
80132.003	2750-0451P	06/18/1999	60/139,459
80132.016	2750-0947P	06/16/2000	09/595,335
80132.004	2750-0452P	06/18/1999	60/139,461
80132.017	2750-0948P	06/16/2000	09/595,329
80132.005	2750-0453P	06/18/1999	60/139,462
80132.018	2750-0949P	06/16/2000	09/595,332
80132.006	2750-0454P	06/18/1999	60/139,457
80132.019	2750-0950P	06/16/2000	09/594,598
80132.007	2750-0455P	06/18/1999	60/139,460
80132.020	2750-0951P	06/16/2000	09/594,595
80132.008	2750-0456P	06/18/1999	60/139,456
00033.003	2750-0928P	06/09/2000	09/592,459
00033.001	2750-0457P	06/10/1999	60/138,540
00033.002	2750-0458P	06/10/1999	60/138,847

Client No.	Attorney No.	Filing Date	Appln. No
80132.021	2750-0952P	06/16/2000	09/594,597
80132.009	2750-0459P	06/18/1999	60/139,463
80132.022	2750-0953P	06/16/2000	09/595,298
80132.010	2750-0460P	06/18/1999	60/139,455
00034.002	2750-0934P	06/14/2000	09/593,710
00034.001	2750-0463P	06/14/1999	60/139,119
00045.002	2750-0975P	06/23/2000	09/602,016
00045.001	2750-0471P	06/24/1999	60/140,695
00048.002	2750-0977P	06/29/2000	09/606,181
00048.001	2750-0473P	06/29/1999	60/140,991
00050.002	2750-0979P	06/30/2000	09/607,081
00050.001	2750-0475P	07/01/1999	60/141,842
00051.002	2750-0980P	06/30/2000	09/610,157
00051.001	2750-0476P	07/01/1999	60/142,154
00052.002	2750-0981P	06/30/2000	09/609,198
00052.001	2750-0477P	07/02/1999	60/142,055
00053.002	2750-0982P	07/06/2000	09/611,409
00053.001	2750-0478P	07/06/1999	60/142,390
00054.002	2750-0983P	07/07/2000	09/612,645
00054.001	2750-0479P	07/08/1999	60/142,803
00058.002	2750-0984P	07/07/2000	09/613,547
00058.001	2750-0480P	07/09/1999	60/142,920

	Client No.	Attorney No.	Filing Date	Appln. No
	80134.016	2750-1068P	07/21/2000	09/620,393
	80134.002	2750-0484P	07/21/1999	60/145,086
	80134.018	2750-1061P	07/14/2000	09/614,450
	80134.004	2750-0486P	07/16/1999	60/144,085
	80134.014	2750-0496P	07/19/1999	60/144,334
	80135.003	2750-1072P	07/21/2000	09/621,900
	80135.001	2750-0501P	07/23/1999	60/145,224
	80135.004	2750-1066P	07/20/2000	09/620,978
	80135.002	2750-0502P	07/20/1999	60/144,884
	80136.004	2750-1074P	07/27/2000	09/628,984
	80136.001	2750-0507P	07/27/1999	60/145,918
	80136.003	2750-0519P	08/05/1999	60/147,192
	80136.005	2750-1075P	07/27/2000	09/628,987
	80136.002	2750-0508P	07/27/1999	60/145,919
	80137.003	2750-1076P	08/02/2000	09/628,985
	80137.001	2750-0511P	08/02/1999	60/146,388

Number 25

Application No. 10/216,621 (2750-1531P) listed above is a continuation of US application No. 09/940,257 filed August 24, 2001. The entire contents of which are hereby incorporated by reference. Application No. 09/940,247 is a continuation-in-part of the following 821 applications, the entire contents of which are also hereby incorporated by reference:

	Client No.	Attorney No.	Filing Date	Appln. No.	
1.	80001.006	2750-0550P	3-Sep-1999	09/391,631	which claims priority to

	Client No.	Attorney No.	Filing Date	Appln. No.	
2.	80001.001	2750-0300P	4-Sep-1998	60/099,671	and
3.	80002.001	2750-0301P	4-Sep-1998	60/099,672	and
4.	80003.001	2750-0302P	11-Sep-1998	60/099,933	and
5.	80004.001	2750-0304P	17-Sep-1998	60/100,864	and
6.	80005.001	2750-0305P	18-Sep-1998	60/101,042	and
7.	80007.001	2750-0307P	24-Sep-1998	60/101,682	and
8.	80008.001	2750-0308P	30-Sep-1998	60/102,533	and
9.	80009.001	2750-0309P	30-Sep-1998	60/102,460	and
10.	80010.001	2750-0310P	5-Oct-1998	60/103,116	and
11.	80011.001	2750-0311P	5-Oct-1998	60/103,141	and
12.	80014.001	2750-0314P	9-Oct-1998	60/103,574	and
13.	80015.001	2750-0315P	13-Oct-1998	60/103,907	and
14.	80024.001	2750-0324P	29-Oct-1998	60/106,105	and
15.	80025.001	2750-0325P	30-Oct-1998	60/106,218	and
16.	80027.001	2750-0327P	6-Nov-1998	60/107,282	and
17.	80030.001	2750-0330P	10-Nov-1998	60/107,836	and
18.	80032.001	2750-0332P	16-Nov-1998	60/108,526	and
19.	80033.001	2750-0333P	17-Nov-1998	60/108,901	and
20.	80036.001	2750-0336P	20-Nov-1998	60/109,267	and
21.	80037.001	2750-0337P	23-Nov-1998	60/109,594	and
22.	80041.001	2750-0341P	30-Nov-1998	60/110,263	and
23.	80042.001	2750-0342P	1-Dec-1998	60/110,495	and
24.	80043.001	2750-0343P	2-Dec-1998	60/110,626	and
25.	80044.001	2750-0344P	3-Dec-1998	60/110,701	and
26.	80045.001	2750-0345P	7-Dec-1998	60/111,339	and
27.	80046.001	2750-0346P	9-Dec-1998	60/111,589	and
28.	80049.001	2750-0349P	14-Dec-1998	60/112,096	and
29.	80050.001	2750-0350P	15-Dec-1998	60/112,224	and
30.	80051.001	2750-0351P	16-Dec-1998	60/112,624	and
31.	80052.001	2750-0352P	17-Dec-1998	60/112,862	and
32.	80063.001	2750-0363P	7-Jan-1999	60/115,152	and
33.	80066.001	2750-0366P	7-Jan-1999	60/115,156	and
34.	80069.001	2750-0369P	8-Jan-1999	60/115,365	and
35.	80071.001	2750-0371P	11-Jan-1999	60/115,339	and
36.	80073.001	2750-0373P	13-Jan-1999	60/115,847	and
37.	80079.001	2750-0379P	21-Jan-1999	60/116,674	and
38.	80082.001	2750-0382P	22-Jan-1999	60/116,962	and
39.	80094.001	2750-0394P	18-Feb-1999	60/120,583	and
40.	80095.001	2750-0395P	22-Feb-1999	60/121,072	and
41.	80101.001	2750-0401P	2-Mar-1999	60/122,568	and
42.	80111.001	2750-0411P	12-Mar-1999	60/123,941	
43.	80010.002	2750-0565P	5-Oct-1999	09/413,198	which claims

	Client No.	Attorney No.	Filing Date	Appln. No.	
					priority to
44.	80010.001	2750-0310P	5-Oct-1998	60/103,116	and
45.	80011.001	2750-0311P	5-Oct-1998	60/103,141	and
46.	80012.001	2750-0312P	6-Oct-1998	60/103,215	and
47.	80013.001	2750-0313P	8-Oct-1998	60/103,554	and
48.	80014.001	2750-0314P	9-Oct-1998	60/103,574	and
49.	80015.001	2750-0315P	13-Oct-1998	60/103,907	and
50.	80016.001	2750-0316P	14-Oct-1998	60/104,268	and
51.	80017.001	2750-0317P	16-Oct-1998	60/104,680	and
52.	80018.001	2750-0318P	19-Oct-1998	60/104,828	and
53.	80019.001	2750-0319P	20-Oct-1998	60/105,008	and
54.	80020.001	2750-0320P	21-Oct-1998	60/105,142	and
55.	80021.001	2750-0321P	22-Oct-1998	60/105,533	and
56.	80022.001	2750-0322P	26-Oct-1998	60/105,571	and
57.	80023.001	2750-0323P	27-Oct-1998	60/105,815	and
58.	80024.001	2750-0324P	29-Oct-1998	60/106,105	and
59.	80025.001	2750-0325P	30-Oct-1998	60/106,218	
60.	80010.003	2750-0566P	5-Oct-1999	09/412,922	which claims priority to
61.	80010.001	2750-0310P	5-Oct-1998	60/103,116	and
62.	80011.001	2750-0311P	5-Oct-1998	60/103,141	and
63.	80012.001	2750-0312P	6-Oct-1998	60/103,215	and
64.	80013.001	2750-0313P	8-Oct-1998	60/103,554	and
65.	80014.001	2750-0314P	9-Oct-1998	60/103,574	and
66.	80015.001	2750-0315P	13-Oct-1998	60/103,907	and
67.	80016.001	2750-0316P	14-Oct-1998	60/104,268	and
68.	80017.001	2750-0317P	16-Oct-1998	60/104,680	and
69.	80018.001	2750-0318P	19-Oct-1998	60/104,828	and
70.	80019.001	2750-0319P	20-Oct-1998	60/105,008	and
71.	80020.001	2750-0320P	21-Oct-1998	60/105,142	and
72.	80021.001	2750-0321P	22-Oct-1998	60/105,533	and
73.	80022.001	2750-0322P	26-Oct-1998	60/105,571	and
74.	80023.001	2750-0323P	27-Oct-1998	60/105,815	and
75.	80024.001	2750-0324P	29-Oct-1998	60/106,105	and
76.	80025.001	2750-0325P	30-Oct-1998	60/106,218	and
77.	80026.001	2750-0326P	2-Nov-1998	60/106,685	and
78.	80027.001	2750-0327P	6-Nov-1998	60/107,282	and
79.	80028.001	2750-0328P	9-Nov-1998	60/107,720	and
80.	80029.001	2750-0329P	9-Nov-1998	60/107,719	and
81.	80030.001	2750-0330P	10-Nov-1998	60/107,836	and
82.	80031.001	2750-0331P	12-Nov-1998	60/108,190	and
83.	80032.001	2750-0332P	16-Nov-1998	60/108,526	and

	Client No.	Attorney No.	Filing Date	Appln. No.	
84.	80033.001	2750-0333P	17-Nov-1998	60/108,901	and
85.	80034.001	2750-0334P	19-Nov-1998	60/109,124	and
86.	80035.001	2750-0335P	19-Nov-1998	60/109,127	and
87.	80036.001	2750-0336P	20-Nov-1998	60/109,267	and
88.	80037.001	2750-0337P	23-Nov-1998	60/109,594	and
89.	80038.001	2750-0338P	25-Nov-1998	60/110,053	and
90.	80039.001	2750-0339P	25-Nov-1998	60/110,050	and
91.	80040.001	2750-0340P	27-Nov-1998	60/110,158	and
92.	80041.001	2750-0341P	30-Nov-1998	60/110,263	and
93.	80042.001	2750-0342P	1-Dec-1998	60/110,495	and
94.	80043.001	2750-0343P	2-Dec-1998	60/110,626	and
95.	80044.001	2750-0344P	3-Dec-1998	60/110,701	and
96.	80045.001	2750-0345P	7-Dec-1998	60/111,339	and
97.	80046.001	2750-0346P	9-Dec-1998	60/111,589	and
98.	80047.001	2750-0347P	10-Dec-1998	60/111,782	and
99.	80048.001	2750-0348P	11-Dec-1998	60/111,812	and
100.	80049.001	2750-0349P	14-Dec-1998	60/112,096	and
101.	80050.001	2750-0350P	15-Dec-1998	60/112,224	and
102.	80051.001	2750-0351P	16-Dec-1998	60/112,624	and
103.	80052.001	2750-0352P	17-Dec-1998	60/112,862	and
104.	80053.001	2750-0353P	18-Dec-1998	60/112,912	and
105.	80054.001	2750-0354P	21-Dec-1998	60/113,248	and
106.	80055.001	2750-0355P	22-Dec-1998	60/113,522	and
107.	80056.001	2750-0356P	23-Dec-1998	60/113,826	and
108.	80057.001	2750-0357P	28-Dec-1998	60/113,998	and
109.	80058.001	2750-0358P	29-Dec-1998	60/114,384	and
110.	80059.001	2750-0359P	30-Dec-1998	60/114,455	and
111.	80060.001	2750-0360P	4-Jan-1999	60/114,740	and
112.	80061.001	2750-0361P	6-Jan-1999	60/114,866	and
113.	80062.001	2750-0362P	7-Jan-1999	60/115,153	and
114.	80063.001	2750-0363P	7-Jan-1999	60/115,152	and
115.	80064.001	2750-0364P	7-Jan-1999	60/115,151	and
116.	80065.001	2750-0365P	7-Jan-1999	60/115,155	and
117.	80066.001	2750-0366P	7-Jan-1999	60/115,156	and
118.	80067.001	2750-0367P	7-Jan-1999	60/115,154	and
119.	80068.001	2750-0368P	8-Jan-1999	60/115,364	and
120.	80069.001	2750-0369P	8-Jan-1999	60/115,365	and
121.	80071.001	2750-0371P	11-Jan-1999	60/115,339	and
122.	80072.001	2750-0372P	12-Jan-1999	60/115,518	and
123.	80073.001	2750-0373P	13-Jan-1999	60/115,847	and
124.	80074.001	2750-0374P	14-Jan-1999	60/115,905	and
125.	80075.001	2750-0375P	15-Jan-1999	60/116,383	and
126.	80076.001	2750-0376P	15-Jan-1999	60/116,384	and

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127.	80077.001	2750-0377P	19-Jan-1999	60/116,329	and
128.	80078.001	2750-0378P	19-Jan-1999	60/116,340	and
129.	80079.001	2750-0379P	21-Jan-1999	60/116,674	and
130.	80080.001	2750-0380P	21-Jan-1999	60/116,672	and
131.	80081.001	2750-0381P	22-Jan-1999	60/116,960	and
132.	80082.001	2750-0382P	22-Jan-1999	60/116,962	and
133.	80083.001	2750-0383P	28-Jan-1999	60/117,756	and
134.	80084.001	2750-0384P	3-Feb-1999	60/118,672	and
135.	80085.001	2750-0385P	4-Feb-1999	60/118,808	and
136.	80086.001	2750-0386P	5-Feb-1999	60/118,778	and
137.	80087.001	2750-0387P	8-Feb-1999	60/119,029	and
138.	80088.001	2750-0388P	9-Feb-1999	60/119,332	and
139.	80089.001	2750-0389P	10-Feb-1999	60/119,462	and
140.	80091.001	2750-0391P	12-Feb-1999	60/119,922	and
141.	80092.001	2750-0392P	16-Feb-1999	60/120,196	and
142.	80093.001	2750-0393P	16-Feb-1999	60/120,198	and
143.	80094.001	2750-0394P	18-Feb-1999	60/120,583	and
144.	80095.001	2750-0395P	22-Feb-1999	60/121,072	and
145.	80096.001	2750-0396P	23-Feb-1999	60/121,334	and
146.	80097.001	2750-0397P	24-Feb-1999	60/121,470	and
147.	80098.001	2750-0398P	25-Feb-1999	60/121,704	and
148.	80099.001	2750-0399P	26-Feb-1999	60/122,107	and
149.	80100.001	2750-0400P	1-Mar-1999	60/122,266	and
150.	80101.001	2750-0401P	2-Mar-1999	60/122,568	and
151.	80102.001	2750-0402P	3-Mar-1999	60/122,611	and
152.	80103.001	2750-0403P	4-Mar-1999	60/121,775	and
153.	80104.001	2750-0404P	5-Mar-1999	60/123,534	and
154.	80106.001	2750-0406P	9-Mar-1999	60/123,680	and
155.	80108.001	2750-0408P	10-Mar-1999	60/123,715	and
156.	80109.001	2750-0409P	10-Mar-1999	60/123,726	and
157.	80110.001	2750-0410P	11-Mar-1999	60/124,263	and
158.	80111.001	2750-0411P	12-Mar-1999	60/123,941	
159.	80026.002	2750-0600P	28-Oct-1999	09/428,944	which claims priority to
160.	80026.001	2750-0326P	2-Nov-1998	60/106,685	and
161.	80027.001	2750-0327P	6-Nov-1998	60/107,282	and
162.	80028.001	2750-0328P	9-Nov-1998	60/107,720	and
163.	80029.001	2750-0329P	9-Nov-1998	60/107,719	and
164.	80030.001	2750-0330P	10-Nov-1998	60/107,836	and
165.	80031.001	2750-0331P	12-Nov-1998	60/108,190	and
166.	80032.001	2750-0332P	16-Nov-1998	60/108,526	and
167.	80033.001	2750-0333P	17-Nov-1998	60/108,901	and

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168.	80034.001	2750-0334P	19-Nov-1998	60/109,124	and
169.	80035.001	2750-0335P	19-Nov-1998	60/109,127	and
170.	80036.001	2750-0336P	20-Nov-1998	60/109,267	and
171.	80037.001	2750-0337P	23-Nov-1998	60/109,594	and
172.	80038.001	2750-0338P	25-Nov-1998	60/110,053	and
173.	80039.001	2750-0339P	25-Nov-1998	60/110,050	and
174.	80040.001	2750-0340P	27-Nov-1998	60/110,158	and
175.	80041.001	2750-0341P	30-Nov-1998	60/110,263	
176.	80042.002	2750-0662P	1-Dec-1999	09/451,320	which claims priority to
177.	80042.001	2750-0342P	1-Dec-1998	60/110,495	and
178.	80043.001	2750-0343P	2-Dec-1998	60/110,626	and
179.	80044.001	2750-0344P	3-Dec-1998	60/110,701	and
180.	80045.001	2750-0345P	7-Dec-1998	60/111,339	and
181.	80046.001	2750-0346P	9-Dec-1998	60/111,589	and
182.	80047.001	2750-0347P	10-Dec-1998	60/111,782	and
183.	80048.001	2750-0348P	11-Dec-1998	60/111,812	and
184.	80049.001	2750-0349P	14-Dec-1998	60/112,096	and
185.	80050.001	2750-0350P	15-Dec-1998	60/112,224	and
186.	80051.001	2750-0351P	16-Dec-1998	60/112,624	and
187.	80052.001	2750-0352P	17-Dec-1998	60/112,862	and
188.	80053.001	2750-0353P	18-Dec-1998	60/112,912	and
189.	80054.001	2750-0354P	21-Dec-1998	60/113,248	and
190.	80055.001	2750-0355P	22-Dec-1998	60/113,522	and
191.	80056.001	2750-0356P	23-Dec-1998	60/113,826	and
192.	80057.001	2750-0357P	28-Dec-1998	60/113,998	and
193.	80058.001	2750-0358P	29-Dec-1998	60/114,384	and
194.	80059.001	2750-0359P	30-Dec-1998	60/114,455	and
195.	80062.001	2750-0362P	7-Jan-1999	60/115,153	and
196.	80063.001	2750-0363P	7-Jan-1999	60/115,152	and
197.	80064.001	2750-0364P	7-Jan-1999	60/115,151	and
198.	80065.001	2750-0365P	7-Jan-1999	60/115,155	and
199.	80066.001	2750-0366P	7-Jan-1999	60/115,156	and
200.	80068.001	2750-0368P	8-Jan-1999	60/115,364	and
201.	80081.001	2750-0381P	22-Jan-1999	60/116,960	
202.	80084.002	2750-0694P	3-Feb-2000	09/497,191	which claims priority to
203.	80084.001	2750-0384P	3-Feb-1999	60/118,672	and
204.	80085.001	2750-0385P	4-Feb-1999	60/118,808	and
205.	80086.001	2750-0386P	5-Feb-1999	60/118,778	and
206.	80087.001	2750-0387P	8-Feb-1999	60/119,029	and

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207.	80088.001	2750-0388P	9-Feb-1999	60/119,332	and
208.	80089.001	2750-0389P	10-Feb-1999	60/119,462	and
209.	80091.001	2750-0391P	12-Feb-1999	60/119,922	and
210.	80092.001	2750-0392P	16-Feb-1999	60/120,196	and
211.	80093.001	2750-0393P	16-Feb-1999	60/120,198	and
212.	80094.001	2750-0394P	18-Feb-1999	60/120,583	and
213.	80095.001	2750-0395P	22-Feb-1999	60/121,072	and
214.	80096.001	2750-0396P	23-Feb-1999	60/121,334	and
215.	80097.001	2750-0397P	24-Feb-1999	60/121,470	and
216.	80098.001	2750-0398P	25-Feb-1999	60/121,704	and
217.	80099.001	2750-0399P	26-Feb-1999	60/122,107	
218.	80100.002	2750-0710P	1-Mar-2000	09/517,537	which claims priority to
219.	80100.001	2750-0400P	1-Mar-1999	60/122,266	and
220.	80101.001	2750-0401P	2-Mar-1999	60/122,568	and
221.	80102.001	2750-0402P	3-Mar-1999	60/122,611	and
222.	80103.001	2750-0403P	4-Mar-1999	60/121,775	and
223.	80104.001	2750-0404P	5-Mar-1999	60/123,534	and
224.	80106.001	2750-0406P	9-Mar-1999	60/123,680	and
225.	80108.001	2750-0408P	10-Mar-1999	60/123,715	and
226.	80109.001	2750-0409P	10-Mar-1999	60/123,726	and
227.	80110.001	2750-0410P	11-Mar-1999	60/124,263	and
228.	80111.001	2750-0411P	12-Mar-1999	60/123,941	
229.	80141.006	2750-1102P	11-Aug-2000	09/637,565	which claims priority to
230.	80141.002	2750-0526P	12-Aug-1999	60/148,342	
231.	80141.007	2750-1103P	11-Aug-2000	09/637,564	which claims priority to
232.	80141.003	2750-0527P	12-Aug-1999	60/148,340	
233.	80141.008	2750-1104P	11-Aug-2000	09/637,792	which claims priority to
234.	80141.004	2750-0528P	12-Aug-1999	60/148,337	
235.	91022.002	2750-1419P	23-Feb-2001	09/790,663	which claims priority to
236.	91022.001	2750-0718P	25-Feb-2000	60/185,140	and
237.	91023.001	2750-0721P	28-Feb-2000	60/185,398	and
238.	91024.001	2750-0724P	29-Feb-2000	60/185,750	

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239.	91025.002	2750-1423P	1-Mar-2001	09/795,359	which claims priority to
240.	91025.001	2750-0727P	1-Mar-2000	60/186,277	and
241.	91026.001	2750-0731P	3-Mar-2000	60/186,670	and
242.	91027.001	2750-0735P	7-Mar-2000	60/187,379	and
243.	91028.001	2750-0738P	9-Mar-2000	60/187,985	and
244.	91030.001	2750-0741P	10-Mar-2000	60/188,174	and
245.	91031.001	2750-0744P	13-Mar-2000	60/188,687	and
246.	91032.001	2750-0747P	15-Mar-2000	60/189,460	and
247.	91033.001	2750-0754P	16-Mar-2000	60/189,958	and
248.	91034.001	2750-0757P	17-Mar-2000	60/189,965	and
249.	91035.001	2750-0760P	20-Mar-2000	60/190,090	and
250.	91036.001	2750-0765P	23-Mar-2000	60/191,549	and
251.	91037.001	2750-0768P	24-Mar-2000	60/191,826	and
252.	91038.001	2750-0771P	27-Mar-2000	60/192,420	and
253.	91039.001	2750-0774P	29-Mar-2000	60/192,855	and
254.	91040.001	2750-0777P	30-Mar-2000	60/193,243	and
255.	91041.001	2750-0780P	31-Mar-2000	60/193,469	
256.	80208.002	2750-1432P	16-Mar-2001	09/804,470	which claims priority to
257.	80208.001	2750-0750P	16-Mar-2000	60/190,120	and
258.	80209.001	2750-0751P	16-Mar-2000	60/189,947	and
259.	80210.001	2750-0752P	16-Mar-2000	60/189,948	and
260.	80211.001	2750-0753P	16-Mar-2000	60/190,121	
261.	91042.002	2750-1434P	4-Apr-2001	09/824,790	which claims priority to
262.	91045.001	2750-0784P	6-Apr-2000	60/194,884	and
263.	91042.001	2750-0785P	4-Apr-2000	60/194,385	and
264.	91043.001	2750-0789P	5-Apr-2000	60/194,682	and
265.	91044.001	2750-0792P	5-Apr-2000	60/194,698	and
266.	91046.001	2750-0797P	7-Apr-2000	60/195,258	and
267.	91047.001	2750-0802P	11-Apr-2000	60/196,168	and
268.	91048.001	2750-0805P	12-Apr-2000	60/196,483	and
269.	91049.001	2750-0814P	14-Apr-2000	60/197,397	and
270.	91050.001	2750-0817P	17-Apr-2000	60/198,268	and
271.	91051.001	2750-0820P	19-Apr-2000	60/198,400	and
272.	91052.001	2750-0823P	20-Apr-2000	60/198,629	and
273.	91053.001	2750-0826P	21-Apr-2000	60/198,765	and
274.	91054.001	2750-0829P	24-Apr-2000	60/199,123	

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275.	80227.003	2750-1437P	11-Apr-2001	09/832,192	which claims priority to
276.	80227.001	2750-0800P	12-Apr-2000	60/196,212	and
277.	80227.002	2750-0801P	11-Apr-2000	60/196,211	and
278.	80231.001	2750-0810P	14-Apr-2000	60/197,869	and
279.	80231.002	2750-0811P	13-Apr-2000	60/196,213	and
280.	80232.001	2750-0812P	17-Apr-2000	60/197,870	and
281.	80232.002	2750-0813P	17-Apr-2000	60/197,871	and
282.	80242.002	2750-0844P	28-Apr-2000	60/200,373	and
283.	80243.002	2750-0846P	28-Apr-2000	60/200,773	
284.	92001.005	2750-1439P	26-Apr-2001	09/842,246	which claims priority to
285.	92001.001	2750-0832P	26-Apr-2000	60/200,034	
286.	80242.003	2750-1440P	1-May-2001	09/845,208	which claims priority to
287.	80242.001	2750-0843P	1-May-2000	60/200,763	and
288.	80243.001	2750-0845P	1-May-2000	60/201,016	and
289.	80244.001	2750-0847P	1-May-2000	60/200,762	and
290.	80244.002	2750-0848P	1-May-2000	60/200,761	and
291.	80250.001	2750-0867P	11-May-2000	60/203,671	and
292.	80250.002	2750-0868P	11-May-2000	60/203,672	and
293.	80251.001	2750-0869P	11-May-2000	60/203,669	and
294.	80251.002	2750-0870P	11-May-2000	60/203,622	
295.	92002.006	2750-1443P	1-May-2001	09/845,318	which claims priority to
296.	92002.002	2750-0842P	1-May-2000	60/201,018	and
297.	92002.003	2750-0890P	17-May-2000	60/205,325	
298.	92001.006	2750-1444P	1-May-2001	09/845,209	which claims priority to
299.	92001.002	2750-0841P	1-May-2000	60/201,017	and
300.	92001.003	2750-0889P	17-May-2000	60/205,233	
301.	80267.004	2750-1448P	1-Jun-2001	09/870,646	which claims priority to
302.	80267.002	2750-0918P	1-Jun-2000	60/208,648	
303.	91068.002	2750-1449P	1-Jun-2001	09/870,476	which claims priority to
304.	91068.001	2750-0919P	1-Jun-2000	60/208,324	and

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305.	91069.001	2750-0922P	5-Jun-2000	60/208,919	and
306.	91070.001	2750-0925P	5-Jun-2000	60/208,917	and
307.	91071.001	2750-0929P	8-Jun-2000	60/210,008	
308.	80268.002	2750-1451P	1-Jun-2001	09/870,664	which claims priority to
309.	80268.001	2750-0921P	1-Jun-2000	60/208,312	and
310.	80269.001	2750-0924P	5-Jun-2000	60/208,918	and
311.	80270.001	2750-0927P	5-Jun-2000	60/208,920	and
312.	80271.001	2750-0931P	8-Jun-2000	60/210,006	and
313.	80272.001	2750-0933P	9-Jun-2000	60/210,564	and
314.	80273.001	2750-0936P	13-Jun-2000	60/211,214	and
315.	80277.001	2750-0963P	22-Jun-2000	60/213,249	and
316.	80280.001	2750-1036P	27-Jun-2000	60/214,535	and
317.	80281.001	2750-1039P	28-Jun-2000	60/214,799	and
318.	80282.001	2750-1041P	30-Jun-2000	60/215,127	
319.	91072.002	2750-1453P	13-Jun-2001	09/878,974	which claims priority to
320.	91072.001	2750-0937P	13-Jun-2000	60/211,210	and
321.	00238.001	2750-0938P	15-Jun-2000	60/211,539	and
322.	00239.001	2750-0956P	19-Jun-2000	60/212,414	and
323.	00240.001	2750-0959P	20-Jun-2000	60/212,677	and
324.	80276.001	2750-0960P	20-Jun-2000	60/212,713	and
325.	91077.001	2750-0964P	22-Jun-2000	60/213,195	and
326.	00246.001	2750-0965P	22-Jun-2000	60/213,221	and
327.	00247.001	2750-0968P	27-Jun-2000	60/214,760	
328.	80286.003	2750-1457P	12-Jul-2001	09/902,613	which claims priority to
329.	80299.002	2750-1256P	1-Aug-2000	60/223,114	
330.	80288.003	2750-1459P	13-Jul-2001	09/903,497	which claims priority to
331.	80288.002	2750-1054P	13-Jul-2000	60/217,846	and
332.	80299.004	2750-1258P	3-Aug-2000	60/223,099	
333.	80286.004	2750-1461P	1-Aug-2001	09/918,556	which claims priority to
334.	80286.001	2750-1049P	1-Aug-2000	60/223,115	
335.	80288.004	2750-1462P	3-Aug-2001	09/920,626	which claims priority to

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336.	80288.001	2750-1053P	3-Aug-2000	60/223,100	and
337.	80294.001	2750-1105P	18-Aug-2000	60/226,325	and
338.	80304.001	2750-1113P	31-Aug-2000	60/237,361	
339.	80285.004	2750-1464P	7-Aug-2001	09/922,661	which claims priority to
340.	80285.001	2750-1047P	7-Aug-2000	60/223,329	and
341.	80302.001	2750-1088P	31-Aug-2000	60/229,521	and
342.	80295.001	2750-1107P	18-Aug-2000	60/226,381	
343.	92001.007	2750-1469P	9-Aug-2001	09/924,702	which claims priority to
344.	92001.004	2750-1114P	9-Aug-2000	60/224,390	
345.	80295.003	2750-1472P	16-Aug-2001	09/930,244	which claims priority to
346.	80302.002	2750-1089P	31-Aug-2000	60/237,362	and
347.	80295.002	2750-1108P	16-Aug-2000	60/225,848	
348.	80294.003	2750-1473P	16-Aug-2001	09/930,231	which claims priority to
349.	80294.002	2750-1106P	16-Aug-2000	60/225,849	
350.	80297.004	2750-1475P	16-Aug-2001	09/930,223	which claims priority to
351.	80297.002	2750-1112P	16-Aug-2000	60/225,847	
352.	80303.003	2750-1477P	20-Aug-2001	09/931,911	which claims priority to
353.	80303.002	2750-1091P	31-Aug-2000	60/229,520	
354.	00170.003	2750-1484P	26-Feb-2002	10/082,096	which is a 1.53(b) continuation of
355.	00170.002	2750-1422P	1-Mar-2001	09/795,347	which claims priority to
356.	00171.001	2750-0711P	2-Mar-2000	60/186,390	and
357.	00170.001	2750-0725P	1-Mar-2000	60/186,283	and
358.	80199.001	2750-0726P	1-Mar-2000	60/186,296	and
359.	80200.001	2750-0728P	2-Mar-2000	60/187,178	and
360.	00172.001	2750-0729P	2-Mar-2000	60/186,386	and
361.	80201.001	2750-0730P	2-Mar-2000	60/186,387	and

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362.	00173.001	2750-0732P	3-Mar-2000	60/186,748	and
363.	80202.001	2750-0733P	3-Mar-2000	60/186,669	and
364.	00174.001	2750-0734P	7-Mar-2000	60/187,378	and
365.	00175.001	2750-0736P	8-Mar-2000	60/187,896	and
366.	80203.001	2750-0737P	8-Mar-2000	60/187,888	and
367.	00177.001	2750-0739P	10-Mar-2000	60/188,187	and
368.	80204.001	2750-0740P	10-Mar-2000	60/188,186	and
369.	00178.001	2750-0742P	10-Mar-2000	60/188,185	and
370.	80205.001	2750-0743P	10-Mar-2000	60/188,175	and
371.	00179.001	2750-0745P	14-Mar-2000	60/189,080	and
372.	80206.001	2750-0746P	14-Mar-2000	60/189,052	and
373.	00180.001	2750-0748P	15-Mar-2000	60/189,461	and
374.	80207.001	2750-0749P	15-Mar-2000	60/189,462	and
375.	00181.001	2750-0755P	16-Mar-2000	60/189,953	and
376.	80212.001	2750-0756P	16-Mar-2000	60/189,959	and
377.	00182.001	2750-0758P	20-Mar-2000	60/190,069	and
378.	80213.001	2750-0759P	20-Mar-2000	60/190,070	and
379.	00183.001	2750-0761P	20-Mar-2000	60/190,545	and
380.	80214.001	2750-0762P	20-Mar-2000	60/190,089	and
381.	00184.001	2750-0763P	22-Mar-2000	60/191,084	and
382.	80215.001	2750-0764P	22-Mar-2000	60/191,097	and
383.	00185.001	2750-0766P	23-Mar-2000	60/191,543	and
384.	80216.001	2750-0767P	23-Mar-2000	60/191,545	and
385.	00186.001	2750-0769P	24-Mar-2000	60/191,823	and
386.	80217.001	2750-0770P	24-Mar-2000	60/191,825	and
387.	00187.001	2750-0772P	27-Mar-2000	60/192,421	and
388.	80218.001	2750-0773P	27-Mar-2000	60/192,308	and
389.	00188.001	2750-0775P	29-Mar-2000	60/192,940	and
390.	80219.001	2750-0776P	29-Mar-2000	60/192,941	and
391.	00189.001	2750-0778P	30-Mar-2000	60/193,244	and
392.	80220.001	2750-0779P	30-Mar-2000	60/193,245	and
393.	00190.001	2750-0781P	31-Mar-2000	60/193,453	and
394.	80221.001	2750-0782P	31-Mar-2000	60/193,455	
395.	92002.008	2750-1486P	28-Feb-2002	10/084,376	which is a 1.53(b) continuation of
396.	92002.007	2750-1470P	9-Aug-2001	09/924,701	which claims priority to
397.	92002.004	2750-1115P	9-Aug-2000	60/224,391	

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398.	00211.003	2750-1489P	4-Mar-2002	10/086,239	which is a 1.53(b) continuation of
399.	00211.002	2750-1441P	1-May-2001	09/845,206	which claims priority to
400.	00211.001	2750-0838P	2-May-2000	60/201,275	and
401.	80241.001	2750-0839P	1-May-2000	60/200,879	and
402.	80245.001	2750-0850P	2-May-2000	60/201,305	and
403.	00212.001	2750-0857P	4-May-2000	60/201,740	and
404.	80246.001	2750-0858P	4-May-2000	60/201,750	and
405.	00213.001	2750-0860P	5-May-2000	60/202,112	and
406.	80247.001	2750-0861P	5-May-2000	60/202,180	and
407.	00214.001	2750-0862P	9-May-2000	60/202,914	and
408.	80248.001	2750-0863P	9-May-2000	60/202,636	and
409.	00215.001	2750-0865P	9-May-2000	60/202,919	and
410.	80249.001	2750-0866P	9-May-2000	60/202,634	and
411.	00216.001	2750-0878P	10-May-2000	60/202,968	and
412.	80252.001	2750-0879P	10-May-2000	60/202,963	and
413.	00217.001	2750-0881P	11-May-2000	60/203,457	and
414.	80253.001	2750-0882P	11-May-2000	60/203,279	and
415.	00219.001	2750-0884P	12-May-2000	60/203,916	and
416.	80254.001	2750-0885P	12-May-2000	60/203,915	and
417.	00220.001	2750-0887P	15-May-2000	60/204,388	and
418.	80255.001	2750-0888P	15-May-2000	60/204,122	and
419.	00221.001	2750-0891P	16-May-2000	60/204,568	and
420.	80256.001	2750-0892P	16-May-2000	60/204,569	and
421.	00222.001	2750-0893P	17-May-2000	60/204,830	and
422.	80257.001	2750-0894P	17-May-2000	60/204,829	and
423.	00223.001	2750-0895P	18-May-2000	60/205,201	and
424.	80258.001	2750-0896P	18-May-2000	60/205,058	and
425.	00224.001	2750-0897P	19-May-2000	60/205,242	and
426.	80259.001	2750-0898P	19-May-2000	60/205,243	and
427.	00225.001	2750-0900P	22-May-2000	60/205,572	and
428.	80260.001	2750-0901P	22-May-2000	60/205,576	and
429.	00226.001	2750-0902P	23-May-2000	60/206,316	and
430.	80261.001	2750-0903P	23-May-2000	60/206,319	and
431.	00227.001	2750-0904P	24-May-2000	60/206,553	and
432.	80262.001	2750-0905P	24-May-2000	60/206,545	and
433.	00228.001	2750-0907P	26-May-2000	60/207,367	and
434.	80263.001	2750-0908P	26-May-2000	60/207,243	and
435.	00229.001	2750-0910P	26-May-2000	60/207,239	and
436.	80264.001	2750-0911P	26-May-2000	60/207,354	and

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437.	00230.001	2750-0913P	30-May-2000	60/207,452	and
438.	80265.001	2750-0914P	30-May-2000	60/207,329	
439.	92002.009	2750-1490P	7-Mar-2002	10/091,527	which is a 1.53(b) continuation of
440.	92002.005	2750-1438P	26-Apr-2001	09/842,088	which claims priority to
441.	92002.001	2750-0833P	26-Apr-2000	60/200,031	
442.	00191.003	2750-1492P	13-Mar-2002	10/095,465	which is a 1.53(b) continuation of
443.	00191.002	2750-1435P	4-Apr-2001	09/824,882	which claims priority to
444.	00191.001	2750-0786P	4-Apr-2000	60/194,404	and
445.	80222.001	2750-0787P	4-Apr-2000	60/194,398	and
446.	00192.001	2750-0790P	5-Apr-2000	60/194,683	and
447.	80223.001	2750-0791P	5-Apr-2000	60/194,697	and
448.	00193.001	2750-0793P	6-Apr-2000	60/194,874	and
449.	80224.001	2750-0794P	6-Apr-2000	60/194,872	and
450.	00194.001	2750-0795P	6-Apr-2000	60/194,885	and
451.	80225.001	2750-0796P	6-Apr-2000	60/195,045	and
452.	00195.001	2750-0798P	7-Apr-2000	60/195,283	and
453.	80226.001	2750-0799P	7-Apr-2000	60/195,257	and
454.	00196.001	2750-0803P	11-Apr-2000	60/196,169	and
455.	80228.001	2750-0804P	11-Apr-2000	60/196,089	and
456.	00197.001	2750-0806P	12-Apr-2000	60/196,487	and
457.	80229.001	2750-0807P	12-Apr-2000	60/196,289	and
458.	00200.001	2750-0808P	12-Apr-2000	60/196,485	and
459.	80230.001	2750-0809P	12-Apr-2000	60/196,486	and
460.	00201.001	2750-0815P	17-Apr-2000	60/197,687	and
461.	80233.001	2750-0816P	17-Apr-2000	60/197,678	and
462.	00202.001	2750-0818P	17-Apr-2000	60/198,133	and
463.	80234.001	2750-0819P	17-Apr-2000	60/197,671	and
464.	00203.001	2750-0821P	19-Apr-2000	60/198,386	and
465.	80235.001	2750-0822P	19-Apr-2000	60/198,373	and
466.	00204.001	2750-0824P	20-Apr-2000	60/198,619	and
467.	80236.001	2750-0825P	20-Apr-2000	60/198,623	and
468.	00206.001	2750-0827P	21-Apr-2000	60/198,767	and
469.	80237.001	2750-0828P	21-Apr-2000	60/198,763	and

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470.	00207.001	2750-0830P	24-Apr-2000	60/199,124	and
471.	80238.001	2750-0831P	24-Apr-2000	60/199,122	and
472.	00208.001	2750-0834P	26-Apr-2000	60/199,828	and
473.	80239.001	2750-0835P	26-Apr-2000	60/199,818	and
474.	00210.001	2750-0836P	27-Apr-2000	60/200,103	and
475.	80240.001	2750-0837P	27-Apr-2000	60/200,102	and
476.	80141.010	2750-1493P	15-Mar-2002	10/097,600	which is a 1.53(b) continuation of
477.	80141.009	2750-1436P	12-Apr-2001	09/832,934	which is a 1.53(b) continuation of
478.	80141.005	2750-1101P	11-Aug-2000	09/637,820	which claims priority to
479.	80141.001	2750-0525P	12-Aug-1999	60/148,347	
480.	91074.003	2750-1494P	15-Mar-2002	10/097,295	which is a 1.53(b) continuation of
481.	91074.002	2750-1452P	15-Jun-2001	09/881,096	which claims priority to
482.	91074.001	2750-0940P	15-Jun-2000	60/211,538	and
483.	91075.001	2750-0958P	19-Jun-2000	60/212,623	and
484.	91076.001	2750-0961P	20-Jun-2000	60/212,727	and
485.	91079.001	2750-0967P	22-Jun-2000	60/213,270	and
486.	91080.001	2750-0970P	27-Jun-2000	60/214,524	
487.	80266.005	2750-1495P	18-Mar-2002		which is a 1.53(b) continuation of
488.	80266.004	2750-1446P	1-Jun-2001	09/870,699	which claims priority to
489.	80266.002	2750-0916P	1-Jun-2000	60/208,421	
490.	80266.006	2750-1496P	18-Mar-2002	10/098,506	which is a 1.53(b) continuation of

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491.	80266.003	2750-1445P	1-Jun-2001	09/870,713	which claims priority to
492.	80266.001	2750-0915P	2-Jun-2000	60/209,338	
493.	80283.003	2750-1499P	25-Mar-2002	10/103,845	which is a 1.53(b) continuation of
494.	80283.002	2750-1454P	5-Jul-2001	09/898,063	which claims priority to
495.	80283.001	2750-1043P	5-Jul-2000	60/216,362	and
496.	80284.001	2750-1046P	11-Jul-2000	60/217,384	and
497.	80291.001	2750-1057P	18-Jul-2000	60/219,033	and
498.	80292.001	2750-1079P	25-Jul-2000	60/220,811	and
499.	80293.001	2750-1081P	25-Jul-2000	60/220,652	
500.	00252.003	2750-1501P	27-Mar-2002	10/106,718	which is a 1.53(b) continuation of
501.	00252.002	2750-1455P	5-Jul-2001	09/898,064	which claims priority to
502.	00252.001	2750-1042P	5-Jul-2000	60/216,361	and
503.	00253.001	2750-1045P	11-Jul-2000	60/217,476	and
504.	00254.001	2750-1056P	18-Jul-2000	60/219,004	and
505.	00255.001	2750-1059P	25-Jul-2000	60/220,647	and
506.	00256.001	2750-1080P	25-Jul-2000	60/220,484	
507.	80287.005	2750-1502P	1-Apr-2002	10/109,638	which is a 1.53(b) continuation of
508.	80287.003	2750-1458P	12-Jul-2001	09/902,614	which claims priority to
509.	80287.002	2750-1052P	12-Jul-2000	60/218,548	and
510.	80299.003	2750-1257P	3-Aug-2000	60/223,116	
511.	80296.004	2750-1504P	10-Apr-2002	10/119,275	which is a 1.53(b) continuation of
512.	80296.003	2750-1474P	16-Aug-2001	09/930,214	which claims priority to

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513.	80303.002	2750-1091P	31-Aug-2000	60/229,520	and
514.	80296.002	2750-1110P	16-Aug-2000	60/225,850	
515.	80287.005	2750-1506P	17-Apr-2002	10/123,117	which is a 1.53(b) continuation of
516.	80287.004	2750-1463P	3-Aug-2001	09/921,135	which claims priority to
517.	80287.001	2750-1051P	3-Aug-2000	60/223,101	and
518.	80303.001	2750-1090P	31-Aug-2000	60/229,519	and
519.	80296.001	2750-1109P	18-Aug-2000	60/226,323	
520.	91081.003	2750-1507P	17-Apr-2002	10/123,222	which is a 1.53(b) continuation of
521.	91081.002	2750-1456P	11-Jul-2001	09/902,093	which claims priority to
522.	91081.001	2750-1044P	11-Jul-2000	60/217,385	and
523.	91082.001	2750-1055P	18-Jul-2000	60/219,021	and
524.	91083.001	2750-1058P	25-Jul-2000	60/220,814	and
525.	91084.001	2750-1083P	14-Aug-2000	60/224,516	and
526.	91085.001	2750-1085P	15-Aug-2000	60/225,302	and
527.	91086.001	2750-1087P	21-Aug-2000	60/226,725	and
528.	91087.001	2750-1163P	23-Aug-2000	60/227,026	and
529.	91088.001	2750-1226P	30-Aug-2000	60/228,897	
530.	80285.005	2750-1508P	17-Apr-2002	10/123,159	which is a 1.53(b) continuation of
531.	80285.003	2750-1460P	13-Jul-2001	09/903,988	which claims priority to
532.	80285.002	2750-1048P	14-Jul-2000	60/218,566	and
533.	80299.001	2750-1255P	3-Aug-2000	60/223,098	
534.	80298.003	2750-1509P	17-Apr-2002	10/123,111	which is a 1.53(b) continuation of
535.	80298.002	2750-1471P	14-Aug-2001	09/928,372	which claims priority to

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536.	80298.001	2750-1082P	14-Aug-2000	60/224,517	and
537.	80300.001	2750-1084P	15-Aug-2000	60/225,303	and
538.	80301.001	2750-1086P	21-Aug-2000	60/226,452	and
539.	80307.001	2750-1162P	23-Aug-2000	60/227,024	and
540.	80308.001	2750-1225P	30-Aug-2000	60/228,898	
541.	80297.005	2750-1510P	18-Apr-2002	10/124,666	which is a 1.53(b) continuation of
542.	80297.003	2750-1476P	17-Aug-2001	09/931,043	which claims priority to
543.	80297.001	2750-1111P	18-Aug-2000	60/226,324	
544.	80365.002	2750-1512P	29-Apr-2002	10/133,891	which is a 1.53(b) continuation of
545.	80365.001	2750-1398P	31-Jan-2001	09/774,340	
546.	80326.003	2750-1518P	29-Apr-2002	10/133,893	which is a 1.53(b) continuation of
547.	80326.001	2750-1285P	19-Oct-2000	09/691,039	
548.	710-0005-55300-U- 00001.02	2750-1519P	29-Apr-2002		which is a 1.53(b) continuation of
549.	710-0005-55300-U- 00001.01	2750-1380P	21-Dec-2000	09/741,043	
550.	80328.003	2750-1520P	29-Apr-2002	10/133,373	which is a 1.53(b) continuation of
551.	80328.001	2750-1289P	19-Oct-2000	09/691,045	
552.	80330.003	2750-1521P	29-Apr-2002	10/133,905	which is a 1.53(b) continuation of

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553.	80330.001	2750-1293P	19-Oct-2000	09/691,019	
554.	80267.005	2750-1522P	29-Apr-2002	10/133,376	which is a 1.53(b) continuation of
555.	80267.003	2750-1447P	1-Jun-2001	09/870,675	which claims priority to
556.	80267.001	2750-0917P	2-Jun-2000	60/208,649	
557.	80060.003	2750-1524P	6-May-2002	10/138,320	which is a 1.53(b) continuation of
558.	80060.002	2750-0683P	4-Jan-2000	09/478,081	which claims priority to
559.	80060.001	2750-0360P	4-Jan-1999	60/114,740	and
560.	80061.001	2750-0361P	6-Jan-1999	60/114,866	and
561.	80067.001	2750-0367P	7-Jan-1999	60/115,154	and
562.	80069.001	2750-0369P	8-Jan-1999	60/115,365	and
563.	80071.001	2750-0371P	11-Jan-1999	60/115,339	and
564.	80072.001	2750-0372P	12-Jan-1999	60/115,518	and
565.	80073.001	2750-0373P	13-Jan-1999	60/115,847	and
566.	80074.001	2750-0374P	14-Jan-1999	60/115,905	and
567.	80075.001	2750-0375P	15-Jan-1999	60/116,383	and
568.	80076.001	2750-0376P	15-Jan-1999	60/116,384	and
569.	80077.001	2750-0377P	19-Jan-1999	60/116,329	and
570.	80078.001	2750-0378P	19-Jan-1999	60/116,340	and
571.	80079.001	2750-0379P	21-Jan-1999	60/116,674	and
572.	80080.001	2750-0380P	21-Jan-1999	60/116,672	and
573.	80082.001	2750-0382P	22-Jan-1999	60/116,962	and
574.	80083.001	2750-0383P	28-Jan-1999	60/117,756	
575.	80289.018	2750-1133P	25-Aug-2000	60/228,025	
576.	80289.019	2750-1134P	25-Aug-2000	60/227,781	
577.	80289.020	2750-1135P	25-Aug-2000	60/227,783	
578.	80289.021	2750-1136P	25-Aug-2000	60/227,731	
579.	80289.022	2750-1137P	25-Aug-2000	60/227,732	
580.	80289.023	2750-1138P	25-Aug-2000	60/227,729	
581.	80289.024	2750-1139P	25-Aug-2000	60/228,167	
582.	80289.025	2750-1140P	25-Aug-2000	60/227,734	
583.	80289.026	2750-1141P	25-Aug-2000	60/227,792	
584.	80289.027	2750-1142P	25-Aug-2000	60/227,733	

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585.	80289.028	2750-1143P	25-Aug-2000	60/227,730	
586.	80289.029	2750-1144P	25-Aug-2000	60/227,770	
587.	80289.030	2750-1145P	25-Aug-2000	60/227,728	
588.	80289.031	2750-1146P	25-Aug-2000	60/227,773	
589.	80289.032	2750-1147P	25-Aug-2000	60/228,033	
590.	80289.033	2750-1148P	25-Aug-2000	60/228,024	
591.	80289.034	2750-1149P	25-Aug-2000	60/227,769	
592.	80289.035	2750-1150P	25-Aug-2000	60/227,780	
593.	80289.036	2750-1151P	25-Aug-2000	60/227,725	
594.	80289.037	2750-1152P	25-Aug-2000	60/227,774	
595.	80289.038	2750-1164P	25-Aug-2000	60/228,163	
596.	80289.039	2750-1165P	25-Aug-2000	60/228,046	
597.	80289.040	2750-1166P	25-Aug-2000	60/228,098	
598.	80289.041	2750-1167P	25-Aug-2000	60/228,047	
599.	80289.042	2750-1168P	25-Aug-2000	60/228,052	
600.	80289.043	2750-1169P	25-Aug-2000	60/228,049	
601.	80289.044	2750-1170P	25-Aug-2000	60/228,132	
602.	80289.045	2750-1171P	25-Aug-2000	60/228,152	
603.	80289.046	2750-1172P	25-Aug-2000	60/228,135	
604.	80289.047	2750-1173P	25-Aug-2000	60/228,322	
605.	80289.048	2750-1174P	25-Aug-2000	60/228,156	
606.	80289.049	2750-1175P	25-Aug-2000	60/228,323	
607.	80289.050	2750-1176P	25-Aug-2000	60/228,133	
608.	80289.051	2750-1177P	25-Aug-2000	60/228,320	
609.	80289.052	2750-1178P	25-Aug-2000	60/228,159	
610.	80289.053	2750-1179P	25-Aug-2000	60/228,151	
611.	80289.054	2750-1180P	25-Aug-2000	60/228,202	
612.	80289.055	2750-1181P	25-Aug-2000	60/228,208	
613.	80289.056	2750-1182P	25-Aug-2000	60/228,153	
614.	80289.057	2750-1183P	25-Aug-2000	60/228,179	
615.	80289.058	2750-1184P	25-Aug-2000	60/228,180	
616.	80289.059	2750-1185P	25-Aug-2000	60/228,209	
617.	80289.060	2750-1186P	25-Aug-2000	60/228,178	
618.	80289.061	2750-1187P	25-Aug-2000	60/228,177	
619.	80289.062	2750-1188P	25-Aug-2000	60/227,976	
620.	80289.063	2750-1189P	25-Aug-2000	60/228,207	
621.	80289.064	2750-1190P	25-Aug-2000	60/228,048	
622.	80289.065	2750-1191P	25-Aug-2000	60/228,096	
623.	80289.066	2750-1192P	25-Aug-2000	60/227,932	
624.	80289.067	2750-1193P	25-Aug-2000	60/227,936	
625.	80289.068	2750-1194P	25-Aug-2000	60/228,044	
626.	80289.069	2750-1195P	25-Aug-2000	60/228,216	
627.	80289.070	2750-1196P	25-Aug-2000	60/228,065	

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628.	80289.071	2750-1197P	25-Aug-2000	60/227,975	
629.	80289.072	2750-1198P	25-Aug-2000	60/228,181	
630.	80289.073	2750-1199P	25-Aug-2000	60/228,063	
631.	80289.074	2750-1200P	25-Aug-2000	60/228,064	
632.	80289.075	2750-1201P	25-Aug-2000	60/228,055	
633.	80289.076	2750-1202P	25-Aug-2000	60/228,074	
634.	80289.077	2750-1203P	25-Aug-2000	60/227,939	
635.	80289.078	2750-1204P	25-Aug-2000	60/227,955	
636.	80289.079	2750-1205P	25-Aug-2000	60/228,053	
637.	80289.080	2750-1206P	25-Aug-2000	60/227,978	
638.	80289.081	2750-1207P	25-Aug-2000	60/227,982	
639.	80289.082	2750-1208P	25-Aug-2000	60/228,189	
640.	80289.083	2750-1209P	25-Aug-2000	60/228,054	
641.	80289.084	2750-1210P	25-Aug-2000	60/228,164	
642.	80289.085	2750-1211P	25-Aug-2000	60/228,161	
643.	80289.086	2750-1212P	25-Aug-2000	60/228,165	
644.	80289.087	2750-1213P	25-Aug-2000	60/228,221	
645.	80289.088	2750-1214P	25-Aug-2000	60/228,240	
646.	80289.089	2750-1215P	25-Aug-2000	60/227,979	
647.	80289.090	2750-1216P	25-Aug-2000	60/227,954	
648.	80289.091	2750-1217P	25-Aug-2000	60/228,217	
649.	80289.092	2750-1218P	25-Aug-2000	60/227,929	
650.	80289.093	2750-1219P	25-Aug-2000	60/228,043	
651.	80289.094	2750-1220P	25-Aug-2000	60/227,931	
652.	80289.095	2750-1221P	25-Aug-2000	60/228,187	
653.	80289.096	2750-1222P	25-Aug-2000	60/228,061	
654.	80289.097	2750-1223P	25-Aug-2000	60/228,150	
655.	80289.098	2750-1224P	25-Aug-2000		
656.	80289.201	2750-2116P	25-Aug-2000	60/227,793	
657.	80289.202	2750-2117P	25-Aug-2000	60/228,031	
658.	80289.203	2750-2118P	25-Aug-2000	60/228,028	
659.	80289.204	2750-2119P	25-Aug-2000	60/228,027	
660.	80289.206	2750-2121P	25-Aug-2000	60/228,026	
661.	80289.207	2750-2122P	25-Aug-2000	60/228,038	
662.	80289.208	2750-2123P	25-Aug-2000	60/228,036	
663.	80289.209	2750-2124P	25-Aug-2000	60/227,790	
664.	80289.210	2750-2125P	25-Aug-2000	60/228,039	
665.	80289.211	2750-2126P	25-Aug-2000	60/228,030	
666.	80289.212	2750-2127P	25-Aug-2000	60/228,032	
667.	80289.213	2750-2128P	25-Aug-2000	60/228,149	
668.	80289.214	2750-2129P	25-Aug-2000	60/228,040	
669.	80289.215	2750-2130P	25-Aug-2000	60/227,777	
670.	80289.216	2750-2131P	25-Aug-2000	60/228,037	

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671.	80289.217	2750-2132P	25-Aug-2000	60/227,791	
672.	80289.099	2750-2133P	25-Aug-2000	60/228,041	
673.	80304.002	2750-1157P	6-Sep-2000	60/231,840	
674.	80305.001	2750-1158P	6-Sep-2000	60/231,837	
675.	80305.002	2750-1159P	6-Sep-2000	60/231,833	
676.	80306.001	2750-1160P	6-Sep-2000	60/231,835	
677.	80306.002	2750-1161P	6-Sep-2000	60/231,834	
678.	80309.001	2750-1227P	6-Sep-2000	60/230,430	
679.	91089.001	2750-1228P	6-Sep-2000	60/230,434	
680.	80310.001	2750-1229P	13-Sep-2000	60/232,044	
681.	91090.001	2750-1230P	13-Sep-2000	60/232,043	
682.	80311.001	2750-1231P	15-Sep-2000	60/232,858	
683.	91091.001	2750-1232P	15-Sep-2000	60/232,865	
684.	80312.001	2750-1233P	18-Sep-2000	60/233,621	
685.	91092.001	2750-1234P	18-Sep-2000	60/233,634	
686.	80313.001	2750-1253P	20-Sep-2000	60/234,179	
687.	91093.001	2750-1254P	20-Sep-2000	60/234,178	
688.	80314.001	2750-1259P	21-Sep-2000	60/234,233	
689.	91094.001	2750-1260P	21-Sep-2000	60/234,217	
690.	91095.001	2750-1261P	21-Sep-2000	60/234,220	
691.	80315.001	2750-1262P	25-Sep-2000	60/234,968	
692.	91096.001	2750-1263P	25-Sep-2000	60/234,979	
693.	80316.001	2750-1264P	25-Sep-2000	60/234,974	
694.	91097.001	2750-1265P	25-Sep-2000	60/235,118	
695.	80317.001	2750-1266P	26-Sep-2000	60/234,949	
696.	91098.001	2750-1267P	27-Sep-2000	60/235,577	
697.	91078.001	2750-1268P	28-Sep-2000	60/235,934	
698.	91099.001	2750-1269P	29-Sep-2000	60/236,380	
699.	80318.001	2750-1270P	2-Oct-2000	60/236,732	
700.	91100.001	2750-1271P	2-Oct-2000	60/237,035	
701.	80319.001	2750-1272P	4-Oct-2000	60/237,379	
702.	91101.001	2750-1273P	4-Oct-2000	60/237,505	
703.	80320.001	2750-1274P	5-Oct-2000	60/237,686	
704.	80321.001	2750-1275P	10-Oct-2000	60/238,473	
705.	91102.001	2750-1276P	10-Oct-2000	60/238,472	
706.	80322.001	2750-1277P	10-Oct-2000	60/238,456	
707.	91103.001	2750-1278P	10-Oct-2000	60/238,421	
708.	80323.001	2750-1279P	11-Oct-2000	60/239,091	
709.	91104.001	2750-1280P	11-Oct-2000	60/239,245	
710.	80324.001	2750-1281P	17-Oct-2000	60/240,862	
711.	91105.001	2750-1282P	17-Oct-2000	60/240,863	
712.	80325.001	2750-1283P	19-Oct-2000	60/241,368	
713.	91106.001	2750-1284P	19-Oct-2000	60/241,367	

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714.	80326.002	2750-1286P	19-Oct-2000	09/691,020	
715.	80327.001	2750-1287P	19-Oct-2000	09/691,044	
716.	80327.002	2750-1288P	19-Oct-2000	09/691,028	
717.	80328.002	2750-1290P	19-Oct-2000	09/691,056	
718.	80329.001	2750-1291P	19-Oct-2000	09/691,038	
719.	80329.002	2750-1292P	19-Oct-2000	09/691,031	
720.	80330.002	2750-1294P	19-Oct-2000	09/691,018	
721.	80331.001	2750-1304P	20-Oct-2000	60/241,751	
722.	91107.001	2750-1305P	20-Oct-2000	60/241,750	
723.	80332.001	2750-1306P	23-Oct-2000	60/242,065	
724.	91108.001	2750-1307P	23-Oct-2000	60/242,072	
725.	80334.001	2750-1320P	24-Oct-2000	60/242,686	
726.	80335.001	2750-1321P	25-Oct-2000	60/242,705	
727.	91109.001	2750-1322P	25-Oct-2000	60/242,706	
728.	80336.001	2750-1323P	26-Oct-2000	60/243,289	
729.	91110.001	2750-1324P	26-Oct-2000	60/243,288	
730.	80337.001	2750-1325P	27-Oct-2000	60/243,398	
731.	91111.001	2750-1326P	27-Oct-2000	60/243,478	
732.	80338.001	2750-1327P	30-Oct-2000	60/243,723	
733.	91112.001	2750-1328P	30-Oct-2000	60/243,735	
734.	80339.001	2750-1341P	1-Nov-2000	60/244,691	
735.	91113.001	2750-1342P	1-Nov-2000	60/244,747	
736.	80340.001	2750-1343P	2-Nov-2000	60/244,923	
737.	91114.001	2750-1344P	2-Nov-2000	60/244,920	
738.	80341.001	2750-1345P	3-Nov-2000	60/245,164	
739.	91115.001	2750-1346P	3-Nov-2000	60/245,165	
740.	80342.001	2750-1359P	6-Nov-2000	60/245,676	
741.	91116.001	2750-1360P	6-Nov-2000	60/245,576	
742.	80343.001	2750-1244P	9-Nov-2000	60/246,732	
743.	80344.001	2750-1245P	13-Nov-2000	60/247,010	
744.	91118.001	2750-1246P	13-Nov-2000	60/247,051	
745.	80346.001	2750-1247P	13-Nov-2000	60/247,050	
746.	91119.001	2750-1248P	13-Nov-2000	60/247,049	
747.	80347.001	2750-1348P	15-Nov-2000	60/248,198	
748.	91120.001	2750-1349P	15-Nov-2000	60/248,197	
749.	91121.001	2750-1350P	16-Nov-2000	60/248,555	
750.	80348.001	2750-1351P	17-Nov-2000	60/249,256	
751.	91122.001	2750-1352P	17-Nov-2000	60/249,257	
752.	80349.001	2750-1353P	20-Nov-2000	60/249,454	
753.	91123.001	2750-1354P	20-Nov-2000	60/249,453	
754.	91124.001	2750-1355P	21-Nov-2000	60/252,080	
755.	80350.001	2750-1356P	22-Nov-2000	60/252,464	
756.	91125.001	2750-1357P	22-Nov-2000	60/252,465	

	Client No.	Attorney No.	Filing Date	Appln. No.	
757.	80351.001	2750-1358P	24-Nov-2000	60/252,598	
758.	91126.001	2750-1361P	24-Nov-2000	60/252,590	
759.	91127.001	2750-1362P	28-Nov-2000	60/253,140	
760.	80352.001	2750-1363P	29-Nov-2000	60/253,722	
761.	91128.001	2750-1364P	29-Nov-2000	60/253,748	
762.	91129.001	2750-1365P	1-Dec-2000	60/250,356	
763.	91130.001	2750-1366P	4-Dec-2000	60/250,46	
764.	91131.001	2750-1367P	6-Dec-2000	60/251,387	
765.	80353.001	2750-1368P	7-Dec-2000	60/251,504	
766.	91132.001	2750-1369P	7-Dec-2000	60/251,508	
767.	80354.001	2750-1370P	8-Dec-2000	60/251,853	
768.	91133.001	2750-1371P	8-Dec-2000	60/251,854	
769.	80355.001	2750-1372P	11-Dec-2000	60/254,174	
770.	91134.001	2750-1373P	11-Dec-2000	60/254,196	
771.	91135.001	2750-1374P	13-Dec-2000	60/254,891	
772.	80356.001	2750-1375P	15-Dec-2000	60/256,503	
773.	91136.001	2750-1376P	15-Dec-2000	60/255,415	
774.	80357.001	2750-1377P	18-Dec-2000	60/255,891	
775.	91137.001	2750-1378P	18-Dec-2000	60/255,892	
776.	91138.001	2750-1379P	19-Dec-2000	60/256,306	
777.	91139.001	2750-1381P	21-Dec-2000	60/256,929	
778.	91140.001	2750-1382P	27-Dec-2000	60/257,978	
779.	80358.001	2750-1383P	29-Dec-2000	09/750,044	
780.	80359.001	2750-1384P	2-Jan-2001	60/258,880	
781.	80360.001	2750-1385P	2-Jan-2001	09/750,910	
782.	80361.001	2750-1386P	3-Jan-2001	09/752,823	
783.	92003.001	2750-1153P	5-Jan-2001	09/754,184	
784.	92003.002	2750-1154P	5-Jan-2001	09/754,185	
785.	80362.001	2750-1388P	19-Jan-2001	60/262,389	
786.	91141.001	2750-1389P	19-Jan-2001	60/262,359	
787.	80363.001	2750-1391P	26-Jan-2001	60/264,026	
788.	91142.001	2750-1392P	26-Jan-2001	60/264,027	
789.	80364.001	2750-1393P	29-Jan-2001	60/264,282	
790.	91143.001	2750-1394P	29-Jan-2001	60/264,257	
791.	710-0004-55300- US-U-30992.01	2750-1395P	31-Jan-2001	09/774,106	
792.	710-0004-55300- US-U-30986.01	2750-1396P	31-Jan-2001	09/774,089	
793.	710-0023-55300- US-U-00001.01	2750-1397P	31-Jan-2001	09/774,090	
794.	80366.001	2750-1399P	1-Feb-2001	09/775,870	
795.	80367.001	2750-1400P	1-Feb-2001	09/776,014	
796.	710-3001-55300- US-U-20046.01	2750-1402P	6-Feb-2001	60/266,468	

	Client No.	Attorney No.	Filing Date	Appln. No.	
	US-P-30946.01				
797.	710-3001-55300- US-P-30946.02	2750-1403P	6-Feb-2001	60/266,469	
798.	710-3001-55300- US-P-31043.01	2750-1404P	7-Feb-2001	60/266,863	
799.	710-0004-55300- US-U-30920.01	2750-1405P	8-Feb-2001	09/778,734	
800.	710-3001-55300- US-P-31053.01	2750-1406P	9-Feb-2001	60/267,425	
801.	710-3001-55300- US-P-31053.02	2750-1407P	9-Feb-2001	60/267,430	
802.	710-3001-55300- US-P-31057.01	2750-1408P	9-Feb-2001	60/267,426	
803.	710-3001-55300- US-P-31070.01	2750-1409P	12-Feb-2001	60/267,707	
804.	710-3001-55300- US-P-31070.02	2750-1410P	12-Feb-2001	60/267,706	
805.	710-3001-55300- US-P-31091.01	2750-1412P	14-Feb-2001	60/268,366	
806.	710-3001-55300- US-P-31096.01	2750-1413P	16-Feb-2001	60/268,921	
807.	710-3001-55300- US-P-31112.01	2750-1414P	21-Feb-2001	60/269,890	
808.	710-3001-55300- US-P-31112.02	2750-1415P	21-Feb-2001	60/269,891	
809.	710-3001-55300- US-P-31130.01	2750-1416P	21-Feb-2001	60/269,892	
810.	710-3001-55300- US-P-31130.02	2750-1417P	21-Feb-2001	60/269,893	
811.	710-3001-55300- US-P-31135.01	2750-1418P	22-Feb-2001	60/270,122	
812.	710-3001-55300- US-P-31145.01	2750-1420P	26-Feb-2001	60/270,913	
813.	710-3001-55300- US-P-31149.01	2750-1421P	26-Feb-2001	60/270,912	
814.	710-3001-55300- US-P-31162.01	2750-1424P	28-Feb-2001	60/271,724	
815.	710-3001-55300- US-P-31162.02	2750-1425P	28-Feb-2001	60/271,725	
816.	710-3001-55300- US-P-31170.01	2750-1427P	2-Mar-2001	60/272,467	
817.	710-3001-55300- US-P-31178.01	2750-1428P	5-Mar-2001	60/272,783	

	Client No.	Attorney No.	Filing Date	Appln. No.	
818.	710-3001-55300-US-P-31190.01	2750-1429P	7-Mar-2001	60/273,554	
819.	710-3001-55300-US-P-31197.01	2750-1430P	7-Mar-2001	60/273,553	
820.	710-3001-55300-US-P-31197.02	2750-1431P	7-Mar-2001	60/273,552	
821.	710-0004-55300-US-U-031308.01	2750-1433P	2-Apr-2001	09/823,082	

Number 26

Application 26 (attorney docket no. 2750-1564P) listed above is a continuation of Application No. 10/191,406 (Attorney No. 2750-1530P), filed on July 10, 2002, the entire contents of which are hereby incorporated by reference. Application No. 10/191,406 is a continuation of Application No. 09/940,255 (attorney no. 2750-1465P) filed August 24, 2001 the entire contents of which are also hereby incorporated by reference. Moreover, Application No. 09/940,255 is a continuation-in-part of all the following Nonprovisional applications to which the present application also incorporates by reference and claims priority under 35 USC §120:

	Country	Appln No	Attorney No	FILING DATE
1.	UNITED STATES	09/391.631	2750-0550P	9/3/99
2.	UNITED STATES	09/413.198	2750-0565P	10/5/99
3.	UNITED STATES	09/412.922	2750-0566P	10/5/99
4.	UNITED STATES	09/428.944	2750-0600P	10/28/99
5.	UNITED STATES	09/451.320	2750-0662P	12/1/99
6.	UNITED STATES	09/478.081	2750-0683P	1/4/00
7.	UNITED STATES	09/497.191	2750-0694P	2/3/00
8.	UNITED STATES	09/517.537	2750-0710P	3/1/00
9.	UNITED STATES	09/637.820	2750-1101P	8/11/00
10.	UNITED STATES	09/637.565	2750-1102P	8/11/00
11.	UNITED STATES	09/637.564	2750-1103P	8/11/00
12.	UNITED STATES	09/637.792	2750-1104P	8/11/00
13.	UNITED STATES	09/691.039	2750-1285P	10/19/00
14.	UNITED STATES	09/691.020	2750-1286P	10/19/00
15.	UNITED STATES	09/691.044	2750-1287P	10/19/00
16.	UNITED STATES	09/691.028	2750-1288P	10/19/00
17.	UNITED STATES	09/691.045	2750-1289P	10/19/00
18.	UNITED STATES	09/691.056	2750-1290P	10/19/00
19.	UNITED STATES	09/691.038	2750-1291P	10/19/00
20.	UNITED STATES	09/691.031	2750-1292P	10/19/00
21.	UNITED STATES	09/691.019	2750-1293P	10/19/00

	Country	Appln No	Attorney No	FILING DATE
22.	UNITED STATES	09/691.018	2750-1294P	10/19/00
23.	UNITED STATES	09/741.043	2750-1380P	12/21/00
24.	UNITED STATES	09/750.044	2750-1383P	12/29/00
25.	UNITED STATES	09/750.910	2750-1385P	1/2/01
26.	UNITED STATES	09/752.823	2750-1386P	1/3/01
27.	UNITED STATES	09/754.184	2750-1153P	1/5/01
28.	UNITED STATES	09/754.185	2750-1154P	1/5/01
29.	UNITED STATES	09/774.106	2750-1395P	1/31/01
30.	UNITED STATES	09/774.089	2750-1396P	1/31/01
31.	UNITED STATES	09/774.090	2750-1397P	1/31/01
32.	UNITED STATES	09/774.340	2750-1398P	1/31/01
33.	UNITED STATES	09/775.870	2750-1399P	2/1/01
34.	UNITED STATES	09/776.014	2750-1400P	2/1/01
35.	UNITED STATES	09/778.734	2750-1405P	2/8/01
36.	UNITED STATES	09/790.663	2750-1419P	2/23/01
37.	UNITED STATES	09/795.347	2750-1422P	3/1/01
38.	UNITED STATES	09/795.359	2750-1423P	3/1/01
39.	UNITED STATES	09/804.470	2750-1432P	3/16/01
40.	UNITED STATES	09/823.082	2750-1433P	4/2/01
41.	UNITED STATES	09/824.790	2750-1434P	4/4/01
42.	UNITED STATES	09/824.882	2750-1435P	4/4/01
43.	UNITED STATES	09/832.192	2750-1437P	4/11/01
44.	UNITED STATES	09/832.934	2750-1436P	4/12/01
45.	UNITED STATES	09/842.088	2750-1438P	4/26/01
46.	UNITED STATES	09/842.246	2750-1439P	4/26/01
47.	UNITED STATES	09/845.208	2750-1440P	5/1/01
48.	UNITED STATES	09/845.206	2750-1441P	5/1/01
49.	UNITED STATES	09/845.318	2750-1443P	5/1/01
50.	UNITED STATES	09/845.209	2750-1444P	5/1/01
51.	UNITED STATES	09/870.713	2750-1445P	6/1/01
52.	UNITED STATES	09/870.699	2750-1446P	6/1/01
53.	UNITED STATES	09/870.675	2750-1447P	6/1/01
54.	UNITED STATES	09/870.646	2750-1448P	6/1/01
55.	UNITED STATES	09/870.476	2750-1449P	6/1/01
56.	UNITED STATES	09/870.664	2750-1451P	6/1/01
57.	UNITED STATES	09/878.974	2750-1453P	6/13/01
58.	UNITED STATES	09/881.096	2750-1452P	6/15/01
59.	UNITED STATES	09/898.063	2750-1454P	7/5/01
60.	UNITED STATES	09/898.064	2750-1455P	7/5/01
61.	UNITED STATES	09/902.093	2750-1456P	7/11/01
62.	UNITED STATES	09/902.613	2750-1457P	7/12/01
63.	UNITED STATES	09/902.614	2750-1458P	7/12/01
64.	UNITED STATES	09/903.497	2750-1459P	7/13/01
65.	UNITED STATES	09/903.988	2750-1460P	7/13/01
66.	UNITED STATES	09/918.556	2750-1461P	8/1/01
67.	UNITED STATES	09/920.626	2750-1462P	8/3/01

	Country	Appln No	Attorney No	FILING DATE
68.	UNITED STATES	09/921.135	2750-1463P	8/3/01
69.	UNITED STATES	09/922.661	2750-1464P	8/7/01
70.	UNITED STATES	09/924.702	2750-1469P	8/9/01
71.	UNITED STATES	09/924.701	2750-1470P	8/9/01
72.	UNITED STATES	09/928.372	2750-1471P	8/14/01
73.	UNITED STATES	09/930.244	2750-1472P	8/16/01
74.	UNITED STATES	09/930.231	2750-1473P	8/16/01
75.	UNITED STATES	09/930.214	2750-1474P	8/16/01
76.	UNITED STATES	09/930.223	2750-1475P	8/16/01
77.	UNITED STATES	09/931.043	2750-1476P	8/17/01
78.	UNITED STATES	09/931.911	2750-1477P	8/20/01

Furthermore, the some of the above-listed 78 nonprovisional applications themselves claim priority under 35 USC §119(e) of the following applications to which the present application also claims priority and incorporates by reference:

		Appln No	Attorney No	FILING	
1.	Nonprovisional application no:	09/391.631	2750-0550P	9/3/99	claims priority of the following provisionals:
	1.	60/099.671	2750-0300P	9/4/98	
	2.	60/099.672	2750-0301P	9/4/98	
	3.	60/099.933	2750-0302P	9/11/98	
	4.	60/100.864	2750-0304P	9/17/98	
	5.	60/101.042	2750-0305P	9/18/98	
	6.	60/101.682	2750-0307P	9/24/98	
	7.	60/102.533	2750-0308P	9/30/98	
	8.	60/102.460	2750-0309P	9/30/98	
	9.	60/103.116	2750-0310P	10/5/98	
	10.	60/103.141	2750-0311P	10/5/98	
	11.	60/103.574	2750-0314P	10/9/98	
	12.	60/103.907	2750-0315P	10/13/98	
	13.	60/106.105	2750-0324P	10/29/98	
	14.	60/106.218	2750-0325P	10/30/98	
	15.	60/107.282	2750-0327P	11/6/98	
	16.	60/107.836	2750-0330P	11/10/98	
	17.	60/108.526	2750-0332P	11/16/98	
	18.	60/108.901	2750-0333P	11/17/98	
	19.	60/109.267	2750-0336P	11/20/98	
	20.	60/109.594	2750-0337P	11/23/98	
	21.	60/110.263	2750-0341P	11/30/98	
	22.	60/110.495	2750-0342P	12/1/98	
	23.	60/110.626	2750-0343P	12/2/98	
	24.	60/110.701	2750-0344P	12/3/98	
	25.	60/111.339	2750-0345P	12/7/98	
	26.	60/111.589	2750-0346P	12/9/98	
	27.	60/112.096	2750-0349P	12/14/98	

	28.	60/112.224	2750-0350P	12/15/98	
	29.	60/112.624	2750-0351P	12/16/98	
	30.	60/112.862	2750-0352P	12/17/98	
	31.	60/115.152	2750-0363P	1/7/99	
	32.	60/115.156	2750-0366P	1/7/99	
	33.	60/115.363	2750-0369P	1/8/99	
	34.	60/115.339	2750-0371P	1/11/99	
	35.	60/115.847	2750-0373P	1/13/99	
	36.	60/116.674	2750-0379P	1/21/99	
	37.	60/116.962	2750-0382P	1/22/99	
	38.	60/120.583	2750-0394P	2/18/99	
	39.	60/121.072	2750-0395P	2/22/99	
	40.	60/122.568	2750-0401P	3/2/99	
	41.	60/123.941	2750-0411P	3/12/99	
2.	Nonprovisional application no:	09/413.198	2750-0565P	10/5/99	claims priority of the following provisionals:
	1.	60/103.116	2750-0310P	10/5/98	
	2.	60/103.141	2750-0311P	10/5/98	
	3.	60/103.215	2750-0312P	10/6/98	
	4.	60/103.554	2750-0313P	10/8/98	
	5.	60/103.574	2750-0314P	10/9/98	
	6.	60/103.907	2750-0315P	10/13/98	
	7.	60/104.268	2750-0316P	10/14/98	
	8.	60/104.680	2750-0317P	10/16/98	
	9.	60/104.828	2750-0318P	10/19/98	
	10.	60/105.008	2750-0319P	10/20/98	
	11.	60/105.142	2750-0320P	10/21/98	
	12.	60/105.533	2750-0321P	10/22/98	
	13.	60/105.571	2750-0322P	10/26/98	
	14.	60/105.815	2750-0323P	10/27/98	
	15.	60/106.105	2750-0324P	10/29/98	
	16.	60/106.218	2750-0325P	10/30/98	
3.	Nonprovisional application no:	09/412.922	2750-0566P	10/5/99	claims priority of the following provisionals:
	1.	60/103.116	2750-0310P	10/5/98	
	2.	60/103.141	2750-0311P	10/5/98	
	3.	60/103.215	2750-0312P	10/6/98	
	4.	60/103.554	2750-0313P	10/8/98	
	5.	60/103.574	2750-0314P	10/9/98	
	6.	60/103.907	2750-0315P	10/13/98	
	7.	60/104.268	2750-0316P	10/14/98	
	8.	60/104.680	2750-0317P	10/16/98	
	9.	60/104.828	2750-0318P	10/19/98	
	10.	60/105.008	2750-0319P	10/20/98	
	11.	60/105.142	2750-0320P	10/21/98	
	12.	60/105.533	2750-0321P	10/22/98	
	13.	60/105.571	2750-0322P	10/26/98	

14.	60/105.815	2750-0323P	10/27/98
15.	60/106.105	2750-0324P	10/29/98
16.	60/106.218	2750-0325P	10/30/98
17.	60/106.685	2750-0326P	11/2/98
18.	60/107.282	2750-0327P	11/6/98
19.	60/107.720	2750-0328P	11/9/98
20.	60/107.719	2750-0329P	11/9/98
21.	60/107.836	2750-0330P	11/10/98
22.	60/108.190	2750-0331P	11/12/98
23.	60/108.526	2750-0332P	11/16/98
24.	60/108.901	2750-0333P	11/17/98
25.	60/109.124	2750-0334P	11/19/98
26.	60/109.127	2750-0335P	11/19/98
27.	60/109.267	2750-0336P	11/20/98
28.	60/109.594	2750-0337P	11/23/98
29.	60/110.053	2750-0338P	11/25/98
30.	60/110.050	2750-0339P	11/25/98
31.	60/110.158	2750-0340P	11/27/98
32.	60/110.263	2750-0341P	11/30/98
33.	60/110.495	2750-0342P	12/1/98
34.	60/110.626	2750-0343P	12/2/98
35.	60/110.701	2750-0344P	12/3/98
36.	60/111.339	2750-0345P	12/7/98
37.	60/111.589	2750-0346P	12/9/98
38.	60/111.782	2750-0347P	12/10/98
39.	60/111.812	2750-0348P	12/11/98
40.	60/112.096	2750-0349P	12/14/98
41.	60/112.224	2750-0350P	12/15/98
42.	60/112.624	2750-0351P	12/16/98
43.	60/112.862	2750-0352P	12/17/98
44.	60/112.912	2750-0353P	12/18/98
45.	60/113.248	2750-0354P	12/21/98
46.	60/113.522	2750-0355P	12/22/98
47.	60/113.826	2750-0356P	12/23/98
48.	60/113.998	2750-0357P	12/28/98
49.	60/114.384	2750-0358P	12/29/98
50.	60/114.455	2750-0359P	12/30/98
51.	60/114.740	2750-0360P	1/4/99
52.	60/114.866	2750-0361P	1/6/99
53.	60/115.153	2750-0362P	1/7/99
54.	60/115.152	2750-0363P	1/7/99
55.	60/115.151	2750-0364P	1/7/99
56.	60/115.155	2750-0365P	1/7/99
57.	60/115.156	2750-0366P	1/7/99
58.	60/115.154	2750-0367P	1/7/99
59.	60/115.364	2750-0368P	1/8/99
60.	60/115.365	2750-0369P	1/8/99

	61.	60/115.339	2750-0371P	1/11/99	
	62.	60/115.518	2750-0372P	1/12/99	
	63.	60/115.847	2750-0373P	1/13/99	
	64.	60/115.905	2750-0374P	1/14/99	
	65.	60/116.383	2750-0375P	1/15/99	
	66.	60/116.384	2750-0376P	1/15/99	
	67.	60/116.329	2750-0377P	1/19/99	
	68.	60/116.340	2750-0378P	1/19/99	
	69.	60/116.674	2750-0379P	1/21/99	
	70.	60/116.672	2750-0380P	1/21/99	
	71.	60/116.960	2750-0381P	1/22/99	
	72.	60/116.962	2750-0382P	1/22/99	
	73.	60/117.756	2750-0383P	1/28/99	
	74.	60/118.672	2750-0384P	2/3/99	
	75.	60/118.808	2750-0385P	2/4/99	
	76.	60/118.778	2750-0386P	2/5/99	
	77.	60/119.029	2750-0387P	2/8/99	
	78.	60/119.332	2750-0388P	2/9/99	
	79.	60/119.462	2750-0389P	2/10/99	
	80.	60/119.922	2750-0391P	2/12/99	
	81.	60/120.196	2750-0392P	2/16/99	
	82.	60/120.198	2750-0393P	2/16/99	
	83.	60/120.583	2750-0394P	2/18/99	
	84.	60/121.072	2750-0395P	2/22/99	
	85.	60/121.334	2750-0396P	2/23/99	
	86.	60/121.470	2750-0397P	2/24/99	
	87.	60/121.704	2750-0398P	2/25/99	
	88.	60/122.107	2750-0399P	2/26/99	
	89.	60/122.266	2750-0400P	3/1/99	
	90.	60/122.568	2750-0401P	3/2/99	
	91.	60/122.611	2750-0402P	3/3/99	
	92.	60/121.775	2750-0403P	3/4/99	
	93.	60/123.534	2750-0404P	3/5/99	
	94.	60/123.680	2750-0406P	3/9/99	
	95.	60/123.715	2750-0408P	3/10/99	
	96.	60/123.726	2750-0409P	3/10/99	
	97.	60/124.263	2750-0410P	3/11/99	
	98.	60/123.941	2750-0411P	3/12/99	
4.	Nonprovisional application no: 09/428.944		2750-0600P	10/28/99	claims priority of the following provisionals:
	1.	60/106.685	2750-0326P	11/2/98	
	2.	60/107.282	2750-0327P	11/6/98	
	3.	60/107.720	2750-0328P	11/9/98	
	4.	60/107.719	2750-0329P	11/9/98	
	5.	60/107.836	2750-0330P	11/10/98	
	6.	60/108.190	2750-0331P	11/12/98	
	7.	60/108.526	2750-0332P	11/16/98	

		8.	60/108.901	2750-0333P	11/17/98	
		9.	60/109.124	2750-0334P	11/19/98	
		10.	60/109.127	2750-0335P	11/19/98	
		11.	60/109.267	2750-0336P	11/20/98	
		12.	60/109.594	2750-0337P	11/23/98	
		13.	60/110.053	2750-0338P	11/25/98	
		14.	60/110.050	2750-0339P	11/25/98	
		15.	60/110.158	2750-0340P	11/27/98	
		16.	60/110.263	2750-0341P	11/30/98	
5.	Nonprovisional application no:		09/451.320	2750-0662P	12/1/99	claims priority of the following provisionals:
		1.	60/110.495	2750-0342P	12/1/98	
		2.	60/110.626	2750-0343P	12/2/98	
		3.	60/110.701	2750-0344P	12/3/98	
		4.	60/111.339	2750-0345P	12/7/98	
		5.	60/111.589	2750-0346P	12/9/98	
		6.	60/111.782	2750-0347P	12/10/98	
		7.	60/111.812	2750-0348P	12/11/98	
		8.	60/112.096	2750-0349P	12/14/98	
		9.	60/112.224	2750-0350P	12/15/98	
		10.	60/112.624	2750-0351P	12/16/98	
		11.	60/112.862	2750-0352P	12/17/98	
		12.	60/112.912	2750-0353P	12/18/98	
		13.	60/113.248	2750-0354P	12/21/98	
		14.	60/113.522	2750-0355P	12/22/98	
		15.	60/113.826	2750-0356P	12/23/98	
		16.	60/113.998	2750-0357P	12/28/98	
		17.	60/114.384	2750-0358P	12/29/98	
		18.	60/114.455	2750-0359P	12/30/98	
		19.	60/115.153	2750-0362P	1/7/99	
		20.	60/115.152	2750-0363P	1/7/99	
		21.	60/115.151	2750-0364P	1/7/99	
		22.	60/115.155	2750-0365P	1/7/99	
		23.	60/115.156	2750-0366P	1/7/99	
		24.	60/115.364	2750-0368P	1/8/99	
		25.	60/116.960	2750-0381P	1/22/99	
6.	Nonprovisional application no:		09/478.081	2750-0683P	1/4/00	claims priority of the following provisionals:
		1.	60/116.674	2750-0379P	1/21/99	
		2.	60/115.518	2750-0372P	1/12/99	
		3.	60/115.154	2750-0367P	1/7/99	
		4.	60/115.365	2750-0369P	1/8/99	
		5.	60/116.384	2750-0376P	1/15/99	
		6.	60/115.339	2750-0371P	1/11/99	
		7.	60/116.340	2750-0378P	1/19/99	
		8.	60/114.866	2750-0361P	1/6/99	
		9.	60/116.962	2750-0382P	1/22/99	

		10.	60/114.740	2750-0360P	1/4/99	
		11.	60/115.905	2750-0374P	1/14/99	
		12.	60/115.847	2750-0373P	1/13/99	
		13.	60/116.672	2750-0380P	1/21/99	
		14.	60/116.383	2750-0375P	1/15/99	
		15.	60/116.329	2750-0377P	1/19/99	
		16.	60/117.756	2750-0383P	1/28/99	
7.	Nonprovisional application no:	09/497.191	2750-0694P	2/3/00	claims priority of the following provisionals:	
	1.	60/120.196	2750-0392P	2/16/99		
	2.	60/121.470	2750-0397P	2/24/99		
	3.	60/122.107	2750-0399P	2/26/99		
	4.	60/121.334	2750-0396P	2/23/99		
	5.	60/119.462	2750-0389P	2/10/99		
	6.	60/120.583	2750-0394P	2/18/99		
	7.	60/121.704	2750-0398P	2/25/99		
	8.	60/120.198	2750-0393P	2/16/99		
	9.	60/121.072	2750-0395P	2/22/99		
	10.	60/119.922	2750-0391P	2/12/99		
	11.	60/118.672	2750-0384P	2/3/99		
	12.	60/118.808	2750-0385P	2/4/99		
	13.	60/118.778	2750-0386P	2/5/99		
	14.	60/119.029	2750-0387P	2/8/99		
	15.	60/119.332	2750-0388P	2/9/99		
8.	Nonprovisional application no:	09/517.537	2750-0710P	3/1/00	claims priority of the following provisionals:	
	1.	60/123.534	2750-0404P	3/5/99		
	2.	60/122.266	2750-0400P	3/1/99		
	3.	60/123.941	2750-0411P	3/12/99		
	4.	60/124.263	2750-0410P	3/11/99		
	5.	60/123.726	2750-0409P	3/10/99		
	6.	60/122.568	2750-0401P	3/2/99		
	7.	60/123.680	2750-0406P	3/9/99		
	8.	60/123.715	2750-0408P	3/10/99		
	9.	60/121.775	2750-0403P	3/4/99		
	10.	60/122.611	2750-0402P	3/3/99		
9.	Nonprovisional application no:	09/637.820	2750-1101P	8/11/00	claims priority of the following provisionals:	
	1.	60/148.347	2750-0525P	8/12/99		
10.	Nonprovisional application no:	09/637.565	2750-1102P	8/11/00	claims priority of the following provisionals:	
	1.	60/148.342	2750-0526P	8/12/99		
11.	Nonprovisional application no:	09/637.564	2750-1103P	8/11/00	claims priority of the following provisionals:	
	1.	60/148.340	2750-0527P	8/12/99		
12.	Nonprovisional application no:	09/637.792	2750-1104P	8/11/00	claims priority of the following provisionals:	

		1.	60/148.337	2750-0528P	8/12/99	
36.	Nonprovisional application no:		09/790.663	2750-1419P	2/23/01	claims priority of the following provisionals:
		1.	60/185.398	2750-0721P	2/28/00	
		2.	60/185.140	2750-0718P	2/25/00	
		3.	60/185.750	2750-0724P	2/29/00	
37.	Nonprovisional application no:		09/795.347	2750-1422P	3/1/01	claims priority of the following provisionals:
		1.	60/186.296	2750-0726P	3/1/00	
		2.	60/186.748	2750-0732P	3/3/00	
		3.	60/186.283	2750-0725P	3/1/00	
		4.	60/191.825	2750-0770P	3/24/00	
		5.	60/190.069	2750-0758P	3/20/00	
		6.	60/189.959	2750-0756P	3/16/00	
		7.	60/190.070	2750-0759P	3/20/00	
		8.	60/190.545	2750-0761P	3/20/00	
		9.	60/190.089	2750-0762P	3/20/00	
		10.	60/191.084	2750-0763P	3/22/00	
		11.	60/191.097	2750-0764P	3/22/00	
		12.	60/191.543	2750-0766P	3/23/00	
		13.	60/189.953	2750-0755P	3/16/00	
		14.	60/191.823	2750-0769P	3/24/00	
		15.	60/192.421	2750-0772P	3/27/00	
		16.	60/186.390	2750-0711P	3/2/00	
		17.	60/192.308	2750-0773P	3/27/00	
		18.	60/187.178	2750-0728P	3/2/00	
		19.	60/192.941	2750-0776P	3/29/00	
		20.	60/193.244	2750-0778P	3/30/00	
		21.	60/193.245	2750-0779P	3/30/00	
		22.	60/193.453	2750-0781P	3/31/00	
		23.	60/193.455	2750-0782P	3/31/00	
		24.	60/191.545	2750-0767P	3/23/00	
		25.	60/187.888	2750-0737P	3/8/00	
		26.	60/186.386	2750-0729P	3/2/00	
		27.	60/192.940	2750-0775P	3/29/00	
		28.	60/189.462	2750-0749P	3/15/00	
		29.	60/186.669	2750-0733P	3/3/00	
		30.	60/187.896	2750-0736P	3/8/00	
		31.	60/186.387	2750-0730P	3/2/00	
		32.	60/188.187	2750-0739P	3/10/00	
		33.	60/188.186	2750-0740P	3/10/00	
		34.	60/188.185	2750-0742P	3/10/00	
		35.	60/188.175	2750-0743P	3/10/00	
		36.	60/189.080	2750-0745P	3/14/00	
		37.	60/189.052	2750-0746P	3/14/00	
		38.	60/189.461	2750-0748P	3/15/00	
		39.	60/187.378	2750-0734P	3/7/00	

38.	Nonprovisional application no:	09/795,359	2750-1423P	3/1/01	claims priority of the following provisionals:
	1.	60/189,460	2750-0747P	3/15/00	
	2.	60/190,090	2750-0760P	3/20/00	
	3.	60/189,965	2750-0757P	3/17/00	
	4.	60/189,958	2750-0754P	3/16/00	
	5.	60/188,687	2750-0744P	3/13/00	
	6.	60/188,174	2750-0741P	3/10/00	
	7.	60/187,985	2750-0738P	3/9/00	
	8.	60/187,379	2750-0735P	3/7/00	
	9.	60/186,277	2750-0727P	3/1/00	
	10.	60/192,855	2750-0774P	3/29/00	
	11.	60/186,670	2750-0731P	3/3/00	
	12.	60/192,420	2750-0771P	3/27/00	
	13.	60/193,469	2750-0780P	3/31/00	
	14.	60/193,243	2750-0777P	3/30/00	
	15.	60/191,826	2750-0768P	3/24/00	
	16.	60/191,549	2750-0765P	3/23/00	
39.	Nonprovisional application no:	09/804,470	2750-1432P	3/16/01	claims priority of the following provisionals:
		60/189,948	2750-0752P	3/16/00	
		60/190,121	2750-0753P	3/16/00	
		60/189,947	2750-0751P	3/16/00	
		60/190,120	2750-0750P	3/16/00	
41.	Nonprovisional application no:	09/824,790	2750-1434P	4/4/01	claims priority of the following provisionals:
	1.	60/199,123	2750-0829P	4/24/00	
	2.	60/194,698	2750-0792P	4/5/00	
	3.	60/196,168	2750-0802P	4/11/00	
	4.	60/197,397	2750-0814P	4/14/00	
	5.	60/195,258	2750-0797P	4/7/00	
	6.	60/194,884	2750-0784P	4/6/00	
	7.	60/196,483	2750-0805P	4/12/00	
	8.	60/194,682	2750-0789P	4/5/00	
	9.	60/194,385	2750-0785P	4/4/00	
	10.	60/198,400	2750-0820P	4/19/00	
	11.	60/198,765	2750-0826P	4/21/00	
	12.	60/198,629	2750-0823P	4/20/00	
	13.	60/198,268	2750-0817P	4/17/00	
42.	Nonprovisional application no:	09/824,882	2750-1435P	4/4/01	claims priority of the following provisionals:
	1.	60/195,045	2750-0796P	4/6/00	
	2.	60/196,089	2750-0804P	4/11/00	
	3.	60/198,373	2750-0822P	4/19/00	
	4.	60/198,386	2750-0821P	4/19/00	
	5.	60/197,687	2750-0815P	4/17/00	
	6.	60/198,133	2750-0818P	4/17/00	

	7.	60/197.671	2750-0819P	4/17/00	
	8.	60/195.283	2750-0798P	4/7/00	
	9.	60/196.289	2750-0807P	4/12/00	
	10.	60/196.486	2750-0809P	4/12/00	
	11.	60/198.763	2750-0828P	4/21/00	
	12.	60/196.169	2750-0803P	4/11/00	
	13.	60/197.678	2750-0816P	4/17/00	
	14.	60/194.874	2750-0793P	4/6/00	
	15.	60/194.885	2750-0795P	4/6/00	
	16.	60/194.872	2750-0794P	4/6/00	
	17.	60/195.257	2750-0799P	4/7/00	
	18.	60/194.697	2750-0791P	4/5/00	
	19.	60/194.683	2750-0790P	4/5/00	
	20.	60/194.398	2750-0787P	4/4/00	
	21.	60/194.404	2750-0786P	4/4/00	
	22.	60/196.487	2750-0806P	4/12/00	
	23.	60/200.102	2750-0837P	4/27/00	
	24.	60/198.623	2750-0825P	4/20/00	
	25.	60/198.767	2750-0827P	4/21/00	
	26.	60/199.122	2750-0831P	4/24/00	
	27.	60/199.124	2750-0830P	4/24/00	
	28.	60/196.485	2750-0808P	4/12/00	
	29.	60/199.828	2750-0834P	4/26/00	
	30.	60/199.818	2750-0835P	4/26/00	
	31.	60/200.103	2750-0836P	4/27/00	
	32.	60/198.619	2750-0824P	4/20/00	
43.	Nonprovisional application no:	09/832.192	2750-1437P	4/11/01	claims priority of the following provisionals:
	1.	60/200.773	2750-0846P	4/28/00	
	2.	60/196.212	2750-0800P	4/12/00	
	3.	60/197.869	2750-0810P	4/14/00	
	4.	60/196.213	2750-0811P	4/13/00	
	5.	60/197.870	2750-0812P	4/17/00	
	6.	60/197.871	2750-0813P	4/17/00	
	7.	60/200.373	2750-0844P	4/28/00	
	8.	60/196.211	2750-0801P	4/11/00	
44.	Nonprovisional application no:	09/832.934	2750-1436P	4/12/01	is a continuation of the following appln:
	1.	09/637.820	2750-1101P	8/11/00	which claims priority of the following:
	2.	60/148.347	2750-0525P	8/12/99	
45.	Nonprovisional application no:	09/842.088	2750-1438P	4/26/01	claims priority of the following provisionals:
	1.	60/200.031	2750-0833P	4/26/00	
46.	Nonprovisional application no:	09/842.246	2750-1439P	4/26/01	claims priority of the following provisionals:
	1.	60/200.034	2750-0832P	4/26/00	

47.	Nonprovisional application no:	09/845.208	2750-1440P	5/1/01	claims priority of the following provisionals:
	1.	60/203.622	2750-0870P	5/11/00	
	2.	60/200.763	2750-0843P	5/1/00	
	3.	60/201.016	2750-0845P	5/1/00	
	4.	60/200.762	2750-0847P	5/1/00	
	5.	60/200.761	2750-0848P	5/1/00	
	6.	60/203.671	2750-0867P	5/11/00	
	7.	60/203.669	2750-0869P	5/11/00	
	8.	60/203.672	2750-0868P	5/11/00	
48.	Nonprovisional application no:	09/845.206	2750-1441P	5/1/01	claims priority of the following provisionals:
	1.	60/204.122	2750-0888P	5/15/00	
	2.	60/207.452	2750-0913P	5/30/00	
	3.	60/207.329	2750-0914P	5/30/00	
	4.	60/205.243	2750-0898P	5/19/00	
	5.	60/204.388	2750-0887P	5/15/00	
	6.	60/204.568	2750-0891P	5/16/00	
	7.	60/204.830	2750-0893P	5/17/00	
	8.	60/204.829	2750-0894P	5/17/00	
	9.	60/205.201	2750-0895P	5/18/00	
	10.	60/207.367	2750-0907P	5/26/00	
	11.	60/205.242	2750-0897P	5/19/00	
	12.	60/203.279	2750-0882P	5/11/00	
	13.	60/205.572	2750-0900P	5/22/00	
	14.	60/205.576	2750-0901P	5/22/00	
	15.	60/206.316	2750-0902P	5/23/00	
	16.	60/206.319	2750-0903P	5/23/00	
	17.	60/206.553	2750-0904P	5/24/00	
	18.	60/206.545	2750-0905P	5/24/00	
	19.	60/205.058	2750-0896P	5/18/00	
	20.	60/202.180	2750-0861P	5/5/00	
	21.	60/207.354	2750-0911P	5/26/00	
	22.	60/204.569	2750-0892P	5/16/00	
	23.	60/201.275	2750-0838P	5/2/00	
	24.	60/200.879	2750-0839P	5/1/00	
	25.	60/201.305	2750-0850P	5/2/00	
	26.	60/201.740	2750-0857P	5/4/00	
	27.	60/203.915	2750-0885P	5/12/00	
	28.	60/202.112	2750-0860P	5/5/00	
	29.	60/203.916	2750-0884P	5/12/00	
	30.	60/202.914	2750-0862P	5/9/00	
	31.	60/202.636	2750-0863P	5/9/00	
	32.	60/202.634	2750-0866P	5/9/00	
	33.	60/202.963	2750-0879P	5/10/00	
	34.	60/203.457	2750-0881P	5/11/00	
	35.	60/202.968	2750-0878P	5/10/00	
	36.	60/201.750	2750-0858P	5/4/00	

		37.	60/207.239	2750-0910P	5/26/00	
		38.	60/207.243	2750-0908P	5/26/00	
		39.	60/202.919	2750-0865P	5/9/00	
49.	Nonprovisional application no:		09/845.318	2750-1443P	5/1/01	claims priority of the following provisionals:
		1.	60/205.325	2750-0890P	5/17/00	
		2.	60/201.018	2750-0842P	5/1/00	
50.	Nonprovisional application no:		09/845.209	2750-1444P	5/1/01	claims priority of the following provisionals:
		1.	60/205.233	2750-0889P	5/17/00	
		2.	60/201.017	2750-0841P	5/1/00	
51.	Nonprovisional application no:		09/870.713	2750-1445P	6/1/01	claims priority of the following provisionals:
		1.	60/209.338	2750-0915P	6/2/00	
52.	Nonprovisional application no:		09/870.699	2750-1446P	6/1/01	claims priority of the following provisionals:
		1.	60/208.421	2750-0916P	6/1/00	
53.	Nonprovisional application no:		09/870.675	2750-1447P	6/1/01	claims priority of the following provisionals:
		1.	60/208.649	2750-0917P	6/2/00	
54.	Nonprovisional application no:		09/870.646	2750-1448P	6/1/01	claims priority of the following provisionals:
		1.	60/208.648	2750-0918P	6/1/00	
55.	Nonprovisional application no:		09/870.476	2750-1449P	6/1/01	claims priority of the following provisionals:
		1.	60/208.324	2750-0919P	6/1/00	
		2.	60/210.008	2750-0929P	6/8/00	
		3.	60/208.917	2750-0925P	6/5/00	
		4.	60/208.919	2750-0922P	6/5/00	
56.	Nonprovisional application no:		09/870.664	2750-1451P	6/1/01	claims priority of the following provisionals:
			60/208.918	2750-0924P	6/5/00	
			60/214.535	2750-1036P	6/27/00	
			60/208.920	2750-0927P	6/5/00	
			60/215.127	2750-1041P	6/30/00	
			60/214.799	2750-1039P	6/28/00	
			60/213.249	2750-0963P	6/22/00	
			60/210.564	2750-0933P	6/9/00	
			60/210.006	2750-0931P	6/8/00	
			60/208.312	2750-0921P	6/1/00	
			60/211.214	2750-0936P	6/13/00	
57.	Nonprovisional application no:		09/878.974	2750-1453P	6/13/01	claims priority of the following provisionals:
		1.	60/211.539	2750-0938P	6/15/00	
		2.	60/214.760	2750-0968P	6/27/00	
		3.	60/213.195	2750-0964P	6/22/00	
		4.	60/213.221	2750-0965P	6/22/00	

	5.	60/212.677	2750-0959P	6/20/00	
	6.	60/212.414	2750-0956P	6/19/00	
	7.	60/211.210	2750-0937P	6/13/00	
	8.	60/212.713	2750-0960P	6/20/00	
58.	Nonprovisional application no:	09/881.096	2750-1452P	6/15/01	claims priority of the following provisionals:
	1.	60/213.270	2750-0967P	6/22/00	
	2.	60/212.727	2750-0961P	6/20/00	
	3.	60/212.623	2750-0958P	6/19/00	
	4.	60/211.538	2750-0940P	6/15/00	
	5.	60/214.524	2750-0970P	6/27/00	
59.	Nonprovisional application no:	09/898.063	2750-1454P	7/5/01	claims priority of the following provisionals:
	1.	60/216.362	2750-1043P	7/5/00	
	2.	60/220.811	2750-1079P	7/25/00	
	3.	60/220.652	2750-1081P	7/25/00	
	4.	60/217.384	2750-1046P	7/11/00	
	5.	60/219.033	2750-1057P	7/18/00	
60.	Nonprovisional application no:	09/898.064	2750-1455P	7/5/01	claims priority of the following provisionals:
	1.	60/217.476	2750-1045P	7/11/00	
	2.	60/216.361	2750-1042P	7/5/00	
	3.	60/220.647	2750-1059P	7/25/00	
	4.	60/220.484	2750-1080P	7/25/00	
	5.	60/219.004	2750-1056P	7/18/00	
61.	Nonprovisional application no:	09/902.093	2750-1456P	7/11/01	claims priority of the following provisionals:
	1.	60/226.725	2750-1087P	8/21/00	
	2.	60/225.302	2750-1085P	8/15/00	
	3.	60/228.897	2750-1226P	8/30/00	
	4.	60/227.026	2750-1163P	8/23/00	
	5.	60/217.385	2750-1044P	7/11/00	
	6.	60/219.021	2750-1055P	7/18/00	
	7.	60/224.516	2750-1083P	8/14/00	
	8.	60/220.814	2750-1058P	7/25/00	
62.	Nonprovisional application no:	09/902.613	2750-1457P	7/12/01	claims priority of the following provisionals:
	1.	60/217.754	2750-1050P	7/12/00	
	2.	60/223.114	2750-1256P	8/1/00	
63.	Nonprovisional application no:	09/902.614	2750-1458P	7/12/01	claims priority of the following provisionals:
	1.	60/223.116	2750-1257P	8/3/00	
	2.	60/218.548	2750-1052P	7/12/00	
64.	Nonprovisional application no:	09/903.497	2750-1459P	7/13/01	claims priority of the following provisionals:
	1.	60/217.846	2750-1054P	7/13/00	
	2.	60/223.099	2750-1258P	8/3/00	

65.	Nonprovisional application no:	09/903.988	2750-1460P	7/13/01	claims priority of the following provisionals:
	1.	60/218.566	2750-1048P	7/14/00	
	2.	60/223.098	2750-1255P	8/3/00	
66.	Nonprovisional application no:	09/918.556	2750-1461P	8/1/01	claims priority of the following provisionals:
	1.	60/223.115	2750-1049P	8/1/00	
67.	Nonprovisional application no:	09/920.626	2750-1462P	8/3/01	claims priority of the following provisionals:
	1.	60/223.100	2750-1053P	8/3/00	
	2.	60/237.361	2750-1113P	8/31/00	
	3.	60/226.325	2750-1105P	8/18/00	
68.	Nonprovisional application no:	09/921.135	2750-1463P	8/3/01	claims priority of the following provisionals:
	1.	60/223.101	2750-1051P	8/3/00	
	2.	60/226.323	2750-1109P	8/18/00	
	3.	60/229.519	2750-1090P	8/31/00	
69.	Nonprovisional application no:	09/922.661	2750-1464P	8/7/01	claims priority of the following provisionals:
	1.	60/229.521	2750-1088P	8/31/00	
	2.	60/226.381	2750-1107P	8/18/00	
	3.	60/223.329	2750-1047P	8/7/00	
70.	Nonprovisional application no:	09/924.702	2750-1469P	8/9/01	claims priority of the following provisionals:
	1.	60/224.390	2750-1114P	8/9/00	
71.	Nonprovisional application no:	09/924.701	2750-1470P	8/9/01	claims priority of the following provisionals:
	1.	60/224.391	2750-1115P	8/9/00	
72.	Nonprovisional application no:	09/928.372	2750-1471P	8/14/01	claims priority of the following provisionals:
	1.	60/227.024	2750-1162P	8/23/00	
	2.	60/228.898	2750-1225P	8/30/00	
	3.	60/225.303	2750-1084P	8/15/00	
	4.	60/224.517	2750-1082P	8/14/00	
	5.	60/226.452	2750-1086P	8/21/00	
73.	Nonprovisional application no:	09/930.244	2750-1472P	8/16/01	claims priority of the following provisionals:
	1.	60/237.362	2750-1089P	8/31/00	
	2.	60/225.848	2750-1108P	8/16/00	
74.	Nonprovisional application no:	09/930.231	2750-1473P	8/16/01	Claims priority of the following provisionals:
	1.	60/225.849	2750-1106P	8/16/00	
75.	Nonprovisional application no:	09/930.214	2750-1474P	8/16/01	Claims priority of the following provisionals:
	1.	60/225.850	2750-1110P	8/16/00	
	2.	60/229.520	2750-1091P	8/31/00	

76.	Nonprovisional application no:	09/930.223	2750-1475P	8/16/01	Claims priority of the following provisionals:
	1.	60/225.847	2750-1112P	8/16/00	
77.	Nonprovisional application no:	09/931.043	2750-1476P	8/17/01	Claims priority of the following provisionals:
	1.	60/226.324	2750-1111P	8/18/00	
78.	Nonprovisional application no:	09/931.911	2750-1477P	8/20/01	Claims priority of the following provisionals:
	1.	60/229.520	2750-1091P	8/31/00	
	Nonprovisional application no:	09/940.255	2750-1465P	8/24/01	Claims priority of the following provisionals:
	1.	60/228.025	2750-1133P	8/25/00	
	2.	60/227.781	2750-1134P	8/25/00	
	3.	60/227.783	2750-1135P	8/25/00	
	4.	60/227.731	2750-1136P	8/25/00	
	5.	60/227.732	2750-1137P	8/25/00	
	6.	60/227.729	2750-1138P	8/25/00	
	7.	60/228.167	2750-1139P	8/25/00	
	8.	60/227.734	2750-1140P	8/25/00	
	9.	60/227.792	2750-1141P	8/25/00	
	10.	60/227.733	2750-1142P	8/25/00	
	11.	60/227.730	2750-1143P	8/25/00	
	12.	60/227.770	2750-1144P	8/25/00	
	13.	60/227.728	2750-1145P	8/25/00	
	14.	60/227.773	2750-1146P	8/25/00	
	15.	60/228.033	2750-1147P	8/25/00	
	16.	60/228.024	2750-1148P	8/25/00	
	17.	60/227.769	2750-1149P	8/25/00	
	18.	60/227.780	2750-1150P	8/25/00	
	19.	60/227.725	2750-1151P	8/25/00	
	20.	60/227.774	2750-1152P	8/25/00	
	21.	60/231.840	2750-1157P	9/6/00	
	22.	60/231.837	2750-1158P	9/6/00	
	23.	60/231.833	2750-1159P	9/6/00	
	24.	60/231.835	2750-1160P	9/6/00	
	25.	60/231.834	2750-1161P	9/6/00	
	26.	60/228.163	2750-1164P	8/25/00	
	27.	60/228.046	2750-1165P	8/25/00	
	28.	60/228.098	2750-1166P	8/25/00	
	29.	60/228.047	2750-1167P	8/25/00	
	30.	60/228.052	2750-1168P	8/25/00	
	31.	60/228.049	2750-1169P	8/25/00	
	32.	60/228.132	2750-1170P	8/25/00	
	33.	60/228.152	2750-1171P	8/25/00	
	34.	60/228.135	2750-1172P	8/25/00	
	35.	60/228.322	2750-1173P	8/25/00	
	36.	60/228.156	2750-1174P	8/25/00	
	37.	60/228.323	2750-1175P	8/25/00	

38.	60/228.133	2750-1176P	8/25/00
39.	60/228.320	2750-1177P	8/25/00
40.	60/228.159	2750-1178P	8/25/00
41.	60/228.151	2750-1179P	8/25/00
42.	60/228.202	2750-1180P	8/25/00
43.	60/228.208	2750-1181P	8/25/00
44.	60/228.153	2750-1182P	8/25/00
45.	60/228.179	2750-1183P	8/25/00
46.	60/228.180	2750-1184P	8/25/00
47.	60/228.209	2750-1185P	8/25/00
48.	60/228.178	2750-1186P	8/25/00
49.	60/228.177	2750-1187P	8/25/00
50.	60/227.976	2750-1188P	8/25/00
51.	60/228.207	2750-1189P	8/25/00
52.	60/228.048	2750-1190P	8/25/00
53.	60/228.096	2750-1191P	8/25/00
54.	60/227.932	2750-1192P	8/25/00
55.	60/227.936	2750-1193P	8/25/00
56.	60/228.044	2750-1194P	8/25/00
57.	60/228.216	2750-1195P	8/25/00
58.	60/228.065	2750-1196P	8/25/00
59.	60/227.975	2750-1197P	8/25/00
60.	60/228.181	2750-1198P	8/25/00
61.	60/228.063	2750-1199P	8/25/00
62.	60/228.064	2750-1200P	8/25/00
63.	60/228.055	2750-1201P	8/25/00
64.	60/228.074	2750-1202P	8/25/00
65.	60/227.939	2750-1203P	8/25/00
66.	60/227.955	2750-1204P	8/25/00
67.	60/228.053	2750-1205P	8/25/00
68.	60/227.978	2750-1206P	8/25/00
69.	60/227.982	2750-1207P	8/25/00
70.	60/228.189	2750-1208P	8/25/00
71.	60/228.054	2750-1209P	8/25/00
72.	60/228.164	2750-1210P	8/25/00
73.	60/228.161	2750-1211P	8/25/00
74.	60/228.165	2750-1212P	8/25/00
75.	60/228.221	2750-1213P	8/25/00
76.	60/228.240	2750-1214P	8/25/00
77.	60/227.979	2750-1215P	8/25/00
78.	60/227.954	2750-1216P	8/25/00
79.	60/228.217	2750-1217P	8/25/00
80.	60/227.929	2750-1218P	8/25/00
81.	60/228.043	2750-1219P	8/25/00
82.	60/227.931	2750-1220P	8/25/00
83.	60/228.187	2750-1221P	8/25/00
84.	60/228.061	2750-1222P	8/25/00

85.	60/228.150	2750-1223P	8/25/00
86.		2750-1224P	8/25/00
87.	60/230.430	2750-1227P	9/6/00
88.	60/230.434	2750-1228P	9/6/00
89.	60/232.044	2750-1229P	9/13/00
90.	60/232.043	2750-1230P	9/13/00
91.	60/232.858	2750-1231P	9/15/00
92.	60/232.865	2750-1232P	9/15/00
93.	60/233.621	2750-1233P	9/18/00
94.	60/233.634	2750-1234P	9/18/00
95.	60/246.732	2750-1244P	11/9/00
96.	60/247.010	2750-1245P	11/13/00
97.	60/247.051	2750-1246P	11/13/00
98.	60/247.050	2750-1247P	11/13/00
99.	60/247.049	2750-1248P	11/13/00
100.	60/234.179	2750-1253P	9/20/00
101.	60/234.178	2750-1254P	9/20/00
102.	60/234.233	2750-1259P	9/21/00
103.	60/234.217	2750-1260P	9/21/00
104.	60/234.220	2750-1261P	9/21/00
105.	60/234.968	2750-1262P	9/25/00
106.	60/234.979	2750-1263P	9/25/00
107.	60/234.974	2750-1264P	9/25/00
108.	60/235.118	2750-1265P	9/25/00
109.	60/234.949	2750-1266P	9/26/00
110.	60/235.577	2750-1267P	9/27/00
111.	60/235.934	2750-1268P	9/28/00
112.	60/236.380	2750-1269P	9/29/00
113.	60/236.732	2750-1270P	10/2/00
114.	60/237.035	2750-1271P	10/2/00
115.	60/237.379	2750-1272P	10/4/00
116.	60/237.505	2750-1273P	10/4/00
117.	60/237.686	2750-1274P	10/5/00
118.	60/238.473	2750-1275P	10/10/00
119.	60/238.472	2750-1276P	10/10/00
120.	60/238.456	2750-1277P	10/10/00
121.	60/238.421	2750-1278P	10/10/00
122.	60/239.091	2750-1279P	10/11/00
123.	60/239.245	2750-1280P	10/11/00
124.	60/240.862	2750-1281P	10/17/00
125.	60/240.863	2750-1282P	10/17/00
126.	60/241.368	2750-1283P	10/19/00
127.	60/241.367	2750-1284P	10/19/00
128.	60/241.751	2750-1304P	10/20/00
129.	60/241.750	2750-1305P	10/20/00
130.	60/242.065	2750-1306P	10/23/00
131.	60/242.072	2750-1307P	10/23/00

132.	60/242.686	2750-1320P	10/24/00
133.	60/242.705	2750-1321P	10/25/00
134.	60/242.706	2750-1322P	10/25/00
135.	60/243.289	2750-1323P	10/26/00
136.	60/243.288	2750-1324P	10/26/00
137.	60/243.398	2750-1325P	10/27/00
138.	60/243.478	2750-1326P	10/27/00
139.	60/243.723	2750-1327P	10/30/00
140.	60/243.735	2750-1328P	10/30/00
141.	60/244.691	2750-1341P	11/1/00
142.	60/244.747	2750-1342P	11/1/00
143.	60/244.923	2750-1343P	11/2/00
144.	60/244.920	2750-1344P	11/2/00
145.	60/245.164	2750-1345P	11/3/00
146.	60/245.165	2750-1346P	11/3/00
147.	60/248.198	2750-1348P	11/15/00
148.	60/248.197	2750-1349P	11/15/00
149.	60/248.555	2750-1350P	11/16/00
150.	60/249.256	2750-1351P	11/17/00
151.	60/249.257	2750-1352P	11/17/00
152.	60/249.454	2750-1353P	11/20/00
153.	60/249.453	2750-1354P	11/20/00
154.	60/252.080	2750-1355P	11/21/00
155.	60/252.464	2750-1356P	11/22/00
156.	60/252.465	2750-1357P	11/22/00
157.	60/252.598	2750-1358P	11/24/00
158.	60/245.676	2750-1359P	11/6/00
159.	60/245.576	2750-1360P	11/6/00
160.	60/252.590	2750-1361P	11/24/00
161.	60/253.140	2750-1362P	11/28/00
162.	60/253.722	2750-1363P	11/29/00
163.	60/253.748	2750-1364P	11/29/00
164.	60/250.356	2750-1365P	12/1/00
165.	60/250.46	2750-1366P	12/4/00
166.	60/251.387	2750-1367P	12/6/00
167.	60/251.504	2750-1368P	12/7/00
168.	60/251.508	2750-1369P	12/7/00
169.	60/251.853	2750-1370P	12/8/00
170.	60/251.854	2750-1371P	12/8/00
171.	60/254.174	2750-1372P	12/11/00
172.	60/254.196	2750-1373P	12/11/00
173.	60/254.891	2750-1374P	12/13/00
174.	60/256.503	2750-1375P	12/15/00
175.	60/255.415	2750-1376P	12/15/00
176.	60/255.891	2750-1377P	12/18/00
177.	60/255.892	2750-1378P	12/18/00
178.	60/256.306	2750-1379P	12/19/00

179.	60/256.929	2750-1381P	12/21/00
180.	60/257.978	2750-1382P	12/27/00
181.	60/258.880	2750-1384P	1/2/01
182.	60/262.389	2750-1388P	1/19/01
183.	60/262.359	2750-1389P	1/19/01
184.	60/264.026	2750-1391P	1/26/01
185.	60/264.027	2750-1392P	1/26/01
186.	60/264.282	2750-1393P	1/29/01
187.	60/264.257	2750-1394P	1/29/01
188.	60/266.468	2750-1402P	2/6/01
189.	60/266.469	2750-1403P	2/6/01
190.	60/266.863	2750-1404P	2/7/01
191.	60/267.425	2750-1406P	2/9/01
192.	60/267.430	2750-1407P	2/9/01
193.	60/267.426	2750-1408P	2/9/01
194.	60/267.707	2750-1409P	2/12/01
195.	60/267.706	2750-1410P	2/12/01
196.	60/268.366	2750-1412P	2/14/01
197.	60/268.921	2750-1413P	2/16/01
198.	60/269.890	2750-1414P	2/21/01
199.	60/269.891	2750-1415P	2/21/01
200.	60/269.892	2750-1416P	2/21/01
201.	60/269.893	2750-1417P	2/21/01
202.	60/270.122	2750-1418P	2/22/01
203.	60/270.913	2750-1420P	2/26/01
204.	60/270.912	2750-1421P	2/26/01
205.	60/271.724	2750-1424P	2/28/01
206.	60/271.725	2750-1425P	2/28/01
207.	60/272.467	2750-1427P	3/2/01
208.	60/272.783	2750-1428P	3/5/01
209.	60/273.554	2750-1429P	3/7/01
210.	60/273.553	2750-1430P	3/7/01
211.	60/273.552	2750-1431P	3/7/01
212.	60/227.793	2750-2116P	8/25/00
213.	60/228.031	2750-2117P	8/25/00
214.	60/228.028	2750-2118P	8/25/00
215.	60/228.027	2750-2119P	8/25/00
216.	60/228.026	2750-2121P	8/25/00
217.	60/228.038	2750-2122P	8/25/00
218.	60/228.036	2750-2123P	8/25/00
219.	60/227.790	2750-2124P	8/25/00
220.	60/228.039	2750-2125P	8/25/00
221.	60/228.030	2750-2126P	8/25/00
222.	60/228.032	2750-2127P	8/25/00
223.	60/228.149	2750-2128P	8/25/00
224.	60/228.040	2750-2129P	8/25/00
225.	60/227.777	2750-2130P	8/25/00

	226.	60/228,037	2750-2131P	8/25/00	
	227.	60/227,791	2750-2132P	8/25/00	
	228.	60/228,041	2750-2133P	8/25/00	

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Application 10/282,058 (2750-1535P) listed above is a continuation-in-part of Application Nos 09/940,258 (Attorney No. 2750-1466P) filed on August 24, 2001 and Application No. 10/162,726 (Attorney No. 2750-1529P) filed on June 6, 2002, the entire contents of both of these applications are hereby incorporated by reference.

Through application nos. 09/940,258 and 10/162,726, the present application also claims priority under 35 USC §119(e) and/or §120 of the following applications, the entire contents of which are also hereby incorporated by reference:

	Attorney No.	Filing Date	Appln. No.	
1.	2750-0550P	9/3/1999	09/391,631	which claims priority to
2.	2750-0300P	9/4/1998	60/099,671	and
3.	2750-0301P	9/4/1998	60/099,672	and
4.	2750-0302P	9/11/1998	60/099,933	and
5.	2750-0304P	9/17/1998	60/100,864	and
6.	2750-0305P	9/18/1998	60/101,042	and
7.	2750-0307P	9/24/1998	60/101,682	and
8.	2750-0308P	9/30/1998	60/102,533	and
9.	2750-0309P	9/30/1998	60/102,460	and
10.	2750-0310P	10/5/1998	60/103,116	and
11.	2750-0311P	10/5/1998	60/103,141	and

	Attorney No.	Filing Date	Appln. No.	
12.	2750-0314P	10/9/1998	60/103,574	and
13.	2750-0315P	10/13/1998	60/103,907	and
14.	2750-0324P	10/29/1998	60/106,105	and
15.	2750-0325P	10/30/1998	60/106,218	and
16.	2750-0327P	11/6/1998	60/107,282	and
17.	2750-0330P	11/10/1998	60/107,836	and
18.	2750-0332P	11/16/1998	60/108,526	and
19.	2750-0333P	11/17/1998	60/108,901	and
20.	2750-0336P	11/20/1998	60/109,267	and
21.	2750-0337P	11/23/1998	60/109,594	and
22.	2750-0341P	11/30/1998	60/110,263	and
23.	2750-0342P	12/1/1998	60/110,495	and
24.	2750-0343P	12/2/1998	60/110,626	and
25.	2750-0344P	12/3/1998	60/110,701	and
26.	2750-0345P	12/7/1998	60/111,339	and
27.	2750-0346P	12/9/1998	60/111,589	and
28.	2750-0349P	12/14/1998	60/112,096	and
29.	2750-0350P	12/15/1998	60/112,224	and
30.	2750-0351P	12/16/1998	60/112,624	and
31.	2750-0352P	12/17/1998	60/112,862	and
32.	2750-0363P	1/7/1999	60/115,152	and

	Attorney No.	Filing Date	Appln. No.	
33.	2750-0366P	1/7/1999	60/115,156	and
34.	2750-0369P	1/8/1999	60/115,365	and
35.	2750-0371P	1/11/1999	60/115,339	and
36.	2750-0373P	1/13/1999	60/115,847	and
37.	2750-0379P	1/21/1999	60/116,674	and
38.	2750-0382P	1/22/1999	60/116,962	and
39.	2750-0394P	2/18/1999	60/120,583	and
40.	2750-0395P	2/22/1999	60/121,072	and
41.	2750-0401P	3/2/1999	60/122,568	and
42.	2750-0411P	3/12/1999	60/123,941	
43.	2750-0565P	10/5/1999	09/413,198	which claims priority to
44.	2750-0310P	10/5/1998	60/103,116	and
45.	2750-0311P	10/5/1998	60/103,141	and
46.	2750-0312P	10/6/1998	60/103,215	and
47.	2750-0313P	10/8/1998	60/103,554	and
48.	2750-0314P	10/9/1998	60/103,574	and
49.	2750-0315P	10/13/1998	60/103,907	and
50.	2750-0316P	10/14/1998	60/104,268	and
51.	2750-0317P	10/16/1998	60/104,680	and
52.	2750-0318P	10/19/1998	60/104,828	and
53.	2750-	10/20/1998	60/105,000	and

	Attorney No.	Filing Date	Appln. No.	
	0319P	8	8	
54.	2750- 0320P	10/21/199 8	60/105,14 2	and
55.	2750- 0321P	10/22/199 8	60/105,53 3	and
56.	2750- 0322P	10/26/199 8	60/105,57 1	and
57.	2750- 0323P	10/27/199 8	60/105,81 5	and
58.	2750- 0324P	10/29/199 8	60/106,10 5	and
59.	2750- 0325P	10/30/199 8	60/106,21 8	
60.	2750- 0566P	10/5/1999	09/412,92 2	which claims priority to
61.	2750- 0310P	10/5/1998	60/103,11 6	and
62.	2750- 0311P	10/5/1998	60/103,14 1	and
63.	2750- 0312P	10/6/1998	60/103,21 5	and
64.	2750- 0313P	10/8/1998	60/103,55 4	and
65.	2750- 0314P	10/9/1998	60/103,57 4	and
66.	2750- 0315P	10/13/199 8	60/103,90 7	and
67.	2750- 0316P	10/14/199 8	60/104,26 8	and
68.	2750- 0317P	10/16/199 8	60/104,68 0	and
69.	2750- 0318P	10/19/199 8	60/104,82 8	and
70.	2750- 0319P	10/20/199 8	60/105,00 8	and
71.	2750- 0320P	10/21/199 8	60/105,14 2	and
72.	2750- 0321P	10/22/199 8	60/105,53 3	and
73.	2750- 0322P	10/26/199 8	60/105,57 1	and

	Attorney No.	Filing Date	Appln. No.	
74.	2750-0323P	10/27/1998	60/105,815	and
75.	2750-0324P	10/29/1998	60/106,105	and
76.	2750-0325P	10/30/1998	60/106,218	and
77.	2750-0326P	11/2/1998	60/106,685	and
78.	2750-0327P	11/6/1998	60/107,282	and
79.	2750-0328P	11/9/1998	60/107,720	and
80.	2750-0329P	11/9/1998	60/107,719	and
81.	2750-0330P	11/10/1998	60/107,836	and
82.	2750-0331P	11/12/1998	60/108,190	and
83.	2750-0332P	11/16/1998	60/108,526	and
84.	2750-0333P	11/17/1998	60/108,901	and
85.	2750-0334P	11/19/1998	60/109,124	and
86.	2750-0335P	11/19/1998	60/109,127	and
87.	2750-0336P	11/20/1998	60/109,267	and
88.	2750-0337P	11/23/1998	60/109,594	and
89.	2750-0338P	11/25/1998	60/110,053	and
90.	2750-0339P	11/25/1998	60/110,050	and
91.	2750-0340P	11/27/1998	60/110,158	and
92.	2750-0341P	11/30/1998	60/110,263	and
93.	2750-0342P	12/1/1998	60/110,495	and
94.	2750-0343P	12/2/1998	60/110,626	and

	Attorney No.	Filing Date	Appln. No.	
95.	2750-0344P	12/3/1998	60/110,701	and
96.	2750-0345P	12/7/1998	60/111,339	and
97.	2750-0346P	12/9/1998	60/111,589	and
98.	2750-0347P	12/10/1998	60/111,782	and
99.	2750-0348P	12/11/1998	60/111,812	and
100.	2750-0349P	12/14/1998	60/112,096	and
101.	2750-0350P	12/15/1998	60/112,224	and
102.	2750-0351P	12/16/1998	60/112,624	and
103.	2750-0352P	12/17/1998	60/112,862	and
104.	2750-0353P	12/18/1998	60/112,912	and
105.	2750-0354P	12/21/1998	60/113,248	and
106.	2750-0355P	12/22/1998	60/113,522	and
107.	2750-0356P	12/23/1998	60/113,826	and
108.	2750-0357P	12/28/1998	60/113,998	and
109.	2750-0358P	12/29/1998	60/114,384	and
110.	2750-0359P	12/30/1998	60/114,455	and
111.	2750-0360P	1/4/1999	60/114,740	and
112.	2750-0361P	1/6/1999	60/114,866	and
113.	2750-0362P	1/7/1999	60/115,153	and
114.	2750-0363P	1/7/1999	60/115,152	and
115.	2750-0364P	1/7/1999	60/115,151	and

	Attorney No.	Filing Date	Appln. No.	
116	2750-0365P	1/7/1999	60/115,15 5	and
117	2750-0366P	1/7/1999	60/115,15 6	and
118	2750-0367P	1/7/1999	60/115,15 4	and
119	2750-0368P	1/8/1999	60/115,36 4	and
120	2750-0369P	1/8/1999	60/115,36 5	and
121	2750-0371P	1/11/1999	60/115,33 9	and
122	2750-0372P	1/12/1999	60/115,51 8	and
123	2750-0373P	1/13/1999	60/115,84 7	and
124	2750-0374P	1/14/1999	60/115,90 5	and
125	2750-0375P	1/15/1999	60/116,38 3	and
126	2750-0376P	1/15/1999	60/116,38 4	and
127	2750-0377P	1/19/1999	60/116,32 9	and
128	2750-0378P	1/19/1999	60/116,34 0	and
129	2750-0379P	1/21/1999	60/116,67 4	and
130	2750-0380P	1/21/1999	60/116,67 2	and
131	2750-0381P	1/22/1999	60/116,96 0	and
132	2750-0382P	1/22/1999	60/116,96 2	and
133	2750-0383P	1/28/1999	60/117,75 6	and
134	2750-0384P	2/3/1999	60/118,67 2	and
135	2750-0385P	2/4/1999	60/118,80 8	and
136	2750-0386P	2/5/1999	60/118,77 8	and

	Attorney No.	Filing Date	Appln. No.	
137	2750-0387P	2/8/1999	60/119,029	and
138	2750-0388P	2/9/1999	60/119,332	and
139	2750-0389P	2/10/1999	60/119,462	and
140	2750-0391P	2/12/1999	60/119,922	and
141	2750-0392P	2/16/1999	60/120,196	and
142	2750-0393P	2/16/1999	60/120,198	and
143	2750-0394P	2/18/1999	60/120,583	and
144	2750-0395P	2/22/1999	60/121,072	and
145	2750-0396P	2/23/1999	60/121,334	and
146	2750-0397P	2/24/1999	60/121,470	and
147	2750-0398P	2/25/1999	60/121,704	and
148	2750-0399P	2/26/1999	60/122,107	and
149	2750-0400P	3/1/1999	60/122,266	and
150	2750-0401P	3/2/1999	60/122,568	and
151	2750-0402P	3/3/1999	60/122,611	and
152	2750-0403P	3/4/1999	60/121,775	and
153	2750-0404P	3/5/1999	60/123,534	and
154	2750-0406P	3/9/1999	60/123,680	and
155	2750-0408P	3/10/1999	60/123,715	and
156	2750-0409P	3/10/1999	60/123,726	and
157	2750-0410P	3/11/1999	60/124,263	and

	Attorney No.	Filing Date	Appln. No.	
158	2750-0411P	3/12/1999	60/123,941	
159	2750-0600P	10/28/1999	09/428,944	which claims priority to
160	2750-0326P	11/2/1998	60/106,685	and
161	2750-0327P	11/6/1998	60/107,282	and
162	2750-0328P	11/9/1998	60/107,720	and
163	2750-0329P	11/9/1998	60/107,719	and
164	2750-0330P	11/10/1999	60/107,836	and
165	2750-0331P	11/12/1999	60/108,190	and
166	2750-0332P	11/16/1999	60/108,526	and
167	2750-0333P	11/17/1999	60/108,901	and
168	2750-0334P	11/19/1999	60/109,124	and
169	2750-0335P	11/19/1999	60/109,127	and
170	2750-0336P	11/20/1999	60/109,267	and
171	2750-0337P	11/23/1999	60/109,594	and
172	2750-0338P	11/25/1999	60/110,053	and
173	2750-0339P	11/25/1999	60/110,050	and
174	2750-0340P	11/27/1999	60/110,158	and
175	2750-0341P	11/30/1999	60/110,263	
176	2750-0662P	12/1/1999	09/451,320	which claims priority to
177	2750-0342P	12/1/1998	60/110,495	and

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178	2750-0343P	12/2/1998	60/110,626	and
179	2750-0344P	12/3/1998	60/110,701	and
180	2750-0345P	12/7/1998	60/111,339	and
181	2750-0346P	12/9/1998	60/111,589	and
182	2750-0347P	12/10/1998	60/111,782	and
183	2750-0348P	12/11/1998	60/111,812	and
184	2750-0349P	12/14/1998	60/112,096	and
185	2750-0350P	12/15/1998	60/112,224	and
186	2750-0351P	12/16/1998	60/112,624	and
187	2750-0352P	12/17/1998	60/112,862	and
188	2750-0353P	12/18/1998	60/112,912	and
189	2750-0354P	12/21/1998	60/113,248	and
190	2750-0355P	12/22/1998	60/113,522	and
191	2750-0356P	12/23/1998	60/113,826	and
192	2750-0357P	12/28/1998	60/113,998	and
193	2750-0358P	12/29/1998	60/114,384	and
194	2750-0359P	12/30/1998	60/114,455	and
195	2750-0362P	1/7/1999	60/115,153	and
196	2750-0363P	1/7/1999	60/115,152	and
197	2750-0364P	1/7/1999	60/115,151	and
198	2750-0365P	1/7/1999	60/115,155	and

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199	2750-0366P	1/7/1999	60/115,156	and
200	2750-0368P	1/8/1999	60/115,364	and
201	2750-0381P	1/22/1999	60/116,960	
202	2750-0694P	2/3/2000	09/497,191	which claims priority to
203	2750-0384P	2/3/1999	60/118,672	and
204	2750-0385P	2/4/1999	60/118,808	and
205	2750-0386P	2/5/1999	60/118,778	and
206	2750-0387P	2/8/1999	60/119,029	and
207	2750-0388P	2/9/1999	60/119,332	and
208	2750-0389P	2/10/1999	60/119,462	and
209	2750-0391P	2/12/1999	60/119,922	and
210	2750-0392P	2/16/1999	60/120,196	and
211	2750-0393P	2/16/1999	60/120,198	and
212	2750-0394P	2/18/1999	60/120,583	and
213	2750-0395P	2/22/1999	60/121,072	and
214	2750-0396P	2/23/1999	60/121,334	and
215	2750-0397P	2/24/1999	60/121,470	and
216	2750-0398P	2/25/1999	60/121,704	and
217	2750-0399P	2/26/1999	60/122,107	
218	2750-0710P	3/1/2000	09/517,537	which claims priority to

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219	2750-0400P	3/1/1999	60/122,266	and
220	2750-0401P	3/2/1999	60/122,568	and
221	2750-0402P	3/3/1999	60/122,611	and
222	2750-0403P	3/4/1999	60/121,775	and
223	2750-0404P	3/5/1999	60/123,534	and
224	2750-0406P	3/9/1999	60/123,680	and
225	2750-0408P	3/10/1999	60/123,715	and
226	2750-0409P	3/10/1999	60/123,726	and
227	2750-0410P	3/11/1999	60/124,263	and
228	2750-0411P	3/12/1999	60/123,941	
229	2750-1102P	8/11/2000	09/637,565	which claims priority to
230	2750-0526P	8/12/1999	60/148,342	
231	2750-1103P	8/11/2000	09/637,564	which claims priority to
232	2750-0527P	8/12/1999	60/148,340	
233	2750-1104P	8/11/2000	09/637,792	which claims priority to
234	2750-0528P	8/12/1999	60/148,337	
235	2750-1419P	2/23/2001	09/790,663	which claims priority to
236	2750-0718P	2/25/2000	60/185,140	and
237	2750-0721P	2/28/2000	60/185,398	and

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238	2750-0724P	2/29/2000	60/185,750	
239	2750-1423P	3/1/2001	09/795,359	which claims priority to
240	2750-0727P	3/1/2000	60/186,277	and
241	2750-0731P	3/3/2000	60/186,670	and
242	2750-0735P	3/7/2000	60/187,379	and
243	2750-0738P	3/9/2000	60/187,985	and
244	2750-0741P	3/10/2000	60/188,174	and
245	2750-0744P	3/13/2000	60/188,687	and
246	2750-0747P	3/15/2000	60/189,460	and
247	2750-0754P	3/16/2000	60/189,958	and
248	2750-0757P	3/17/2000	60/189,965	and
249	2750-0760P	3/20/2000	60/190,090	and
250	2750-0765P	3/23/2000	60/191,549	and
251	2750-0768P	3/24/2000	60/191,826	and
252	2750-0771P	3/27/2000	60/192,420	and
253	2750-0774P	3/29/2000	60/192,855	and
254	2750-0777P	3/30/2000	60/193,243	and
255	2750-0780P	3/31/2000	60/193,469	
256	2750-1432P	3/16/2001	09/804,470	which claims priority to
257	2750-0750P	3/16/2000	60/190,120	and

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258	2750-0751P	3/16/2000	60/189,947	and
259	2750-0752P	3/16/2000	60/189,948	and
260	2750-0753P	3/16/2000	60/190,121	
261	2750-1434P	4/4/2001	09/824,790	which claims priority to
262	2750-0784P	4/6/2000	60/194,884	and
263	2750-0785P	4/4/2000	60/194,385	and
264	2750-0789P	4/5/2000	60/194,682	and
265	2750-0792P	4/5/2000	60/194,698	and
266	2750-0797P	4/7/2000	60/195,258	and
267	2750-0802P	4/11/2000	60/196,168	and
268	2750-0805P	4/12/2000	60/196,483	and
269	2750-0814P	4/14/2000	60/197,397	and
270	2750-0817P	4/17/2000	60/198,268	and
271	2750-0820P	4/19/2000	60/198,400	and
272	2750-0823P	4/20/2000	60/198,629	and
273	2750-0826P	4/21/2000	60/198,765	and
274	2750-0829P	4/24/2000	60/199,123	
275	2750-1437P	4/11/2001	09/832,192	which claims priority to
276	2750-0800P	4/12/2000	60/196,212	and
277	2750-0801P	4/11/2000	60/196,211	and

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278	2750-0810P	4/14/2000	60/197,869	and
279	2750-0811P	4/13/2000	60/196,213	and
280	2750-0812P	4/17/2000	60/197,870	and
281	2750-0813P	4/17/2000	60/197,871	and
282	2750-0844P	4/28/2000	60/200,373	and
283	2750-0846P	4/28/2000	60/200,773	
284	2750-1439P	4/26/2001	09/842,246	which claims priority to
285	2750-0832P	4/26/2000	60/200,034	
286	2750-1440P	5/1/2001	09/845,208	which claims priority to
287	2750-0843P	5/1/2000	60/200,763	and
288	2750-0845P	5/1/2000	60/201,016	and
289	2750-0847P	5/1/2000	60/200,762	and
290	2750-0848P	5/1/2000	60/200,761	and
291	2750-0867P	5/11/2000	60/203,671	and
292	2750-0868P	5/11/2000	60/203,672	and
293	2750-0869P	5/11/2000	60/203,669	and
294	2750-0870P	5/11/2000	60/203,622	
295	2750-1443P	5/1/2001	09/845,318	which claims priority to
296	2750-0842P	5/1/2000	60/201,018	and
297	2750-	5/17/2000	60/205,32	

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	0890P		5	
298	2750-1444P	5/1/2001	09/845,209	which claims priority to
299	2750-0841P	5/1/2000	60/201,017	and
300	2750-0889P	5/17/2000	60/205,233	
301	2750-1448P	6/1/2001	09/870,646	which claims priority to
302	2750-0918P	6/1/2000	60/208,648	
303	2750-1449P	6/1/2001	09/870,476	which claims priority to
304	2750-0919P	6/1/2000	60/208,324	and
305	2750-0922P	6/5/2000	60/208,919	and
306	2750-0925P	6/5/2000	60/208,917	and
307	2750-0929P	6/8/2000	60/210,008	
308	2750-1451P	6/1/2001	09/870,664	which claims priority to
309	2750-0921P	6/1/2000	60/208,312	and
310	2750-0924P	6/5/2000	60/208,918	and
311	2750-0927P	6/5/2000	60/208,920	and
312	2750-0931P	6/8/2000	60/210,006	and
313	2750-0933P	6/9/2000	60/210,564	and
314	2750-0936P	6/13/2000	60/211,214	and
315	2750-0963P	6/22/2000	60/213,249	and
316	2750-	6/27/2000	60/214,53	and

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	1036P		5	
317	2750- 1039P	6/28/2000	60/214,79 9	and
318	2750- 1041P	6/30/2000	60/215,12 7	
319	2750- 1453P	6/13/2001	09/878,97 4	which claims priority to
320	2750- 0937P	6/13/2000	60/211,21 0	and
321	2750- 0938P	6/15/2000	60/211,53 9	and
322	2750- 0956P	6/19/2000	60/212,41 4	and
323	2750- 0959P	6/20/2000	60/212,67 7	and
324	2750- 0960P	6/20/2000	60/212,71 3	and
325	2750- 0964P	6/22/2000	60/213,19 5	and
326	2750- 0965P	6/22/2000	60/213,22 1	and
327	2750- 0968P	6/27/2000	60/214,76 0	
328	2750- 1457P	7/12/2001	09/902,61 3	which claims priority to
329	2750- 1256P	8/1/2000	60/223,11 4	
330	2750- 1459P	7/13/2001	09/903,49 7	which claims priority to
331	2750- 1054P	7/13/2000	60/217,84 6	and
332	2750- 1258P	8/3/2000	60/223,09 9	
333	2750- 1461P	8/1/2001	09/918,55 6	which claims priority to
334	2750- 1049P	8/1/2000	60/223,11 5	

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335	2750-1462P	8/3/2001	09/920,626	which claims priority to
336	2750-1053P	8/3/2000	60/223,100	and
337	2750-1105P	8/18/2000	60/226,325	and
338	2750-1113P	8/31/2000	60/237,361	
339	2750-1464P	8/7/2001	09/922,661	which claims priority to
340	2750-1047P	8/7/2000	60/223,329	and
341	2750-1088P	8/31/2000	60/229,521	and
342	2750-1107P	8/18/2000	60/226,381	
343	2750-1469P	8/9/2001	09/924,702	which claims priority to
344	2750-1114P	8/9/2000	60/224,390	
345	2750-1472P	8/16/2001	09/930,244	which claims priority to
346	2750-1089P	8/31/2000	60/237,362	and
347	2750-1108P	8/16/2000	60/225,848	
348	2750-1473P	8/16/2001	09/930,231	which claims priority to
349	2750-1106P	8/16/2000	60/225,849	
350	2750-1475P	8/16/2001	09/930,223	which claims priority to
351	2750-1112P	8/16/2000	60/225,847	
352	2750-1477P	8/20/2001	09/931,911	which claims priority to

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353	2750-1091P	8/31/2000	60/229,520	
354	2750-1484P	2/26/2002	10/082,096	which is a 1.53(b) continuation of
355	2750-1422P	3/1/2001	09/795,347	which claims priority to
356	2750-0711P	3/2/2000	60/186,390	and
357	2750-0725P	3/1/2000	60/186,283	and
358	2750-0726P	3/1/2000	60/186,296	and
359	2750-0728P	3/2/2000	60/187,178	and
360	2750-0729P	3/2/2000	60/186,386	and
361	2750-0730P	3/2/2000	60/186,387	and
362	2750-0732P	3/3/2000	60/186,748	and
363	2750-0733P	3/3/2000	60/186,669	and
364	2750-0734P	3/7/2000	60/187,378	and
365	2750-0736P	3/8/2000	60/187,896	and
366	2750-0737P	3/8/2000	60/187,888	and
367	2750-0739P	3/10/2000	60/188,187	and
368	2750-0740P	3/10/2000	60/188,186	and
369	2750-0742P	3/10/2000	60/188,185	and
370	2750-0743P	3/10/2000	60/188,175	and
371	2750-0745P	3/14/2000	60/189,080	and
372	2750-0746P	3/14/2000	60/189,052	and
373	2750-	3/15/2000	60/189,46	and

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	0748P		1	
374	2750- 0749P	3/15/2000	60/189,46 2	and
375	2750- 0755P	3/16/2000	60/189,95 3	and
376	2750- 0756P	3/16/2000	60/189,95 9	and
377	2750- 0758P	3/20/2000	60/190,06 9	and
378	2750- 0759P	3/20/2000	60/190,07 0	and
379	2750- 0761P	3/20/2000	60/190,54 5	and
380	2750- 0762P	3/20/2000	60/190,08 9	and
381	2750- 0763P	3/22/2000	60/191,08 4	and
382	2750- 0764P	3/22/2000	60/191,09 7	and
383	2750- 0766P	3/23/2000	60/191,54 3	and
384	2750- 0767P	3/23/2000	60/191,54 5	and
385	2750- 0769P	3/24/2000	60/191,82 3	and
386	2750- 0770P	3/24/2000	60/191,82 5	and
387	2750- 0772P	3/27/2000	60/192,42 1	and
388	2750- 0773P	3/27/2000	60/192,30 8	and
389	2750- 0775P	3/29/2000	60/192,94 0	and
390	2750- 0776P	3/29/2000	60/192,94 1	and
391	2750- 0778P	3/30/2000	60/193,24 4	and
392	2750- 0779P	3/30/2000	60/193,24 5	and
393	2750- 0781P	3/31/2000	60/193,45 3	and
394	2750-	3/31/2000	60/193,45	

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	0782P		5	
395	2750- 1486P	2/28/2002	10/084,37 6	which is a 1.53(b) continuation of
396	2750- 1470P	8/9/2001	09/924,70 1	which claims priority to
397	2750- 1115P	8/9/2000	60/224,39 1	
398	2750- 1489P	3/4/2002	10/086,23 9	which is a 1.53(b) continuation of
399	2750- 1441P	5/1/2001	09/845,20 6	which claims priority to
400	2750- 0838P	5/2/2000	60/201,27 5	and
401	2750- 0839P	5/1/2000	60/200,87 9	and
402	2750- 0850P	5/2/2000	60/201,30 5	and
403	2750- 0857P	5/4/2000	60/201,74 0	and
404	2750- 0858P	5/4/2000	60/201,75 0	and
405	2750- 0860P	5/5/2000	60/202,11 2	and
406	2750- 0861P	5/5/2000	60/202,18 0	and
407	2750- 0862P	5/9/2000	60/202,91 4	and
408	2750- 0863P	5/9/2000	60/202,63 6	and
409	2750- 0865P	5/9/2000	60/202,91 9	and
410	2750- 0866P	5/9/2000	60/202,63 4	and
411	2750- 0878P	5/10/2000	60/202,96 8	and
412	2750- 0879P	5/10/2000	60/202,96 3	and
413	2750- 0881P	5/11/2000	60/203,45 7	and
414	2750-	5/11/2000	60/203,27	and

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	0882P		9	
415	2750- 0884P	5/12/2000	60/203,91 6	and
416	2750- 0885P	5/12/2000	60/203,91 5	and
417	2750- 0887P	5/15/2000	60/204,38 8	and
418	2750- 0888P	5/15/2000	60/204,12 2	and
419	2750- 0891P	5/16/2000	60/204,56 8	and
420	2750- 0892P	5/16/2000	60/204,56 9	and
421	2750- 0893P	5/17/2000	60/204,83 0	and
422	2750- 0894P	5/17/2000	60/204,82 9	and
423	2750- 0895P	5/18/2000	60/205,20 1	and
424	2750- 0896P	5/18/2000	60/205,05 8	and
425	2750- 0897P	5/19/2000	60/205,24 2	and
426	2750- 0898P	5/19/2000	60/205,24 3	and
427	2750- 0900P	5/22/2000	60/205,57 2	and
428	2750- 0901P	5/22/2000	60/205,57 6	and
429	2750- 0902P	5/23/2000	60/206,31 6	and
430	2750- 0903P	5/23/2000	60/206,31 9	and
431	2750- 0904P	5/24/2000	60/206,55 3	and
432	2750- 0905P	5/24/2000	60/206,54 5	and
433	2750- 0907P	5/26/2000	60/207,36 7	and
434	2750- 0908P	5/26/2000	60/207,24 3	and
435	2750-	5/26/2000	60/207,23	and

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	0910P		9	
436	2750- 0911P	5/26/2000	60/207,35 4	and
437	2750- 0913P	5/30/2000	60/207,45 2	and
438	2750- 0914P	5/30/2000	60/207,32 9	
439	2750- 1490P	3/7/2002	10/091,52 7	which is a 1.53(b) continuation of
440	2750- 1438P	4/26/2001	09/842,08 8	which claims priority to
441	2750- 0833P	4/26/2000	60/200,03 1	
442	2750- 1492P	3/13/2002	10/095,46 5	which is a 1.53(b) continuation of
443	2750- 1435P	4/4/2001	09/824,88 2	which claims priority to
444	2750- 0786P	4/4/2000	60/194,40 4	and
445	2750- 0787P	4/4/2000	60/194,39 8	and
446	2750- 0790P	4/5/2000	60/194,68 3	and
447	2750- 0791P	4/5/2000	60/194,69 7	and
448	2750- 0793P	4/6/2000	60/194,87 4	and
449	2750- 0794P	4/6/2000	60/194,87 2	and
450	2750- 0795P	4/6/2000	60/194,88 5	and
451	2750- 0796P	4/6/2000	60/195,04 5	and
452	2750- 0798P	4/7/2000	60/195,28 3	and
453	2750- 0799P	4/7/2000	60/195,25 7	and
454	2750- 0803P	4/11/2000	60/196,16 9	and
455	2750-	4/11/2000	60/196,08	and

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	0804P		9	
456	2750-0806P	4/12/2000	60/196,487	and
457	2750-0807P	4/12/2000	60/196,289	and
458	2750-0808P	4/12/2000	60/196,485	and
459	2750-0809P	4/12/2000	60/196,486	and
460	2750-0815P	4/17/2000	60/197,687	and
461	2750-0816P	4/17/2000	60/197,678	and
462	2750-0818P	4/17/2000	60/198,133	and
463	2750-0819P	4/17/2000	60/197,671	and
464	2750-0821P	4/19/2000	60/198,386	and
465	2750-0822P	4/19/2000	60/198,373	and
466	2750-0824P	4/20/2000	60/198,619	and
467	2750-0825P	4/20/2000	60/198,623	and
468	2750-0827P	4/21/2000	60/198,767	and
469	2750-0828P	4/21/2000	60/198,763	and
470	2750-0830P	4/24/2000	60/199,124	and
471	2750-0831P	4/24/2000	60/199,122	and
472	2750-0834P	4/26/2000	60/199,828	and
473	2750-0835P	4/26/2000	60/199,818	and
474	2750-0836P	4/27/2000	60/200,103	and
475	2750-0837P	4/27/2000	60/200,102	

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476	2750-1493P	3/15/2002	10/097,600	which is a 1.53(b) continuation of
477	2750-1436P	4/12/2001	09/832,934	which is a 1.53(b) continuation of
478	2750-1101P	8/11/2000	09/637,820	which claims priority to
479	2750-0525P	8/12/1999	60/148,347	
480	2750-1494P	3/15/2002	10/097,295	which is a 1.53(b) continuation of
481	2750-1452P	6/15/2001	09/881,096	which claims priority to
482	2750-0940P	6/15/2000	60/211,538	and
483	2750-0958P	6/19/2000	60/212,623	and
484	2750-0961P	6/20/2000	60/212,727	and
485	2750-0967P	6/22/2000	60/213,270	and
486	2750-0970P	6/27/2000	60/214,524	
487	2750-1495P	3/18/2002		which is a 1.53(b) continuation of
488	2750-1446P	6/1/2001	09/870,699	which claims priority to
489	2750-0916P	6/1/2000	60/208,421	
490	2750-1496P	3/18/2002	10/098,506	which is a 1.53(b) continuation of
491	2750-1445P	6/1/2001	09/870,713	which claims priority to
492	2750-0915P	6/2/2000	60/209,338	
493	2750-1499P	3/25/2002	10/103,845	which is a 1.53(b) continuation of
494	2750-1454P	7/5/2001	09/898,063	which claims priority to

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495	2750-1043P	7/5/2000	60/216,362	and
496	2750-1046P	7/11/2000	60/217,384	and
497	2750-1057P	7/18/2000	60/219,033	and
498	2750-1079P	7/25/2000	60/220,811	and
499	2750-1081P	7/25/2000	60/220,652	
500	2750-1501P	3/27/2002	10/106,718	which is a 1.53(b) continuation of
501	2750-1455P	7/5/2001	09/898,064	which claims priority to
502	2750-1042P	7/5/2000	60/216,361	and
503	2750-1045P	7/11/2000	60/217,476	and
504	2750-1056P	7/18/2000	60/219,004	and
505	2750-1059P	7/25/2000	60/220,647	and
506	2750-1080P	7/25/2000	60/220,484	
507	2750-1502P	4/1/2002		which is a 1.53(b) continuation of
508	2750-1458P	7/12/2001	09/902,614	which claims priority to
509	2750-1052P	7/12/2000	60/218,548	and
510	2750-1257P	8/3/2000	60/223,116	
511	2750-1504P	4/10/2002		which is a 1.53(b) continuation of
512	2750-1474P	8/16/2001	09/930,214	which claims priority to
513	2750-1091P	8/31/2000	60/229,520	and
514	2750-	8/16/2000	60/225,85	

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	1110P		0	
515	2750-1506P	4/17/2002		which is a 1.53(b) continuation of
516	2750-1463P	8/3/2001	09/921,135	which claims priority to
517	2750-1051P	8/3/2000	60/223,101	and
518	2750-1090P	8/31/2000	60/229,519	and
519	2750-1109P	8/18/2000	60/226,323	
520	2750-1507P	4/17/2002		which is a 1.53(b) continuation of
521	2750-1456P	7/11/2001	09/902,093	which claims priority to
522	2750-1044P	7/11/2000	60/217,385	and
523	2750-1055P	7/18/2000	60/219,021	and
524	2750-1058P	7/25/2000	60/220,814	and
525	2750-1083P	8/14/2000	60/224,516	and
526	2750-1085P	8/15/2000	60/225,302	and
527	2750-1087P	8/21/2000	60/226,725	and
528	2750-1163P	8/23/2000	60/227,026	and
529	2750-1226P	8/30/2000	60/228,897	
530	2750-1508P	4/17/2002		which is a 1.53(b) continuation of
531	2750-1460P	7/13/2001	09/903,988	which claims priority to
532	2750-1048P	7/14/2000	60/218,566	and
533	2750-1255P	8/3/2000	60/223,098	

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534	2750-1509P	4/17/2002		which is a 1.53(b) continuation of
535	2750-1471P	8/14/2001	09/928,372	which claims priority to
536	2750-1082P	8/14/2000	60/224,517	and
537	2750-1084P	8/15/2000	60/225,303	and
538	2750-1086P	8/21/2000	60/226,452	and
539	2750-1162P	8/23/2000	60/227,024	and
540	2750-1225P	8/30/2000	60/228,898	
541	2750-1510P	4/18/2002		which is a 1.53(b) continuation of
542	2750-1476P	8/17/2001	09/931,043	which claims priority to
543	2750-1111P	8/18/2000	60/226,324	
544	2750-1512P	4/29/2002		which is a 1.53(b) continuation of
545	2750-1398P	1/31/2001	09/774,340	
546	2750-1518P	4/29/2002		which is a 1.53(b) continuation of
547	2750-1285P	10/19/2000	09/691,039	
548	2750-1519P	4/29/2002		which is a 1.53(b) continuation of
549	2750-1380P	12/21/2000	09/741,043	
550	2750-1520P	4/29/2002		which is a 1.53(b) continuation of
551	2750-1289P	10/19/2000	09/691,045	

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552	2750-1521P	4/29/2002		which is a 1.53(b) continuation of
553	2750-1293P	10/19/2000	09/691,019	
554	2750-1522P	4/29/2002		which is a 1.53(b) continuation of
555	2750-1447P	6/1/2001	09/870,675	which claims priority to
556	2750-0917P	6/2/2000	60/208,649	
557	2750-1524P	5/6/2002		which is a 1.53(b) continuation of
558	2750-0683P	1/4/2000	09/478,081	which claims priority to
559	2750-0360P	1/4/1999	60/114,740	and
560	2750-0361P	1/6/1999	60/114,866	and
561	2750-0367P	1/7/1999	60/115,154	and
562	2750-0369P	1/8/1999	60/115,365	and
563	2750-0371P	1/11/1999	60/115,339	and
564	2750-0372P	1/12/1999	60/115,518	and
565	2750-0373P	1/13/1999	60/115,847	and
566	2750-0374P	1/14/1999	60/115,905	and
567	2750-0375P	1/15/1999	60/116,383	and
568	2750-0376P	1/15/1999	60/116,384	and
569	2750-0377P	1/19/1999	60/116,329	and
570	2750-0378P	1/19/1999	60/116,340	and
571	2750-	1/21/1999	60/116,67	and

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	0379P		4	
572	2750- 0380P	1/21/1999	60/116,67 2	and
573	2750- 0382P	1/22/1999	60/116,96 2	and
574	2750- 0383P	1/28/1999	60/117,75 6	
575	2750- 1133P	08/25/200 05	60/228,02 5	
576	2750- 1134P	08/25/200 01	60/227,78 1	
577	2750- 1135P	08/25/200 03	60/227,78 3	
578	2750- 1136P	08/25/200 01	60/227,73 1	
579	2750- 1137P	08/25/200 02	60/227,73 2	
580	2750- 1138P	08/25/200 09	60/227,72 9	
581	2750- 1139P	08/25/200 07	60/228,16 7	
582	2750- 1140P	08/25/200 04	60/227,73 4	
583	2750- 1141P	08/25/200 02	60/227,79 2	
584	2750- 1142P	08/25/200 03	60/227,73 3	
585	2750- 1143P	08/25/200 00	60/227,73 0	
586	2750- 1144P	08/25/200 00	60/227,77 0	
587	2750- 1145P	08/25/200 08	60/227,72 8	
588	2750- 1146P	08/25/200 03	60/227,77 3	
589	2750- 1147P	08/25/200 03	60/228,03 3	
590	2750- 1148P	08/25/200 04	60/228,02 4	
591	2750- 1149P	08/25/200 09	60/227,76 9	

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592	2750- 1150P	08/25/200 00	60/227,78 00	
593	2750- 1151P	08/25/200 05	60/227,72 05	
594	2750- 1152P	08/25/200 04	60/227,77 04	
595	2750- 1164P	08/25/200 03	60/228,16 03	
596	2750- 1165P	08/25/200 06	60/228,04 06	
597	2750- 1166P	08/25/200 08	60/228,09 08	
598	2750- 1167P	08/25/200 07	60/228,04 07	
599	2750- 1168P	08/25/200 02	60/228,05 02	
600	2750- 1169P	08/25/200 09	60/228,04 09	
601	2750- 1170P	08/25/200 02	60/228,13 02	
602	2750- 1171P	08/25/200 02	60/228,15 02	
603	2750- 1172P	08/25/200 05	60/228,13 05	
604	2750- 1173P	08/25/200 02	60/228,32 02	
605	2750- 1174P	08/25/200 06	60/228,15 06	
606	2750- 1175P	08/25/200 03	60/228,32 03	
607	2750- 1176P	08/25/200 03	60/228,13 03	
608	2750- 1177P	08/25/200 00	60/228,32 00	
609	2750- 1178P	08/25/200 09	60/228,15 09	
610	2750- 1179P	08/25/200 01	60/228,15 01	
611	2750- 1180P	08/25/200 02	60/228,20 02	
612	2750- 1181P	08/25/200 08	60/228,20 08	

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613	2750-1182P	08/25/2000	60/228,1503	
614	2750-1183P	08/25/2000	60/228,1709	
615	2750-1184P	08/25/2000	60/228,1800	
616	2750-1185P	08/25/2000	60/228,2009	
617	2750-1186P	08/25/2000	60/228,1708	
618	2750-1187P	08/25/2000	60/228,1707	
619	2750-1188P	08/25/2000	60/227,9706	
620	2750-1189P	08/25/2000	60/228,2007	
621	2750-1190P	08/25/2000	60/228,0408	
622	2750-1191P	08/25/2000	60/228,0906	
623	2750-1192P	08/25/2000	60/227,9302	
624	2750-1193P	08/25/2000	60/227,9306	
625	2750-1194P	08/25/2000	60/228,0404	
626	2750-1195P	08/25/2000	60/228,2106	
627	2750-1196P	08/25/2000	60/228,0605	
628	2750-1197P	08/25/2000	60/227,9705	
629	2750-1198P	08/25/2000	60/228,1801	
630	2750-1199P	08/25/2000	60/228,0603	
631	2750-1200P	08/25/2000	60/228,0604	
632	2750-1201P	08/25/2000	60/228,0505	
633	2750-1202P	08/25/2000	60/228,0704	

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634	2750- 1203P	08/25/200 09	60/227,93	
635	2750- 1204P	08/25/200 05	60/227,95	
636	2750- 1205P	08/25/200 03	60/228,05	
637	2750- 1206P	08/25/200 08	60/227,97	
638	2750- 1207P	08/25/200 02	60/227,98	
639	2750- 1208P	08/25/200 09	60/228,18	
640	2750- 1209P	08/25/200 04	60/228,05	
641	2750- 1210P	08/25/200 04	60/228,16	
642	2750- 1211P	08/25/200 01	60/228,16	
643	2750- 1212P	08/25/200 05	60/228,16	
644	2750- 1213P	08/25/200 01	60/228,22	
645	2750- 1214P	08/25/200 00	60/228,24	
646	2750- 1215P	08/25/200 09	60/227,97	
647	2750- 1216P	08/25/200 04	60/227,95	
648	2750- 1217P	08/25/200 07	60/228,21	
649	2750- 1218P	08/25/200 09	60/227,92	
650	2750- 1219P	08/25/200 03	60/228,04	
651	2750- 1220P	08/25/200 01	60/227,93	
652	2750- 1221P	08/25/200 07	60/228,18	
653	2750- 1222P	08/25/200 01	60/228,06	
654	2750- 1223P	08/25/200 00	60/228,15	

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655	2750- 1224P	08/25/200 0		
656	2750- 2116P	08/25/200 03	60/227,79	
657	2750- 2117P	08/25/200 01	60/228,03	
658	2750- 2118P	08/25/200 08	60/228,02	
659	2750- 2119P	08/25/200 07	60/228,02	
660	2750- 2121P	08/25/200 06	60/228,02	
661	2750- 2122P	08/25/200 08	60/228,03	
662	2750- 2123P	08/25/200 06	60/228,03	
663	2750- 2124P	08/25/200 00	60/227,79	
664	2750- 2125P	08/25/200 09	60/228,03	
665	2750- 2126P	08/25/200 00	60/228,03	
666	2750- 2127P	08/25/200 02	60/228,03	
667	2750- 2128P	08/25/200 09	60/228,14	
668	2750- 2129P	08/25/200 00	60/228,04	
669	2750- 2130P	08/25/200 07	60/227,77	
670	2750- 2131P	08/25/200 07	60/228,03	
671	2750- 2132P	08/25/200 01	60/227,79	
672	2750- 2133P	08/25/200 01	60/228,04	
673	2750- 1157P	09/06/200 00	60/231,84	
674	2750- 1158P	09/06/200 07	60/231,83	
675	2750- 1159P	09/06/200 03	60/231,83	

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676	2750- 1160P	09/06/200 05	60/231,83	
677	2750- 1161P	09/06/200 04	60/231,83	
678	2750- 1227P	09/06/200 00	60/230,43	
679	2750- 1228P	09/06/200 04	60/230,43	
680	2750- 1229P	09/13/200 04	60/232,04	
681	2750- 1230P	09/13/200 03	60/232,04	
682	2750- 1231P	09/15/200 08	60/232,85	
683	2750- 1232P	09/15/200 05	60/232,86	
684	2750- 1233P	09/18/200 01	60/233,62	
685	2750- 1234P	09/18/200 04	60/233,63	
686	2750- 1253P	09/20/200 09	60/234,17	
687	2750- 1254P	09/20/200 08	60/234,17	
688	2750- 1259P	09/21/200 03	60/234,23	
689	2750- 1260P	09/21/200 07	60/234,21	
690	2750- 1261P	09/21/200 00	60/234,22	
691	2750- 1262P	09/25/200 08	60/234,96	
692	2750- 1263P	09/25/200 09	60/234,97	
693	2750- 1264P	09/25/200 04	60/234,97	
694	2750- 1265P	09/25/200 08	60/235,11	
695	2750- 1266P	09/26/200 09	60/234,94	
696	2750- 1267P	09/27/200 07	60/235,57	

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697	2750- 1268P	09/28/200 04	60/235,93	
698	2750- 1269P	09/29/200 00	60/236,38	
699	2750- 1270P	10/02/200 02	60/236,73	
700	2750- 1271P	10/02/200 05	60/237,03	
701	2750- 1272P	10/04/200 09	60/237,37	
702	2750- 1273P	10/04/200 05	60/237,50	
703	2750- 1274P	10/05/200 06	60/237,68	
704	2750- 1275P	10/10/200 03	60/238,47	
705	2750- 1276P	10/10/200 02	60/238,47	
706	2750- 1277P	10/10/200 06	60/238,45	
707	2750- 1278P	10/10/200 01	60/238,42	
708	2750- 1279P	10/11/200 01	60/239,09	
709	2750- 1280P	10/11/200 05	60/239,24	
710	2750- 1281P	10/17/200 02	60/240,86	
711	2750- 1282P	10/17/200 03	60/240,86	
712	2750- 1283P	10/19/200 08	60/241,36	
713	2750- 1284P	10/19/200 07	60/241,36	
714	2750- 1286P	10/19/200 00	09/691,02	
715	2750- 1287P	10/19/200 04	09/691,04	
716	2750- 1288P	10/19/200 08	09/691,02	
717	2750- 1290P	10/19/200 06	09/691,05	

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718	2750- 1291P	10/19/200 08	09/691,03	
719	2750- 1292P	10/19/200 01	09/691,03	
720	2750- 1294P	10/19/200 08	09/691,01	
721	2750- 1304P	10/20/200 01	60/241,75	
722	2750- 1305P	10/20/200 00	60/241,75	
723	2750- 1306P	10/23/200 05	60/242,06	
724	2750- 1307P	10/23/200 02	60/242,07	
725	2750- 1320P	10/24/200 06	60/242,68	
726	2750- 1321P	10/25/200 05	60/242,70	
727	2750- 1322P	10/25/200 06	60/242,70	
728	2750- 1323P	10/26/200 09	60/243,28	
729	2750- 1324P	10/26/200 08	60/243,28	
730	2750- 1325P	10/27/200 08	60/243,39	
731	2750- 1326P	10/27/200 08	60/243,47	
732	2750- 1327P	10/30/200 03	60/243,72	
733	2750- 1328P	10/30/200 05	60/243,73	
734	2750- 1341P	11/01/200 01	60/244,69	
735	2750- 1342P	11/01/200 07	60/244,74	
736	2750- 1343P	11/02/200 03	60/244,92	
737	2750- 1344P	11/02/200 00	60/244,92	
738	2750- 1345P	11/03/200 04	60/245,16	

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739	2750- 1346P	11/03/200 05	60/245,16	
740	2750- 1359P	11/06/200 06	60/245,67	
741	2750- 1360P	11/06/200 06	60/245,57	
742	2750- 1244P	11/09/200 02	60/246,73	
743	2750- 1245P	11/13/200 00	60/247,01	
744	2750- 1246P	11/13/200 01	60/247,05	
745	2750- 1247P	11/13/200 00	60/247,05	
746	2750- 1248P	11/13/200 09	60/247,04	
747	2750- 1348P	11/15/200 08	60/248,19	
748	2750- 1349P	11/15/200 07	60/248,19	
749	2750- 1350P	11/16/200 05	60/248,55	
750	2750- 1351P	11/17/200 06	60/249,25	
751	2750- 1352P	11/17/200 07	60/249,25	
752	2750- 1353P	11/20/200 04	60/249,45	
753	2750- 1354P	11/20/200 03	60/249,45	
754	2750- 1355P	11/21/200 00	60/252,08	
755	2750- 1356P	11/22/200 04	60/252,46	
756	2750- 1357P	11/22/200 05	60/252,46	
757	2750- 1358P	11/24/200 08	60/252,59	
758	2750- 1361P	11/24/200 00	60/252,59	
759	2750- 1362P	11/28/200 00	60/253,14	

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760	2750- 1363P	11/29/200 02	60/253,72	
761	2750- 1364P	11/29/200 08	60/253,74	
762	2750- 1365P	12/01/200 06	60/250,35	
763	2750- 1366P	12/04/200 04	60/250,46	
764	2750- 1367P	12/06/200 07	60/251,38	
765	2750- 1368P	12/07/200 04	60/251,50	
766	2750- 1369P	12/07/200 08	60/251,50	
767	2750- 1370P	12/08/200 03	60/251,85	
768	2750- 1371P	12/08/200 04	60/251,85	
769	2750- 1372P	12/11/200 04	60/254,17	
770	2750- 1373P	12/11/200 06	60/254,19	
771	2750- 1374P	12/13/200 01	60/254,89	
772	2750- 1375P	12/15/200 03	60/256,50	
773	2750- 1376P	12/15/200 05	60/255,41	
774	2750- 1377P	12/18/200 01	60/255,89	
775	2750- 1378P	12/18/200 02	60/255,89	
776	2750- 1379P	12/19/200 06	60/256,30	
777	2750- 1381P	12/21/200 09	60/256,92	
778	2750- 1382P	12/27/200 08	60/257,97	
779	2750- 1383P	12/29/200 04	09/750,04	
780	2750- 1384P	01/02/200 10	60/258,88	

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781	2750- 1385P	01/02/200 1 0	09/750,91	
782	2750- 1386P	01/03/200 1 3	09/752,82	
783	2750- 1153P	01/05/200 1 4	09/754,18	
784	2750- 1154P	01/05/200 1 5	09/754,18	
785	2750- 1388P	01/19/200 1 9	60/262,38	
786	2750- 1389P	01/19/200 1 9	60/262,35	
787	2750- 1391P	01/26/200 1 6	60/264,02	
788	2750- 1392P	01/26/200 1 7	60/264,02	
789	2750- 1393P	01/29/200 1 2	60/264,28	
790	2750- 1394P	01/29/200 1 7	60/264,25	
791	2750- 1395P	01/31/200 1 6	09/774,10	
792	2750- 1396P	01/31/200 1 9	09/774,08	
793	2750- 1397P	01/31/200 1 0	09/774,09	
794	2750- 1399P	02/01/200 1 0	09/775,87	
795	2750- 1400P	02/01/200 1 4	09/776,01	
796	2750- 1402P	02/06/200 1 8	60/266,46	
797	2750- 1403P	02/06/200 1 9	60/266,46	
798	2750- 1404P	02/07/200 1 3	60/266,86	
799	2750- 1405P	02/08/200 1 4	09/778,73	
800	2750- 1406P	02/09/200 1 5	60/267,42	
801	2750- 1407P	02/09/200 1 0	60/267,43	

	Attorney No.	Filing Date	Appln. No.	
802	2750- 1408P	02/09/200 1 6	60/267,42	
803	2750- 1409P	02/12/200 1 7	60/267,70	
804	2750- 1410P	02/12/200 1 6	60/267,70	
805	2750- 1412P	02/14/200 1 6	60/268,36	
806	2750- 1413P	02/16/200 1 1	60/268,92	
807	2750- 1414P	02/21/200 1 0	60/269,89	
808	2750- 1415P	02/21/200 1 1	60/269,89	
809	2750- 1416P	02/21/200 1 2	60/269,89	
810	2750- 1417P	02/21/200 1 3	60/269,89	
811	2750- 1418P	02/22/200 1 2	60/270,12	
812	2750- 1420P	02/26/200 1 3	60/270,91	
813	2750- 1421P	02/26/200 1 2	60/270,91	
814	2750- 1424P	02/28/200 1 4	60/271,72	
815	2750- 1425P	02/28/200 1 5	60/271,72	
816	2750- 1427P	03/02/200 1 7	60/272,46	
817	2750- 1428P	03/05/200 1 3	60/272,78	
818	2750- 1429P	03/07/200 1 4	60/273,55	
819	2750- 1430P	03/07/200 1 3	60/273,55	
820	2750- 1431P	03/07/200 1 2	60/273,55	
821	2750- 1433P	04/02/200 1 2	09/823,08	
822	2750- 1480P	08/24/200 1 0	09/940,23	

Number 28

Application No. 10/376,785 (attorney no. 2750-1551P) listed above claims priority under 35 USC §119(e) of the following application, the entire contents of which are also hereby incorporated by reference:

Country	Attorney No.	Appln. No.	Filed
United States	2750-1485P	60/361,089	March 1, 2002

Number 29

Application No. 10/376,797 (attorney no. 2750-1552P) listed above claims priority under 35 USC §119(e) of the following application, the entire contents of which are also hereby incorporated by reference:

Country	Attorney No.	Appln. No.	Filed
United States	2750-1487P	60/361,110	March 1, 2002

Number 30

Application No. 09/513,996 (attorney no. 2750-0709P) listed above is a continuation-in-part of the following provisional applications, the entire contents of which are hereby incorporated by reference, and the present application also claims priority of these provisional applications under 35 USC §119(e):

Country	Filing Date	Attorney No.	Client No.	Application No.
United States	2/25/99	2750-0390P	80090.001	60/121,825
United States	3/5/99	2750-0405P	80105.001	60/123,180
United States	3/9/99	2750-0407P	80107.001	60/123,548
United States	3/23/99	2750-0412P	80112.001	60/125,788
United States	3/25/99	2750-0413P	80113.001	60/126,264
United States	3/29/99	2750-0414P	80114.001	60/126,785
United States	4/1/99	2750-0415P	80115.001	60/127,462
United States	4/6/99	2750-0416P	91000.001	60/128,234
United States	4/8/99	2750-0417P	91001.001	60/128,714
United States	4/16/99	2750-0418P	80118.001	60/129,845
United States	4/19/99	2750-0420P	80120.001	60/130,077

Country	Filing Date	Attorney No.	Client No.	Application No.
United States	4/21/99	2750-0421P	80121.001	60/130,449
United States	4/23/99	2750-0422P	80122.001	60/130,891
United States	4/23/99	2750-0303P	80115.002	60/130,510
United States	4/28/99	2750-0423P	80123.001	60/131,449
United States	4/30/99	2750-0424P	80124.001	60/132,407
United States	4/30/99	2750-0425P	80125.001	60/132,048
United States	5/4/99	2750-0426P	80126.001	60/132,484
United States	5/5/99	2750-0427P	80127.001	60/132,485
United States	5/6/99	2750-0428P	91002.001	60/132,487
United States	5/6/99	2750-0429P	80129.001	60/132,486
United States	5/7/99	2750-0430P	80130.001	60/132,863
United States	5/11/99	2750-0431P	80131.001	60/134,256
United States	5/14/99	2750-0433P	00025.001	60/134,221
United States	5/14/99	2750-0435P	80117.001	60/134,218
United States	5/14/99	2750-0432P	91006.001	60/134,370
United States	5/14/99	2750-0434P	80116.001	60/134,219
United States	5/18/99	2750-0436P	91007.001	60/134,768
United States	5/19/99	2750-0437P	91008.001	60/134,941
United States	5/20/99	2750-0438P	91009.001	60/135,124
United States	5/21/99	2750-0439P	91010.001	60/135,353
United States	5/24/99	2750-0440P	91011.001	60/135,629
United States	5/25/99	2750-0441P	91012.001	60/136,021
United States	5/27/99	2750-0442P	91013.001	60/136,392
United States	5/28/99	2750-0444P	91014.001	60/136,782
United States	6/1/99	2750-0445P	91015.001	60/137,222
United States	6/3/99	2750-0446P	91016.001	60/137,528
United States	6/4/99	2750-0447P	91017.001	60/137,502
United States	6/7/99	2750-0449P	91018.001	60/137,724
United States	6/8/99	2750-0450P	91019.001	60/138,094
United States	6/10/99	2750-0457P	00033.001	60/138,540
United States	6/10/99	2750-0458P	00033.002	60/138,847
United States	6/14/99	2750-0463P	00034.001	60/139,119
United States	6/16/99	2750-0462P	80132.012	60/139,452
United States	6/16/99	2750-0461P	80132.011	60/139,453
United States	6/17/99	2750-0464P	00037.001	60/139,492
United States	6/18/99	2750-0452P	80132.004	60/139,461
United States	6/18/99	2750-0466P	00039.001	60/139,750
United States	6/18/99	2750-0459P	80132.009	60/139,463
United States	6/18/99	2750-0454P	80132.006	60/139,457
United States	6/18/99	2750-0451P	80132.003	60/139,459
United States	6/18/99	2750-0453P	80132.005	60/139,462
United States	6/18/99	2750-0460P	80132.010	60/139,455

Country	Filing Date	Attorney No.	Client No.	Application No.
United States	6/18/99	2750-0443P	80132.001	60/139,458
United States	6/18/99	2750-0448P	80132.002	60/139,454
United States	6/18/99	2750-0456P	80132.008	60/139,456
United States	6/18/99	2750-0455P	80132.007	60/139,460
United States	6/18/99	2750-0465P	00038.001	60/139,763
United States	6/21/99	2750-0467P	00042.001	60/139,817
United States	6/22/99	2750-0468P	00043.001	60/139,899
United States	6/23/99	2750-0469P	00044.001	60/140,354
United States	6/23/99	2750-0470P	00042.002	60/140,353
United States	6/24/99	2750-0471P	00045.001	60/140,695
United States	6/28/99	2750-0472P	00046.001	60/140,823
United States	6/29/99	2750-0473P	00048.001	60/140,991
United States	6/30/99	2750-0474P	00049.001	60/141,287
United States	7/1/99	2750-0476P	00051.001	60/142,154
United States	7/1/99	2750-0475P	00050.001	60/141,842
United States	7/2/99	2750-0477P	00052.001	60/142,055
United States	7/6/99	2750-0478P	00053.001	60/142,390
United States	7/8/99	2750-0479P	00054.001	60/142,803
United States	7/9/99	2750-0480P	00058.001	60/142,920
United States	7/12/99	2750-0481P	00059.001	60/142,977
United States	7/13/99	2750-0482P	00060.001	60/143,542
United States	7/14/99	2750-0489P	00061.001	60/143,624
United States	7/15/99	2750-0490P	00062.001	60/144,005
United States	7/16/99	2750-0486P	80134.004	60/144,085
United States	7/16/99	2750-0485P	80134.003	60/144,086
United States	7/19/99	2750-0494P	80134.010	60/144,333
United States	7/19/99	2750-0495P	80134.013	60/144,335
United States	7/19/99	2750-0497P	00064.001	60/144,325
United States	7/19/99	2750-0496P	80134.014	60/144,334
United States	7/19/99	2750-0488P	80134.006	60/144,332
United States	7/19/99	2750-0492P	80134.008	60/144,331
United States	7/20/99	2750-0502P	80135.002	60/144,884
United States	7/20/99	2750-0499P	80134.012	60/144,352
United States	7/20/99	2750-0500P	00065.001	60/144,632
United States	7/21/99	2750-0503P	00066.001	60/144,814
United States	7/21/99	2750-0484P	80134.002	60/145,086
United States	7/21/99	2750-0483P	80134.001	60/145,088
United States	7/22/99	2750-0504P	00067.001	60/145,192
United States	7/22/99	2750-0491P	80134.007	60/145,085
United States	7/22/99	2750-0487P	80134.005	60/145,089
United States	7/22/99	2750-0493P	80134.009	60/145,087
United States	7/23/99	2750-0498P	80134.011	60/145,145

Country	Filing Date	Attorney No.	Client No.	Application No.
United States	7/23/99	2750-0501P	80135.001	60/145,224
United States	7/23/99	2750-0505P	00069.001	60/145,218
United States	7/26/99	2750-0506P	00070.001	60/145,276
United States	7/27/99	2750-0508P	80136.002	60/145,919
United States	7/27/99	2750-0509P	00071.001	60/145,913
United States	7/27/99	2750-0507P	80136.001	60/145,918
United States	7/28/99	2750-0510P	00072.001	60/145,951
United States	8/2/99	2750-0511P	80137.001	60/146,388
United States	8/2/99	2750-0512P	80137.002	60/146,389
United States	8/2/99	2750-0513P	00073.001	60/146,386
United States	8/3/99	2750-0514P	00074.001	60/147,038
United States	8/4/99	2750-0517P	80138.002	60/147,302
United States	8/4/99	2750-0515P	00076.001	60/147,204
United States	8/5/99	2750-0518P	00077.001	60/147,260
United States	8/5/99	2750-0519P	80136.003	60/147,192
United States	8/6/99	2750-0516P	80138.001	60/147,303
United States	8/6/99	2750-0520P	00079.001	60/147,416
United States	8/9/99	2750-0521P	00080.001	60/147,493
United States	8/9/99	2750-0523P	80139.002	60/147,935
United States	8/10/99	2750-0522P	80139.001	60/148,171
United States	8/11/99	2750-0524P	00081.001	60/148,319
United States	8/12/99	2750-0530P	00082.001	60/148,341
United States	8/13/99	2750-0529P	00083.001	60/148,565
United States	8/13/99	2750-0532P	80142.002	60/148,684
United States	8/16/99	2750-0531P	80142.001	60/149,368
United States	8/17/99	2750-0537P	00084.001	60/149,175
United States	8/18/99	2750-0538P	00085.001	60/149,426
United States	8/20/99	2750-0539P	00086.001	60/149,722
United States	8/20/99	2750-0541P	80143.002	60/149,929
United States	8/20/99	2750-0542P	00087.001	60/149,723
United States	8/23/99	2750-0543P	00088.001	60/149,902
United States	8/23/99	2750-0540P	80143.001	60/149,930
United States	8/25/99	2750-0544P	00089.001	60/150,566
United States	8/26/99	2750-0547P	00090.001	60/150,884
United States	8/27/99	2750-0545P	80144.001	60/151,065
United States	8/27/99	2750-0546P	80144.002	60/151,066
United States	8/27/99	2750-0548P	00091.001	60/151,080
United States	8/30/99	2750-0549P	00092.001	60/151,303
United States	8/31/99	2750-0552P	00093.001	60/151,438
United States	9/1/99	2750-0553P	00094.001	60/151,930
United States	9/7/99	2750-0554P	00095.001	60/152,363
United States	9/10/99	2750-0555P	00096.001	60/153,070

Country	Filing Date	Attorney No.	Client No.	Application No.
United States	9/13/99	2750-0556P	00098.001	60/153,758
United States	9/15/99	2750-0557P	00099.001	60/154,018
United States	9/16/99	2750-0558P	00101.001	60/154,039
United States	9/20/99	2750-0559P	00102.001	60/154,779
United States	9/22/99	2750-0560P	00103.001	60/155,139
United States	9/23/99	2750-0561P	00104.001	60/155,486
United States	9/24/99	2750-0562P	00105.001	60/155,659
United States	9/28/99	2750-0563P	00106.001	60/156,458
United States	9/29/99	2750-0564P	00107.001	60/156,596
United States	10/4/99	2750-0570P	00108.001	60/157,117
United States	10/5/99	2750-0571P	00109.001	60/157,753
United States	10/6/99	2750-0572P	00110.001	60/157,865
United States	10/7/99	2750-0575P	00111.001	60/158,029
United States	10/8/99	2750-0576P	00112.001	60/158,232
United States	10/12/99	2750-0577P	00113.001	60/158,369
United States	10/13/99	2750-0583P	80148.002	60/159,294
United States	10/13/99	2750-0574P	80145.002	60/159,295
United States	10/13/99	2750-0579P	80146.002	60/159,293
United States	10/14/99	2750-0580P	80147.001	60/159,638
United States	10/14/99	2750-0581P	80147.002	60/159,637
United States	10/14/99	2750-0582P	80148.001	60/159,329
United States	10/14/99	2750-0578P	80146.001	60/159,331
United States	10/14/99	2750-0573P	80145.001	60/159,330
United States	10/18/99	2750-0584P	00116.001	60/159,584
United States	10/21/99	2750-0585P	00118.001	60/160,815
United States	10/21/99	2750-0590P	80150.002	60/160,767
United States	10/21/99	2750-0589P	80150.001	60/160,768
United States	10/21/99	2750-0588P	00119.001	60/160,741
United States	10/21/99	2750-0587P	80149.002	60/160,770
United States	10/21/99	2750-0586P	80149.001	60/160,814
United States	10/22/99	2750-0593P	80151.002	60/160,981
United States	10/22/99	2750-0591P	00120.001	60/160,980
United States	10/22/99	2750-0592P	80151.001	60/160,989
United States	10/25/99	2750-0594P	00121.001	60/161,405
United States	10/25/99	2750-0596P	80152.002	60/161,404
United States	10/25/99	2750-0595P	80152.001	60/161,406
United States	10/26/99	2750-0597P	00122.001	60/161,361
United States	10/26/99	2750-0598P	80153.001	60/161,360
United States	10/26/99	2750-0599P	80153.002	60/161,359
United States	10/28/99	2750-0601P	00123.001	60/161,920
United States	10/28/99	2750-0602P	80154.001	60/161,992
United States	10/28/99	2750-0603P	80154.002	60/161,993

Country	Filing Date	Attorney No.	Client No.	Application No.
United States	10/29/99	2750-0604P	00124.001	60/162,143
United States	10/29/99	2750-0605P	80155.001	60/162,142
United States	10/29/99	2750-0606P	80155.002	60/162,228
United States	11/1/99	2750-0609P	80156.002	60/162,895
United States	11/1/99	2750-0608P	80156.001	60/162,891
United States	11/1/99	2750-0607P	00125.001	60/162,894
United States	11/2/99	2750-0610P	00126.001	60/163,093
United States	11/2/99	2750-0611P	80157.001	60/163,092
United States	11/2/99	2750-0612P	80157.002	60/163,091
United States	11/3/99	2750-0613P	00127.001	60/163,249
United States	11/3/99	2750-0614P	80158.001	60/163,248
United States	11/3/99	2750-0615P	80158.002	60/163,281
United States	11/4/99	2750-0618P	80159.002	60/163,380
United States	11/4/99	2750-0617P	80159.001	60/163,381
United States	11/4/99	2750-0616P	00128.001	60/163,379
United States	11/8/99	2750-0620P	80160.001	60/164,151
United States	11/8/99	2750-0621P	80160.002	60/164,150
United States	11/8/99	2750-0619P	00129.001	60/164,146
United States	11/9/99	2750-0623P	80161.002	60/164,260
United States	11/9/99	2750-0625P	80162.002	60/164,259
United States	11/10/99	2750-0630P	80164.002	60/164,548
United States	11/10/99	2750-0624P	80162.001	60/164,317
United States	11/10/99	2750-0626P	80163.001	60/164,321
United States	11/10/99	2750-0627P	80163.002	60/164,318
United States	11/10/99	2750-0628P	00131.001	60/164,544
United States	11/10/99	2750-0629P	80164.001	60/164,545
United States	11/10/99	2750-0622P	80161.001	60/164,319
United States	11/12/99	2750-0634P	00133.001	60/164,870
United States	11/12/99	2750-0635P	80166.001	60/164,959
United States	11/12/99	2750-0636P	80166.002	60/164,962
United States	11/12/99	2750-0633P	80165.002	60/164,960
United States	11/12/99	2750-0632P	80165.001	60/164,871
United States	11/12/99	2750-0631P	00132.001	60/164,961
United States	11/15/99	2750-0637P	00134.001	60/164,927
United States	11/15/99	2750-0638P	80167.001	60/164,929
United States	11/15/99	2750-0639P	80167.002	60/164,926
United States	11/16/99	2750-0640P	00135.001	60/165,669
United States	11/16/99	2750-0641P	80168.001	60/165,671
United States	11/16/99	2750-0642P	80168.002	60/165,661
United States	11/17/99	2750-0643P	00136.001	60/165,919
United States	11/17/99	2750-0644P	80169.001	60/165,918
United States	11/17/99	2750-0645P	80169.002	60/165,911

Country	Filing Date	Attorney No.	Client No.	Application No.
United States	11/18/99	2750-0648P	80170.002	60/166,158
United States	11/18/99	2750-0646P	00137.001	60/166,157
United States	11/18/99	2750-0647P	80170.001	60/166,173
United States	11/19/99	2750-0651P	80171.002	60/166,412
United States	11/19/99	2750-0649P	00139.001	60/166,419
United States	11/19/99	2750-0650P	80171.001	60/166,411
United States	11/22/99	2750-0652P	00140.001	60/166,733
United States	11/22/99	2750-0653P	80172.001	60/166,750
United States	11/23/99	2750-0655P	80173.002	60/167,362
United States	11/24/99	2750-0654P	80173.001	60/167,382
United States	11/24/99	2750-0656P	00141.001	60/167,233
United States	11/24/99	2750-0657P	80174.001	60/167,234
United States	11/24/99	2750-0658P	80174.002	60/167,235
United States	11/30/99	2750-0659P	00142.001	60/167,904
United States	11/30/99	2750-0660P	80175.001	60/167,908
United States	11/30/99	2750-0661P	80175.002	60/167,902
United States	12/1/99	2750-0663P	00143.001	60/168,232
United States	12/1/99	2750-0664P	80176.001	60/168,233
United States	12/1/99	2750-0665P	80176.002	60/168,231
United States	12/2/99	2750-0666P	00144.001	60/168,546
United States	12/2/99	2750-0667P	80177.001	60/168,549
United States	12/2/99	2750-0668P	80177.002	60/168,548
United States	12/3/99	2750-0670P	80178.001	60/168,673
United States	12/3/99	2750-0669P	00145.001	60/168,675
United States	12/3/99	2750-0671P	80178.002	60/168,674
United States	12/7/99	2750-0673P	80179.001	60/169,278
United States	12/7/99	2750-0674P	80179.002	60/169,302
United States	12/7/99	2750-0672P	00147.001	60/169,298
United States	12/8/99	2750-0675P	80180.001	60/169,692
United States	12/8/99	2750-0676P	80180.002	60/169,691
United States	12/16/99	2750-0677P	00149.001	60/171,107
United States	12/16/99	2750-0679P	80181.002	60/171,098
United States	12/16/99	2750-0678P	80181.001	60/171,114
United States	1/19/00	2750-0681P	80182.002	60/176,866
United States	1/19/00	2750-0685P	80183.002	60/176,867
United States	1/19/00	2750-0688P	80184.002	60/176,910
United States	1/26/00	2750-0689P	00152.001	UNKNOWN
United States	1/27/00	2750-0690P	00153.002	60/178,547
United States	1/27/00	2750-0691P	80185.001	60/177,666
United States	1/27/00	2750-0682P	80183.001	60/178,546
United States	1/27/00	2750-0680P	80182.001	60/178,544
United States	1/27/00	2750-0687P	80184.001	60/178,545

Country	Filing Date	Attorney No.	Client No.	Application No.
United States	1/28/00	2750-0693P	80186.001	60/178,755
United States	1/28/00	2750-0692P	00155.001	60/178,754
United States	2/1/00	2750-0695P	00157.001	60/179,395
United States	2/1/00	2750-0696P	80187.001	60/179,388
United States	2/3/00	2750-0697P	00158.001	60/180,039
United States	2/3/00	2750-0698P	80188.001	60/180,139
United States	2/4/00	2750-0700P	80189.001	60/180,207
United States	2/4/00	2750-0699P	00159.001	60/180,206
United States	2/7/00	2750-0701P	00160.001	60/180,695
United States	2/7/00	2750-0702P	80190.001	60/180,696
United States	2/9/00	2750-0703P	00161.001	60/181,228
United States	2/9/00	2750-0704P	80191.001	60/181,214
United States	2/10/00	2750-0705P	00162.001	60/181,476
United States	2/10/00	2750-0706P	80192.002	60/181,551
United States	2/15/00	2750-0707P	00163.001	60/182,477
United States	2/15/00	2750-0708P	80193.001	60/182,516
United States	2/15/00	2750-0712P	00164.001	60/182,512
United States	2/15/00	2750-0713P	80194.001	60/182,478
United States	2/17/00	2750-0715P	80195.001	60/183,165
United States	2/17/00	2750-0714P	00165.001	60/183,166

Number 31

Application No. 09/935,625 (attorney no. 2750-1481P) listed above is a continuation-in-part of the following applications, the entire contents of which are also hereby incorporated by reference:

Country	Attorney Docket No.	Application No.	Filed
United States	2750-1156P	60/228,279	8/25/00
United States	2750-2137P	Unknown	8/25/00
United States	2750-2136P	60/228,247	8/25/00
United States	2750-2135P	60/228,246	8/25/00
United States	2750-1155P	60/228,224	8/25/00

Number 32

Application No. 10/375,265 (attorney no. 2750-1550P) listed above is a continuation of Application No. 10/156,052 (Attorney No. 2750-1525P), filed May 29, 2002, which is a continuation of Application No. 09/935,350 (Attorney No. 2750-1478P), filed on August 23,

2001. The entire contents of the two above-mentioned applications are hereby incorporated by reference.

Moreover, Application No. 09/935,350 (Attorney No. 2750-1478P) is a conversion of the following provisional applications, to which the present application claims priority under 35 USC §119(e), the entire contents of which are hereby incorporated by reference:

Country	Attorney No.	Filed	Application No.
United States	2750-1116P	August 23, 2000	60/228,095
United States	2750-1117P	August 23, 2000	60/228,094
United States	2750-1118P	August 23, 2000	60/228,126
United States	2750-1119P	August 25, 2000	60/228,029
United States	2750-1120P	August 25, 2000	60/227,779
United States	2750-1121P	August 25, 2000	60/227,782
United States	2750-1122P	August 23, 2000	60/228,092
United States	2750-1123P	August 23, 2000	60/228,125
United States	2750-1124P	August 23, 2000	60/228,127
United States	2750-1125P	August 24, 2000	60/228,091
United States	2750-1126P	August 25, 2000	60/227,771
United States	2750-1127P	August 25, 2000	60/227,727
United States	2750-1128P	August 25, 2000	60/227,726
United States	2750-1129P	August 24, 2000	60/228,090
United States	2750-1130P	August 24, 2000	60/227,776
United States	2750-1131P	August 23, 2000	60/228,093
United States	2750-1132P	August 23, 2000	60/227,778

Number 33

Application No. 10/376,766 (attorney no. 2750-1553P) listed above claims priority under 35 USC §119(e) of the following application, the entire contents of which are also hereby incorporated by reference:

Country	Attorney No.	Appln. No.	Filed
United States	2750-1488P	60/361,109	March 1, 2002

Number 34

Application No. 09/686,093 (attorney no. 2750-1033P) listed above claims priority under 35 USC §119(e) of the following application, the entire contents of which are hereby incorporated by reference:

Country	Filing Date	Attorney No.	Client No.	Application No.
United States	Oct. 12, 1999	2750-0577P	00113.001	60/158,369

Number 35

Application No. 09/680,498 (attorney no. 2750-1032P) listed above claims priority under 35 USC §119(e) of the following application, the entire contents of which are hereby incorporated by reference:

Country	Filing Date	Attorney No.	Client No.	Application No.
United States	October 8, 1999	2750-0576P	00112.001	60/158,232

Number 36

Application No. 09/671,635 (attorney no. 2750-1026P) listed above claims priority under 35 USC §119(e) of the following application, the entire contents of which are hereby incorporated by reference:

Country	Filing Date	Attorney No.	Client No.	Application No.
United States	09/28/1999	2750-0563P	00106.001	60/156,458

Number 37

Application No. 09/667,517 (attorney no. 2750-1024P) listed above claims priority under 35 USC §119(e) of the following application, the entire contents of which are hereby incorporated by reference:

Country	Filing Date	Attorney No.	Client No.	Application No.
United States	09/23/99	2750-561P	00104.00 1	60/155,486

Number 38

Application No. 09/665,714 (attorney no. 2750-1022P) listed above claims priority under 35 USC §119(e) of the following application, the entire contents of which are hereby incorporated by reference:

Country	Filing Date	Attorney No.	Client No.	Application No.
United States	09/20/99	2750-559P	00102.00 1	60/154,779

Number 39

Application No. 09/621,323 (attorney no. 2750-0990P) listed above claims priority under 35 USC §119(e) of the following application, the entire contents of which are hereby incorporated by reference:

Country	Filing Date	Attorney No.	Client No.	Application No.
United States	07/20/99	2750-	00065.00	60/144,632

States		0500P	1	
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Number 40

Application No. 09/633,191 (attorney no. 2750-1000P) listed above claims priority under 35 USC §119(e) of the following application, the entire contents of which are hereby incorporated by reference:

Country	Filing Date	Attorney No.	Client No.	Application No.
United States	08/05/1999	2750-0518P	00077.001	60/147,260

Number 41

Application No. 09/651,370 (attorney no. 2750-1014P) listed above claims priority under 35 USC §119(e) of the following application, the entire contents of which are hereby incorporated by reference:

Country	Filing Date	Attorney No.	Client No.	Application No.
United States	08/30/1999	2750-0549P	00092.001	60/151,303

Number 42

Application No. 10/426,837 (attorney no. 2750-1558P) listed above claims priority under 35 USC §119(e) of provisional application nos: 60/376,553 filed May 1, 2002 (att. docket no. 2750-1497P) and 60/376,517 filed May 1, 2002 (att. docket no. 2750-1498P) the entire contents of which are hereby incorporated by reference.

Number 43

Application No. 09/702,841 (attorney no. 2750-1330P) listed above claims priority under 35 USC §119(e) of the following application, the entire contents of which are hereby incorporated by reference:

Country	Filing Date	Attorney No.	Client No.	Application No.
United States	11/1/1999	2750-608P	80156.00 1	60/162,891

Number 44

Application No. 09/696,751 (attorney no. 2750-1309P) listed above claims priority under 35 USC §119(e) of the following application, the entire contents of which are hereby incorporated by reference:

Country	Filing Date	Attorney No.	Client No.	Application No.
United States	10/25/1999	2750-595P	80152.00 1	60/161,406

Number 45

Application No. 10/356,562 (attorney no. 2750-1547P) is a continuation of Application No. 10/132,279 (Attorney No. 2750-1513P), filed on April 26, 2002, the entire contents of which are hereby incorporated by reference.

Application No. 10/132,279 (Attorney No. 2750-1513P) is a continuation-in-part of the following nonprovisional applications, to which the present application claims priority under §120, the entire contents of which are also hereby incorporated by reference:

	Country	Client No.	Attorney	Appln. No.	Fi	A.	Stat
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1.	United States	80001.006	2750-0550P	09/391,631	9/3/99	Pending at the time of filing
2.	United States	80010.003	2750-0566P	09/412,922	10/5/99	Pending at the time of filing
3.	United States	80010.002	2750-0565P	09/413,198	10/5/99	Pending at the time of filing
4.	United States	80026.002	2750-0600P	09/428,944	10/28/99	Pending at the time of filing
5.	United States	80042.002	2750-0662P	09/451,320	12/1/99	Pending at the time of filing
6.	United States	80060.002	2750-0683P	09/478,081	1/4/00	Pending at the time of filing
7.	United States	80084.002	2750-0694P	09/497,191	2/3/00	Pending at the time of filing
8.	United States	80141.008	2750-1104P	09/637,792	8/11/00	Pending at the time of filing
9.	United States	80141.007	2750-1103P	09/637,564	8/11/00	Pending at the time of filing
10.	United States	80141.006	2750-1102P	09/637,565	8/11/00	Pending at the time of filing
11.	United States	80141.010	2750-1493P	10/097,600	3/15/02	Pending at the time of filing

Through the eleven nonprovisional applications listed above, the present application also claims priority under 35 USC §119(e) of the following provisional applications, the entire contents of which are hereby incorporated by reference:

1. Appln. No. 09/391,631 (Attorney No. 2750-0550P) filed 9/3/99 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln.	Attorney	Filing Date
1.	United	60/099.67	2750-0300P	9/4/98
2.	United	60/099.67	2750-0301P	9/4/98
3.	United	60/099.93	2750-0302P	9/11/98
4.	United	60/100.86	2750-0304P	9/17/98
5.	United	60/101.04	2750-0305P	9/18/98
6.	United	60/101.68	2750-0307P	9/24/98
7.	United	60/102.53	2750-0308P	9/30/98
8.	United	60/102.46	2750-0309P	9/30/98
9.	United	60/103.11	2750-0310P	10/5/98
10.	United	60/103.14	2750-0311P	10/5/98
11.	United	60/103.57	2750-0314P	10/9/98
12.	United	60/103.90	2750-0315P	10/13/98
13.	United	60/106.10	2750-0324P	10/29/98
14.	United	60/106.21	2750-0325P	10/30/98
15.	United	60/107.28	2750-0327P	11/6/98

	Country	Appln.	Attorney	Filing Date
16.	United	60/107.83	2750-0330P	11/10/98
17.	United	60/108.52	2750-0332P	11/16/98
18.	United	60/108.90	2750-0333P	11/17/98
19.	United	60/109.26	2750-0336P	11/20/98
20.	United	60/109.59	2750-0337P	11/23/98
21.	United	60/110.26	2750-0341P	11/30/98
22.	United	60/110.49	2750-0342P	12/1/98
23.	United	60/110.62	2750-0343P	12/2/98
24.	United	60/110.70	2750-0344P	12/3/98
25.	United	60/111.33	2750-0345P	12/7/98
26.	United	60/111.58	2750-0346P	12/9/98
27.	United	60/112.09	2750-0349P	12/14/98
28.	United	60/112.22	2750-0350P	12/15/98
29.	United	60/112.62	2750-0351P	12/16/98
30.	United	60/112.86	2750-0352P	12/17/98
31.	United	60/115.15	2750-0363P	1/7/99
32.	United	60/115.15	2750-0366P	1/7/99
33.	United	60/115.36	2750-0369P	1/8/99
34.	United	60/115.33	2750-0371P	1/11/99
35.	United	60/115.84	2750-0373P	1/13/99
36.	United	60/116.67	2750-0379P	1/21/99
37.	United	60/116.96	2750-0382P	1/22/99
38.	United	60/120.58	2750-0394P	2/18/99
39.	United	60/121.07	2750-0395P	2/22/99
40.	United	60/122.56	2750-0401P	3/2/99
41.	United	60/123.94	2750-0411P	3/12/99

2. Appln. No. 09/412,922 (Attorney No. 2750-0566P) filed 10/5/99 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
1.	United	60/103.116	2750-0310P	10/5/98
2.	United	60/103.141	2750-0311P	10/5/98
3.	United	60/103.215	2750-0312P	10/6/98
4.	United	60/103.554	2750-0313P	10/8/98
5.	United	60/103.574	2750-0314P	10/9/98
6.	United	60/103.907	2750-0315P	10/13/98
7.	United	60/104.268	2750-0316P	10/14/98
8.	United	60/104.680	2750-0317P	10/16/98
9.	United	60/104.828	2750-0318P	10/19/98
10.	United	60/105.008	2750-0319P	10/20/98
11.	United	60/105.142	2750-0320P	10/21/98
12.	United	60/105.533	2750-0321P	10/22/98
13.	United	60/105.571	2750-0322P	10/26/98
14.	United	60/105.815	2750-0323P	10/27/98

	Country	Appln. No.	Attorney No.	Filing Date
15	United	60/106.105	2750-0324P	10/29/98
16	United	60/106.218	2750-0325P	10/30/98
17	United	60/106.685	2750-0326P	11/2/98
18	United	60/107.282	2750-0327P	11/6/98
19	United	60/107.720	2750-0328P	11/9/98
20	United	60/107.719	2750-0329P	11/9/98
21	United	60/107.836	2750-0330P	11/10/98
22	United	60/108.190	2750-0331P	11/12/98
23	United	60/108.526	2750-0332P	11/16/98
24	United	60/108.901	2750-0333P	11/17/98
25	United	60/109.124	2750-0334P	11/19/98
26	United	60/109.127	2750-0335P	11/19/98
27	United	60/109.267	2750-0336P	11/20/98
28	United	60/109.594	2750-0337P	11/23/98
29	United	60/110.053	2750-0338P	11/25/98
30	United	60/110.050	2750-0339P	11/25/98
31	United	60/110.158	2750-0340P	11/27/98
32	United	60/110.263	2750-0341P	11/30/98
33	United	60/110.495	2750-0342P	12/1/98
34	United	60/110.626	2750-0343P	12/2/98
35	United	60/110.701	2750-0344P	12/3/98
36	United	60/111.339	2750-0345P	12/7/98
37	United	60/111.589	2750-0346P	12/9/98
38	United	60/111.782	2750-0347P	12/10/98
39	United	60/111.812	2750-0348P	12/11/98
40	United	60/112.096	2750-0349P	12/14/98
41	United	60/112.224	2750-0350P	12/15/98
42	United	60/112.624	2750-0351P	12/16/98
43	United	60/112.862	2750-0352P	12/17/98
44	United	60/112.912	2750-0353P	12/18/98
45	United	60/113.248	2750-0354P	12/21/98
46	United	60/113.522	2750-0355P	12/22/98
47	United	60/113.826	2750-0356P	12/23/98
48	United	60/113.998	2750-0357P	12/28/98
49	United	60/114.384	2750-0358P	12/29/98
50	United	60/114.455	2750-0359P	12/30/98
51	United	60/114.740	2750-0360P	1/4/99
52	United	60/114.866	2750-0361P	1/6/99
53	United	60/115.153	2750-0362P	1/7/99
54	United	60/115.152	2750-0363P	1/7/99
55	United	60/115.151	2750-0364P	1/7/99
56	United	60/115.155	2750-0365P	1/7/99
57	United	60/115.156	2750-0366P	1/7/99
58	United	60/115.154	2750-0367P	1/7/99
59	United	60/115.364	2750-0368P	1/8/99
60	United	60/115.365	2750-0369P	1/8/99

	Country	Appln. No.	Attorney No.	Filing Date
61	United	60/115.339	2750-0371P	1/11/99
62	United	60/115.518	2750-0372P	1/12/99
63	United	60/115.847	2750-0373P	1/13/99
64	United	60/115.905	2750-0374P	1/14/99
65	United	60/116.383	2750-0375P	1/15/99
66	United	60/116.384	2750-0376P	1/15/99
67	United	60/116.329	2750-0377P	1/19/99
68	United	60/116.340	2750-0378P	1/19/99
69	United	60/116.674	2750-0379P	1/21/99
70	United	60/116.672	2750-0380P	1/21/99
71	United	60/116.960	2750-0381P	1/22/99
72	United	60/116.962	2750-0382P	1/22/99
73	United	60/117.756	2750-0383P	1/28/99
74	United	60/118.672	2750-0384P	2/3/99
75	United	60/118.808	2750-0385P	2/4/99
76	United	60/118.778	2750-0386P	2/5/99
77	United	60/119.029	2750-0387P	2/8/99
78	United	60/119.332	2750-0388P	2/9/99
79	United	60/119.462	2750-0389P	2/10/99
80	United	60/119.922	2750-0391P	2/12/99
81	United	60/120.196	2750-0392P	2/16/99
82	United	60/120.198	2750-0393P	2/16/99
83	United	60/120.583	2750-0394P	2/18/99
84	United	60/121.072	2750-0395P	2/22/99
85	United	60/121.334	2750-0396P	2/23/99
86	United	60/121.470	2750-0397P	2/24/99
87	United	60/121.704	2750-0398P	2/25/99
88	United	60/122.107	2750-0399P	2/26/99
89	United	60/122.266	2750-0400P	3/1/99
90	United	60/122.568	2750-0401P	3/2/99
91	United	60/122.611	2750-0402P	3/3/99
92	United	60/121.775	2750-0403P	3/4/99
93	United	60/123.534	2750-0404P	3/5/99
94	United	60/123.680	2750-0406P	3/9/99
95	United	60/123.715	2750-0408P	3/10/99
96	United	60/123.726	2750-0409P	3/10/99
97	United	60/124.263	2750-0410P	3/11/99
98	United	60/123.941	2750-0411P	3/12/99

3. Appln. No. 09/413,198 (Attorney No. 2750-0565P) filed 10/5/99 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
1.	United	60/103.116	2750-0310P	10/5/98
2.	United	60/103.141	2750-0311P	10/5/98

	Country	Appln. No.	Attorney No.	Filing Date
3.	United	60/103.215	2750-0312P	10/6/98
4.	United	60/103.554	2750-0313P	10/8/98
5.	United	60/103.574	2750-0314P	10/9/98
6.	United	60/103.907	2750-0315P	10/13/98
7.	United	60/104.268	2750-0316P	10/14/98
8.	United	60/104.680	2750-0317P	10/16/98
9.	United	60/104.828	2750-0318P	10/19/98
10.	United	60/105.008	2750-0319P	10/20/98
11.	United	60/105.142	2750-0320P	10/21/98
12.	United	60/105.533	2750-0321P	10/22/98
13.	United	60/105.571	2750-0322P	10/26/98
14.	United	60/105.815	2750-0323P	10/27/98
15.	United	60/106.105	2750-0324P	10/29/98
16.	United	60/106.218	2750-0325P	10/30/98

4. Appln. No. 09/428,944 (Attorney No. 2750-0600P) filed 10/28/99 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
1.	United	60/106.685	2750-0326P	11/2/98
2.	United	60/107.282	2750-0327P	11/6/98
3.	United	60/107.720	2750-0328P	11/9/98
4.	United	60/107.719	2750-0329P	11/9/98
5.	United	60/107.836	2750-0330P	11/10/98
6.	United	60/108.190	2750-0331P	11/12/98
7.	United	60/108.526	2750-0332P	11/16/98
8.	United	60/108.901	2750-0333P	11/17/98
9.	United	60/109.124	2750-0334P	11/19/98
10.	United	60/109.127	2750-0335P	11/19/98
11.	United	60/109.267	2750-0336P	11/20/98
12.	United	60/109.594	2750-0337P	11/23/98
13.	United	60/110.053	2750-0338P	11/25/98
14.	United	60/110.050	2750-0339P	11/25/98
15.	United	60/110.158	2750-0340P	11/27/98
16.	United	60/110.263	2750-0341P	11/30/98

5. Appln. No. 09/451,320 (Attorney No. 2750-0662P) filed 12/1/99 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
1.	United	60/110.495	2750-0342P	12/1/98
2.	United	60/110.626	2750-0343P	12/2/98
3.	United	60/110.701	2750-0344P	12/3/98
4.	United	60/111.339	2750-0345P	12/7/98

5.	United	60/111.589	2750-0346P	12/9/98
6.	United	60/111.782	2750-0347P	12/10/98
7.	United	60/111.812	2750-0348P	12/11/98
8.	United	60/112.096	2750-0349P	12/14/98
9.	United	60/112.224	2750-0350P	12/15/98
10.	United	60/112.624	2750-0351P	12/16/98
11.	United	60/112.862	2750-0352P	12/17/98
12.	United	60/112.912	2750-0353P	12/18/98
13.	United	60/113.248	2750-0354P	12/21/98
14.	United	60/113.522	2750-0355P	12/22/98
15.	United	60/113.826	2750-0356P	12/23/98
16.	United	60/113.998	2750-0357P	12/28/98
17.	United	60/114.384	2750-0358P	12/29/98
18.	United	60/114.455	2750-0359P	12/30/98
19.	United	60/115.153	2750-0362P	1/7/99
20.	United	60/115.152	2750-0363P	1/7/99
21.	United	60/115.151	2750-0364P	1/7/99
22.	United	60/115.155	2750-0365P	1/7/99
23.	United	60/115.156	2750-0366P	1/7/99
24.	United	60/115.364	2750-0368P	1/8/99
25.	United	60/116.960	2750-0381P	1/22/99

6. Appln. No. 09/478,081 (Attorney No. 2750-0683P) filed 1/4/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
1.	United	60/114.740	2750-0360P	1/4/99
2.	United	60/114.866	2750-0361P	1/6/99
3.	United	60/115.154	2750-0367P	1/7/99
4.	United	60/115.365	2750-0369P	1/8/99
5.	United	60/115.339	2750-0371P	1/11/99
6.	United	60/115.518	2750-0372P	1/12/99
7.	United	60/115.847	2750-0373P	1/13/99
8.	United	60/115.905	2750-0374P	1/14/99
9.	United	60/116.383	2750-0375P	1/15/99
10.	United	60/116.384	2750-0376P	1/15/99
11.	United	60/116.329	2750-0377P	1/19/99
12.	United	60/116.340	2750-0378P	1/19/99
13.	United	60/116.674	2750-0379P	1/21/99
14.	United	60/116.672	2750-0380P	1/21/99
15.	United	60/116.962	2750-0382P	1/22/99
16.	United	60/117.756	2750-0383P	1/28/99

7. Appln. No. 09/497,191 (Attorney No. 2750-0694P) filed 2/3/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
1.	United	60/118.672	2750-0384P	2/3/99
2.	United	60/118.808	2750-0385P	2/4/99
3.	United	60/118.778	2750-0386P	2/5/99
4.	United	60/119.029	2750-0387P	2/8/99
5.	United	60/119.332	2750-0388P	2/9/99
6.	United	60/119.462	2750-0389P	2/10/99
7.	United	60/119.922	2750-0391P	2/12/99
8.	United	60/120.196	2750-0392P	2/16/99
9.	United	60/120.198	2750-0393P	2/16/99
10.	United	60/120.583	2750-0394P	2/18/99
11.	United	60/121.072	2750-0395P	2/22/99
12.	United	60/121.334	2750-0396P	2/23/99
13.	United	60/121.470	2750-0397P	2/24/99
14.	United	60/121.704	2750-0398P	2/25/99
15.	United	60/122.107	2750-0399P	2/26/99

8. Appln. No. 09/637,792 (Attorney No. 2750-1104P) filed 8/11/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United	60/148.337	2750-0528P	8/12/99

9. Appln. No. 09/637,564 (Attorney No. 2750-1103P) filed 8/11/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United	60/148.340	2750-0527P	8/12/99

10. Appln. No. 09/637,565 (Attorney No. 2750-1102P) filed 8/11/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United	60/148.342	2750-0526P	8/12/99

11. Appln. No. 10/097,600 (Attorney No. 2750-1493P) filed 3/15/02 is a continuation of Appln. No. 09/832,934 (Attorney No. 2750-1436P) filed 4/12/01, which is a continuation of Appln. No. 09/637,820 (Attorney No. 2750-1101P) filed 8/11/00, through which it claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United	60/148.347	2750-0525P	8/12/99

Number 46

Application No. 10/336,799 (attorney no. 2750-1540P) listed above is a continuation of Application No. 10/132,257 (attorney no. 2750-1514P), filed on April 26, 2002, the entire contents of which are hereby incorporated by reference.

Through Application No. 10/132,257, the present application claims priority under 35 USC §119(e) and §120 of the following applications, the entire contents of which are hereby incorporated by reference:

	Country	Client No.	Attorney No.	Application No.	Filed	B. Sta
1.	United States	91000.002	2750-0783P	09/543,680	4/6/00	Pending at the time of filing 10/132,257
2.	United States	91002.002	2750-0851P	09/565,308	5/5/00	Pending at the time of filing 10/132,257
3.	United States	91007.002	2750-0876P	09/573,655	5/18/00	Pending at the time of filing 10/132,257
4.	United States	00033.003	2750-0928P	09/592,459	6/9/00	Pending at the time of filing 10/132,257
5.	United States	00034.002	2750-0934P	09/593,710	6/14/00	Pending at the time of filing 10/132,257
6.	United States	00045.002	2750-0975P	09/602,016	6/23/00	Pending at the time of filing 10/132,257
7.	United States	00048.002	2750-0977P	09/606,181	6/29/00	Pending at the time of filing 10/132,257
8.	United States	00050.002	2750-0979P	09/607,081	6/30/00	Pending at the time of filing 10/132,257
9.	United States	00051.002	2750-0980P	09/610,157	6/30/00	Pending
10.	United States	00052.002	2750-0981P	09/609,198	6/30/00	Pending at the time of filing 10/132,257
11.	United States	00053.002	2750-0982P	09/611,409	7/6/00	Pending
12.	United States	00054.002	2750-0983P	09/612,645	7/7/00	Pending at the time of filing 10/132,257

13.	United States	00058.002	2750-0984P	09/613,547	7/7/00	Pending at the time of filing 10/132.257
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Through the applications listed above, the present application also claims priority under 35 USC §119(e) of the following applications, the entire contents of which are hereby incorporated by reference:

	C.	D.	Attorney No.	Application	Filed	E.
14.	United States	91000.001	2750-0416P	60/128,234	4/6/99	Converted
15.	United States	91001.001	2750-0417P	60/128,714	4/8/99	Converted
16.	United States	91002.001	2750-0428P	60/132,487	5/6/99	Converted
17.	United States	91007.001	2750-0436P	60/134,768	5/18/99	Converted
18.	United States	91008.001	2750-0437P	60/134,941	5/19/99	Converted
19.	United States	91009.001	2750-0438P	60/135,124	5/20/99	Converted
20.	United States	91010.001	2750-0439P	60/135,353	5/21/99	Converted
21.	United States	91011.001	2750-0440P	60/135,629	5/24/99	Converted
22.	United States	91012.001	2750-0441P	60/136,021	5/25/99	Converted
23.	United States	91013.001	2750-0442P	60/136,392	5/27/99	Converted
24.	United States	91014.001	2750-0444P	60/136,782	5/28/99	Converted
25.	United States	91015.001	2750-0445P	60/137,222	6/1/99	Converted
26.	United States	91016.001	2750-0446P	60/137,528	6/3/99	Converted
27.	United States	91017.001	2750-0447P	60/137,502	6/4/99	Converted
28.	United States	91018.001	2750-0449P	60/137,724	6/7/99	Converted
29.	United States	91019.001	2750-0450P	60/138,094	6/8/99	Converted
30.	United States	00033.001	2750-0457P	60/138,540	6/10/99	Converted
31.	United States	00033.002	2750-0458P	60/138,847	6/10/99	Converted
32.	United States	00034.001	2750-0463P	60/139,119	6/14/99	Converted
33.	United States	00045.001	2750-0471P	60/140,695	6/24/99	Converted
34.	United States	00048.001	2750-0473P	60/140,991	6/29/99	Converted
35.	United States	00050.001	2750-0475P	60/141,842	7/1/99	Converted
36.	United States	00051.001	2750-0476P	60/142,154	7/1/99	Converted
37.	United States	00052.001	2750-0477P	60/142,055	7/2/99	Converted
38.	United States	00053.001	2750-0478P	60/142,390	7/6/99	Converted
39.	United States	00054.001	2750-0479P	60/142,803	7/8/99	Converted
40.	United States	00058.001	2750-0480P	60/142,920	7/9/99	Converted

Number 47

Application No. 10/347,322 (attorney no. 2750-1546P) is a continuation of Application No. 10/132,256 (Attorney No. 2750-1515P), filed on April 26, 2002, the entire contents of which are hereby incorporated by reference.

Application No. 10/132,256 (Attorney No. 2750-1515P) is a continuation-in-part of the following nonprovisional applications, to which the present application claims priority under §120, the entire contents of which are hereby incorporated by reference:

	Attorney	Appln.	Filed	Status
1.	2750-0942P	09/595,326	6/16/00	Pending at the time of filing 10/132,256
2.	2750-1303P	09/692,696	10/20/00	Pending at the time of filing 10/132,256
3.	2750-1296P	09/692,154	10/20/00	Pending at the time of filing 10/132,256
4.	2750-1297P	09/692,714	10/20/00	Pending at the time of filing 10/132,256
5.	2750-1299P	09/692,148	10/20/00	Pending at the time of filing 10/132,256
6.	2750-1300P	09/692,717	10/20/00	Pending at the time of filing 10/132,256
7.	2750-1302P	09/692,152	10/20/00	Pending at the time of filing 10/132,256
8.	2750-1309P	09/696,751	10/25/00	Pending at the time of filing 10/132,256
9.	2750-1310P	09/695,387	10/25/00	Pending at the time of filing 10/132,256
10.	2750-1312P	09/696,284	10/26/00	Pending at the time of filing 10/132,256
11.	2750-1313P	09/696,017	10/26/00	Pending at the time of filing 10/132,256
12.	2750-1315P	09/697,056	10/27/00	Pending at the time of filing 10/132,256
13.	2750-1316P	09/697,145	10/27/00	Pending at the time of filing 10/132,256
14.	2750-1318P	09/697,081	10/27/00	Pending at the time of filing 10/132,256
15.	2750-1319P	09/697,076	10/27/00	Pending at the time of filing 10/132,256
16.	2750-1331P	09/702,873	11/1/00	Pending at the time of filing 10/132,256

	Attorney	Appln.	Filed	Status
17.	2750-1330P	09/702,841	11/1/00	Pending at the time of filing 10/132,256
18.	2750-1334P	09/703,619	11/2/00	Pending at the time of filing 10/132,256
19.	2750-1333P	09/703,627	11/2/00	Pending at the time of filing 10/132,256
20.	2750-1336P	09/704,550	11/3/00	Pending at the time of filing 10/132,256
21.	2750-1337P	09/704,836	11/3/00	Pending at the time of filing 10/132,256
22.	2750-1339P	09/704,541	11/3/00	Pending at the time of filing 10/132,256
23.	2750-1340P	09/704,540	11/3/00	Pending at the time of filing 10/132,256
24.	2750-1347P	09/708,092	11/8/00	Pending at the time of filing 10/132,256
25.	2750-1249P	09/726,578	12/1/00	Pending at the time of filing 10/132,256
26.	2750-1390P	09/769,525	1/26/01	Pending at the time of filing 10/132,256
27.	2750-1401P	09/774,806	2/1/01	Pending at the time of filing 10/132,256
28.	2750-1451P	09/870,664	6/1/01	Pending at the time of filing 10/132,256
29.	2750-1484P	10/082,096	2/26/02	Pending at the time of filing 10/132,256
30.	2750-1489P	10/086,239	3/4/02	Pending at the time of filing 10/132,256
31.	2750-1491P	10/094,538	3/11/02	Pending at the time of filing 10/132,256
32.	2750-1492P	10/095,465	3/13/02	Pending at the time of filing 10/132,256
33.	2750-1494P	10/097,295	3/15/02	Pending at the time of filing 10/132,256
34.	2750-1499P	10/103,845	3/25/02	Pending at the time of filing 10/132,256
35.	2750-1509P	10/123,111	4/17/02	Pending at the time of filing 10/132,256

Through the thirty-five nonprovisional applications listed above, the present application also claims priority under 35 USC §119(e) of the following provisional applications, the entire contents of which are hereby incorporated by reference:

1. Appln. No. 09/595,326 (Attorney No. 2750-0942P) filed 6/16/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/139,763	2750-0465P	6/18/99

2. Appln. No. 09/692,696 (Attorney No. 2750-1303P) filed 10/20/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/160,981	2750-0593P	10/22/99

3. Appln. No. 09/692,154 (Attorney No. 2750-1296P) filed 10/20/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/160,814	2750-0586P	10/21/99

4. Appln. No. 09/692,714 (Attorney No. 2750-1297P) filed 10/20/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/160,770	2750-0587P	10/21/99

5. Appln. No. 09/692,148 (Attorney No. 2750-1299P) filed 10/20/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/160,768	2750-0589P	10/21/99

6. Appln. No. 09/692,717 (Attorney No. 2750-1300P) filed 10/20/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/160,767	2750-0590P	10/21/99

7. Appln. No. 09/692,152 (Attorney No. 2750-1302P) filed 10/20/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/160,989	2750-0592P	10/22/99

8. Appln. No. 09/696,751 (Attorney No. 2750-1309P) filed 10/25/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/161,406	2750-0595P	10/25/99

9. Appln. No. 09/695,387 (Attorney No. 2750-1310P) filed 10/25/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/161,404	2750-0596P	10/25/99

10. Appln. No. 09/696,284 (Attorney No. 2750-1312P) filed 10/26/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/161,360	2750-0598P	10/26/99

11. Appln. No. 09/696,017 (Attorney No. 2750-1313P) filed 10/26/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/161,359	2750-0599P	10/26/99

12. Appln. No. 09/697,056 (Attorney No. 2750-1315P) filed 10/27/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/161,992	2750-0602P	10/28/99

13. Appln. No. 09/697,145 (Attorney No. 2750-1316P) filed 10/27/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/161,993	2750-0603P	10/28/99

14. Appln. No. 09/697,081 (Attorney No. 2750-1318P) filed 10/27/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/162,142	2750-0605P	10/29/99

15. Appln. No. 09/697,076 (Attorney No. 2750-1319P) filed 10/27/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/162,228	2750-0606P	10/29/99

16. Appln. No. 09/702,873 (Attorney No. 2750-1331P) filed 11/1/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/162,895	2750-0609P	11/1/99

17. Appln. No. 09/702,841 (Attorney No. 2750-1330P) filed 11/1/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/162,891	2750-0608P	11/1/99

18. Appln. No. 09/703,619 (Attorney No. 2750-1334P) filed 11/2/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/163,091	2750-0612P	11/2/99

19. Appln. No. 09/703,627 (Attorney No. 2750-1333P) filed 11/2/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/163,092	2750-0611P	11/2/99

20. Appln. No. 09/704,550 (Attorney No. 2750-1336P) filed 11/3/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/163,248	2750-0614P	11/3/99

21. Appln. No. 09/704,836 (Attorney No. 2750-1337P) filed 11/3/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/163,281	2750-0615P	11/3/99

22. Appln. No. 09/704,541 (Attorney No. 2750-1339P) filed 11/3/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/163,381	2750-0617P	11/4/99

23. Appln. No. 09/704,540 (Attorney No. 2750-1340P) filed 11/3/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/163,380	2750-0618P	11/4/99

24. Appln. No. 09/708,092 (Attorney No. 2750-1347P) filed 11/8/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
1.	United States	60/165,918	2750-0644P	11/17/99
2.	United States	60/166,733	2750-0652P	11/22/99
3.	United States	60/165,661	2750-0642P	11/16/99
4.	United States	60/165,919	2750-0643P	11/17/99
5.	United States	60/165,911	2750-0645P	11/17/99
6.	United States	60/166,173	2750-0647P	11/18/99
7.	United States	60/166,158	2750-0648P	11/18/99
8.	United States	60/166,419	2750-0649P	11/19/99
9.	United States	60/166,157	2750-0646P	11/18/99
10.	United States	60/166,412	2750-0651P	11/19/99
11.	United States	60/165,669	2750-0640P	11/16/99
12.	United States	60/166,750	2750-0653P	11/22/99
13.	United States	60/167,233	2750-0656P	11/24/99

14.	United States	60/167,234	2750-0657P	11/24/99
15.	United States	60/167,235	2750-0658P	11/24/99
16.	United States	60/167,904	2750-0659P	11/30/99
17.	United States	60/167,908	2750-0660P	11/30/99
18.	United States	60/166,411	2750-0650P	11/19/99
19.	United States	60/164,960	2750-0633P	11/12/99
20.	United States	60/164,146	2750-0619P	11/8/99
21.	United States	60/164,151	2750-0620P	11/8/99
22.	United States	60/164,150	2750-0621P	11/8/99
23.	United States	60/164,544	2750-0628P	11/10/99
24.	United States	60/164,545	2750-0629P	11/10/99
25.	United States	60/164,548	2750-0630P	11/10/99
26.	United States	60/165,671	2750-0641P	11/16/99
27.	United States	60/164,871	2750-0632P	11/12/99
28.	United States	60/167,902	2750-0661P	11/30/99
29.	United States	60/164,870	2750-0634P	11/12/99
30.	United States	60/164,959	2750-0635P	11/12/99
31.	United States	60/164,962	2750-0636P	11/12/99
32.	United States	60/164,927	2750-0637P	11/15/99
33.	United States	60/164,929	2750-0638P	11/15/99
34.	United States	60/164,926	2750-0639P	11/15/99
35.	United States	60/164,961	2750-0631P	11/12/99

25. Appln. No. 09/726,578 (Attorney No. 2750-1249P) filed 12/1/00 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
1.	United States	60/169,302	2750-0674P	12/7/99
2.	United States	60/168,231	2750-0665P	12/1/99
3.	United States	60/168,549	2750-0667P	12/2/99
4.	United States	60/168,548	2750-0668P	12/2/99
5.	United States	60/168,675	2750-0669P	12/3/99
6.	United States	60/168,673	2750-0670P	12/3/99
7.	United States	60/168,674	2750-0671P	12/3/99
8.	United States	60/168,232	2750-0663P	12/1/99
9.	United States	60/169,278	2750-0673P	12/7/99
10.	United States	60/168,233	2750-0664P	12/1/99
11.	United States	60/171,107	2750-0677P	12/16/99
12.	United States	60/171,114	2750-0678P	12/16/99
13.	United States	60/171,098	2750-0679P	12/16/99
14.	United States	60/169,298	2750-0672P	12/7/99
15.	United States	60/168,546	2750-0666P	12/2/99

26. Appln. No. 09/769,525 (Attorney No. 2750-1390P) filed 1/26/01 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
1.	United States	60/178,547	2750-0690P	1/27/00
2.	United States	60/178,755	2750-0693P	1/28/00
3.	United States	60/177,666	2750-0691P	1/27/00
4.	United States	60/178,754	2750-0692P	1/28/00

27. Appln. No. 09/774,806 (Attorney No. 2750-1401P) filed 2/1/01 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
1.	United States	60/182,477	2750-0707P	2/15/00
2.	United States	60/180,696	2750-0702P	2/7/00
3.	United States	60/183,166	2750-0714P	2/17/00
4.	United States	60/183,165	2750-0715P	2/17/00
5.	United States	60/182,512	2750-0712P	2/15/00
6.	United States	60/182,516	2750-0708P	2/15/00
7.	United States	60/181,551	2750-0706P	2/10/00
8.	United States	60/181,476	2750-0705P	2/10/00
9.	United States	60/184,667	2750-0716P	2/24/00
10.	United States	60/181,228	2750-0703P	2/9/00
11.	United States	60/185,397	2750-0723P	2/28/00
12.	United States	60/180,695	2750-0701P	2/7/00
13.	United States	60/180,207	2750-0700P	2/4/00
14.	United States	60/181,214	2750-0704P	2/9/00
15.	United States	60/180,139	2750-0698P	2/3/00
16.	United States	60/179,388	2750-0696P	2/1/00
17.	United States	60/179,395	2750-0695P	2/1/00
18.	United States	60/185,119	2750-0720P	2/25/00
19.	United States	60/180,039	2750-0697P	2/3/00
20.	United States	60/184,658	2750-0717P	2/24/00
21.	United States	60/185,396	2750-0722P	2/28/00
22.	United States	60/180,206	2750-0699P	2/4/00
23.	United States	60/185,118	2750-0719P	2/25/00

28. Appln. No. 09/870,664 (Attorney No. 2750-1451P) filed 6/1/01 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
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1.	United States	60/208,918	2750-0924P	6/5/00
2.	United States	60/214,535	2750-1036P	6/27/00
3.	United States	60/208,920	2750-0927P	6/5/00
4.	United States	60/215,127	2750-1041P	6/30/00
5.	United States	60/214,799	2750-1039P	6/28/00
6.	United States	60/213,249	2750-0963P	6/22/00
7.	United States	60/210,564	2750-0933P	6/9/00
8.	United States	60/210,006	2750-0931P	6/8/00
9.	United States	60/208,312	2750-0921P	6/1/00
10.	United States	60/211,214	2750-0936P	6/13/00

29. Appln. No. 10/082,096 (Attorney No. 2750-1484P) filed 2/26/02 is a continuation of Appln No. 09/795,347 (Attorney No. 2750-1422P) filed 3/1/01 and claims priority under 35 USC §119(e) of the following provisional applications claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
1.	United States	60/192,308	2750-0773P	3/27/00
2.	United States	60/189,959	2750-0756P	3/16/00
3.	United States	60/190,069	2750-0758P	3/20/00
4.	United States	60/190,070	2750-0759P	3/20/00
5.	United States	60/190,545	2750-0761P	3/20/00
6.	United States	60/190,089	2750-0762P	3/20/00
7.	United States	60/191,084	2750-0763P	3/22/00
8.	United States	60/191,097	2750-0764P	3/22/00
9.	United States	60/191,543	2750-0766P	3/23/00
10.	United States	60/191,545	2750-0767P	3/23/00
11.	United States	60/191,823	2750-0769P	3/24/00
12.	United States	60/192,421	2750-0772P	3/27/00
13.	United States	60/189,461	2750-0748P	3/15/00
14.	United States	60/192,940	2750-0775P	3/29/00
15.	United States	60/192,941	2750-0776P	3/29/00
16.	United States	60/193,244	2750-0778P	3/30/00
17.	United States	60/193,245	2750-0779P	3/30/00
18.	United States	60/193,453	2750-0781P	3/31/00
19.	United States	60/193,455	2750-0782P	3/31/00
20.	United States	60/191,825	2750-0770P	3/24/00
21.	United States	60/187,378	2750-0734P	3/7/00
22.	United States	60/186,390	2750-0711P	3/2/00
23.	United States	60/186,283	2750-0725P	3/1/00
24.	United States	60/186,296	2750-0726P	3/1/00

25.	United States	60/187,178	2750-0728P	3/2/00
26.	United States	60/186,386	2750-0729P	3/2/00
27.	United States	60/186,387	2750-0730P	3/2/00
28.	United States	60/189,953	2750-0755P	3/16/00
29.	United States	60/186,669	2750-0733P	3/3/00
30.	United States	60/189,462	2750-0749P	3/15/00
31.	United States	60/187,896	2750-0736P	3/8/00
32.	United States	60/187,888	2750-0737P	3/8/00
33.	United States	60/188,187	2750-0739P	3/10/00
34.	United States	60/188,186	2750-0740P	3/10/00
35.	United States	60/188,185	2750-0742P	3/10/00
36.	United States	60/188,175	2750-0743P	3/10/00
37.	United States	60/189,080	2750-0745P	3/14/00
38.	United States	60/189,052	2750-0746P	3/14/00
39.	United States	60/186,748	2750-0732P	3/3/00

30. Appln. No. 10/086,239 (Attorney No. 2750-1489P) filed 3/4/02 is a continuation of Appln No. 09/845,206 (Attorney No. 2750-1441P) filed 5/1/01 and claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
1.	United States	60/201,305	2750-0850P	5/2/00
2.	United States	60/206,319	2750-0903P	5/23/00
3.	United States	60/204,829	2750-0894P	5/17/00
4.	United States	60/201,275	2750-0838P	5/2/00
5.	United States	60/205,058	2750-0896P	5/18/00
6.	United States	60/205,242	2750-0897P	5/19/00
7.	United States	60/205,243	2750-0898P	5/19/00
8.	United States	60/205,572	2750-0900P	5/22/00
9.	United States	60/204,569	2750-0892P	5/16/00
10.	United States	60/206,316	2750-0902P	5/23/00
11.	United States	60/204,830	2750-0893P	5/17/00
12.	United States	60/206,553	2750-0904P	5/24/00
13.	United States	60/206,545	2750-0905P	5/24/00
14.	United States	60/207,367	2750-0907P	5/26/00
15.	United States	60/207,243	2750-0908P	5/26/00
16.	United States	60/207,239	2750-0910P	5/26/00
17.	United States	60/207,354	2750-0911P	5/26/00
18.	United States	60/207,452	2750-0913P	5/30/00
19.	United States	60/207,329	2750-0914P	5/30/00
20.	United States	60/205,576	2750-0901P	5/22/00
21.	United States	60/202,636	2750-0863P	5/9/00

22.	United States	60/200,879	2750-0839P	5/1/00
23.	United States	60/201,740	2750-0857P	5/4/00
24.	United States	60/201,750	2750-0858P	5/4/00
25.	United States	60/202,112	2750-0860P	5/5/00
26.	United States	60/205,201	2750-0895P	5/18/00
27.	United States	60/202,914	2750-0862P	5/9/00
28.	United States	60/204,568	2750-0891P	5/16/00
29.	United States	60/202,919	2750-0865P	5/9/00
30.	United States	60/202,634	2750-0866P	5/9/00
31.	United States	60/202,968	2750-0878P	5/10/00
32.	United States	60/202,963	2750-0879P	5/10/00
33.	United States	60/203,457	2750-0881P	5/11/00
34.	United States	60/203,279	2750-0882P	5/11/00
35.	United States	60/203,916	2750-0884P	5/12/00
36.	United States	60/203,915	2750-0885P	5/12/00
37.	United States	60/204,388	2750-0887P	5/15/00
38.	United States	60/204,122	2750-0888P	5/15/00
39.	United States	60/202,180	2750-0861P	5/5/00

31. Appln. No. 10/094,538 (Attorney No. 2750-1491P) filed 3/11/02 is a continuation of Appln No. 09/783,606 (Attorney No. 2750-1411P) filed 2/15/01 and claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
	United States	60/182,478	2750-0713P	2/15/00

32. Appln. No. 10/095,465 (Attorney No. 2750-1492P) filed 3/13/02 is a continuation of Appln No. 09/824,882 (Attorney No. 2750-1435P) filed 4/4/01 and claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
1.	United States	60/199,828	2750-0834P	4/26/00
2.	United States	60/198,619	2750-0824P	4/20/00
3.	United States	60/195,045	2750-0796P	4/6/00
4.	United States	60/194,404	2750-0786P	4/4/00
5.	United States	60/196,486	2750-0809P	4/12/00
6.	United States	60/196,487	2750-0806P	4/12/00
7.	United States	60/196,169	2750-0803P	4/11/00
8.	United States	60/196,089	2750-0804P	4/11/00
9.	United States	60/196,485	2750-0808P	4/12/00
10.	United States	60/194,874	2750-0793P	4/6/00

11.	United States	60/197,671	2750-0819P	4/17/00
12.	United States	60/194,872	2750-0794P	4/6/00
13.	United States	60/194,697	2750-0791P	4/5/00
14.	United States	60/194,683	2750-0790P	4/5/00
15.	United States	60/199,122	2750-0831P	4/24/00
16.	United States	60/198,623	2750-0825P	4/20/00
17.	United States	60/197,678	2750-0816P	4/17/00
18.	United States	60/198,133	2750-0818P	4/17/00
19.	United States	60/197,687	2750-0815P	4/17/00
20.	United States	60/198,386	2750-0821P	4/19/00
21.	United States	60/198,373	2750-0822P	4/19/00
22.	United States	60/194,398	2750-0787P	4/4/00
23.	United States	60/200,102	2750-0837P	4/27/00
24.	United States	60/195,283	2750-0798P	4/7/00
25.	United States	60/196,289	2750-0807P	4/12/00
26.	United States	60/199,124	2750-0830P	4/24/00
27.	United States	60/195,257	2750-0799P	4/7/00
28.	United States	60/199,818	2750-0835P	4/26/00
29.	United States	60/200,103	2750-0836P	4/27/00
30.	United States	60/198,767	2750-0827P	4/21/00
31.	United States	60/198,763	2750-0828P	4/21/00
32.	United States	60/194,885	2750-0795P	4/6/00

33. Appln. No. 10/097,295 (Attorney No. 2750-1494P) filed 3/15/02 is a continuation of Appln No. 09/881,096 (Attorney No. 2750-1452P) filed 6/15/01 and claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
1.	United States	60/212,727	2750-0961P	6/20/00
2.	United States	60/212,623	2750-0958P	6/19/00
3.	United States	60/213,270	2750-0967P	6/22/00
4.	United States	60/214,524	2750-0970P	6/27/00
5.	United States	60/211,538	2750-0940P	6/15/00

34. Appln. No. 10/103,845 (Attorney No. 2750-1499P) filed 3/25/02 is a continuation of Appln No. 09/898,063 (Attorney No. 2750-1454P) filed 7/5/01 and claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
1.	United States	60/219,033	2750-1057P	7/18/00
2.	United States	60/216,362	2750-1043P	7/5/00

3.	United States	60/217,384	2750-1046P	7/11/00
4.	United States	60/220,811	2750-1079P	7/25/00
5.	United States	60/220,652	2750-1081P	7/25/00

35. Appln. No. 10/123,111 (Attorney No. 2750-1509P) filed 4/17/02 is a continuation of Appln No. 09/928,372 (Attorney No. 2750-1471P) filed 8/14/01 and claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
1.	United States	60/225,303	2750-1084P	8/15/00
2.	United States	60/227,024	2750-1162P	8/23/00
3.	United States	60/228,898	2750-1225P	8/30/00
4.	United States	60/224,517	2750-1082P	8/14/00
5.	United States	60/226,452	2750-1086P	8/21/00

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Application 10/406,556 (attorney no. 2750-1555P) listed above is a continuation Application No. 10/132,277 (Attorney No. 2750-1516P), filed on April 26, 2002, the entire contents of which are hereby incorporated by reference.

Application No. 10/132,277 (Attorney No. 2750-1516P) is a continuation-in-part of the following nonprovisional applications, to which the present application also claims priority, the entire contents of which are hereby incorporated by reference:

	Country	Client No.	Attorney No.	Appln. No.	Filed
1.	United States	91006.002	2750-0875P	09/570,581	5/12/00
2.	United States	00037.002	2750-0941P	09/595,334	6/16/00
3.	United States	00039.002	2750-0943P	09/596,577	6/16/00
4.	United States	00042.003	2750-0971P	09/602,660	6/21/00
5.	United States	00043.002	2750-0972P	09/602,152	6/22/00
6.	United States	00044.002	2750-0973P	09/602,025	6/23/00
7.	United States	00046.002	2750-0976P	09/605,843	6/28/00
8.	United States	00049.002	2750-0978P	09/608,960	6/30/00
9.	United States	00059.002	2750-0985P	09/615,007	7/12/00
10.	United States	00060.002	2750-0986P	09/615,748	7/13/00
11.	United States	00061.002	2750-0987P	09/617,525	7/14/00
12.	United States	00062.002	2750-0988P	09/617,203	7/14/00
13.	United States	00064.002	2750-0989P	09/620,421	7/19/00
14.	United States	00065.002	2750-0990P	09/621,323	7/20/00
15.	United States	00066.002	2750-0991P	09/621,630	7/21/00
16.	United States	00067.002	2750-0992P	09/621,660	7/21/00

	Country	Client No.	Attorney No.	Appln. No.	Filed
17.	United States	00069.002	2750-0993P	09/621.902	7/21/00
18.	United States	00070.002	2750-0994P	09/616.628	7/26/00
19.	United States	00071.002	2750-0995P	09/628.986	7/27/00
20.	United States	00072.002	2750-0996P	09/628.552	7/28/00
21.	United States	00073.002	2750-0997P	09/632.340	8/2/00
22.	United States	00074.002	2750-0998P	09/632.349	8/3/00
23.	United States	00076.002	2750-0999P	09/633.051	8/4/00
24.	United States	00077.002	2750-1000P	09/633.191	8/4/00
25.	United States	00079.002	2750-1001P	09/633.239	8/4/00
26.	United States	00080.002	2750-1002P	09/635.277	8/9/00
27.	United States	00081.002	2750-1003P	09/637.837	8/11/00
28.	United States	00082.002	2750-1004P	09/636.555	8/11/00
29.	United States	00083.002	2750-1005P	09/637.563	8/11/00
30.	United States	00084.002	2750-1006P	09/641.198	8/17/00
31.	United States	00087.002	2750-1009P	09/640.695	8/18/00
32.	United States	00085.002	2750-1007P	09/641.359	8/18/00
33.	United States	00086.002	2750-1008P	09/641.375	8/18/00
34.	United States	00088.002	2750-1010P	09/643.854	8/23/00
35.	United States	00089.002	2750-1011P	09/645.440	8/25/00
36.	United States	00090.002	2750-1012P	09/648.708	8/25/00
37.	United States	00091.002	2750-1013P	09/645.441	8/25/00
38.	United States	00092.002	2750-1014P	09/651.370	8/30/00
39.	United States	00093.002	2750-1015P	09/653.466	8/31/00
40.	United States	00094.002	2750-1016P	09/654.547	9/1/00
41.	United States	00095.002	2750-1017P	09/657.454	9/7/00
42.	United States	00096.002	2750-1018P	09/657.569	9/8/00
43.	United States	00098.002	2750-1019P	09/660.883	9/13/00
44.	United States	00099.002	2750-1020P	09/663.196	9/15/00
45.	United States	00101.002	2750-1021P	09/663.195	9/15/00
46.	United States	00102.002	2750-1022P	09/665.714	9/20/00
47.	United States	00103.002	2750-1023P	09/667.597	9/22/00
48.	United States	00104.002	2750-1024P	09/667.517	9/22/00
49.	United States	00105.002	2750-1025P	09/667.229	9/22/00
50.	United States	00106.002	2750-1026P	09/671.635	9/28/00
51.	United States	00107.002	2750-1027P	09/672.075	9/29/00
52.	United States	00108.002	2750-1028P	09/679.203	10/4/00
53.	United States	00109.002	2750-1029P	09/678.223	10/5/00
54.	United States	00110.002	2750-1030P	09/680.499	10/6/00
55.	United States	00111.002	2750-1031P	09/680.490	10/6/00
56.	United States	00112.002	2750-1032P	09/680.498	10/6/00
57.	United States	00113.002	2750-1033P	09/686.093	10/12/00
58.	United States	00116.002	2750-1034P	09/690.745	10/18/00
59.	United States	00120.002	2750-1301P	09/692.108	10/20/00
60.	United States	00119.002	2750-1298P	09/692.153	10/20/00
61.	United States	00118.002	2750-1295P	09/692.157	10/20/00

	Country	Client No.	Attorney No.	Appln. No.	Filed
62.	United States	00121.002	2750-1308P	09/695,391	10/25/00
63.	United States	00122.002	2750-1311P	09/696,305	10/26/00
64.	United States	00123.002	2750-1314P	09/697,080	10/27/00
65.	United States	00124.002	2750-1317P	09/697,718	10/27/00
66.	United States	00125.002	2750-1329P	09/702,840	11/1/00
67.	United States	00126.002	2750-1332P	09/703,932	11/2/00
68.	United States	00127.002	2750-1335P	09/704,559	11/3/00
69.	United States	00128.002	2750-1338P	09/704,542	11/3/00
70.	United States	00129.002	2750-1347P	09/708,092	11/8/00
71.	United States	00143.002	2750-1249P	09/726,578	12/1/00
72.	United States	00153.002	2750-1390P	09/769,525	1/26/01
73.	United States	00157.002	2750-1401P	09/774,806	2/1/01
74.	United States	00231.002	2750-1450P	09/870,652	6/1/01
75.	United States	91072.002	2750-1453P	09/878,974	6/13/01
76.	United States	00170.003	2750-1484P	10/082,096	2/26/02
77.	United States	00211.003	2750-1489P	10/086,239	3/4/02
78.	United States	00191.003	2750-1492P	10/095,465	3/13/02
79.	United States	00252.003	2750-1501P	10/106,718	3/27/02
80.	United States	80298.003	2750-1509P	10/132,111	4/17/02

Through the applications listed above, the present application also claims priority under 35 USC §119(e), §119(a-d) and §120 of the following applications, the entire contents of which are hereby incorporated by reference:

	Country	Client No.	Attorney No.	Appln.	Filed
81.	United States	91006.001	2750-0432P	60/134,370	5/14/99
82.	United States	00037.001	2750-0464P	60/139,492	6/17/99
83.	United States	00038.001	2750-0465P	60/139,763	6/18/99
84.	United States	00039.001	2750-0466P	60/139,750	6/18/99
85.	United States	00042.001	2750-0467P	60/139,817	6/21/99
86.	United States	00043.001	2750-0468P	60/139,899	6/22/99
87.	United States	00042.002	2750-0470P	60/140,353	6/23/99
88.	United States	00044.001	2750-0469P	60/140,354	6/23/99
89.	United States	00046.001	2750-0472P	60/140,823	6/28/99
90.	United States	00049.001	2750-0474P	60/141,287	6/30/99
91.	United States	00059.001	2750-0481P	60/142,977	7/12/99
92.	United States	00060.001	2750-0482P	60/143,542	7/13/99
93.	United States	00061.001	2750-0489P	60/143,624	7/14/99
94.	United States	00062.001	2750-0490P	60/144,005	7/15/99
95.	United States	00064.001	2750-0497P	60/144,325	7/19/99
96.	United States	00065.001	2750-0500P	60/144,632	7/20/99
97.	United States	00066.001	2750-0503P	60/144,814	7/21/99
98.	United States	00067.001	2750-0504P	60/145,192	7/22/99
99.	United States	00069.001	2750-0505P	60/145,218	7/23/99

	Country	Client No.	Attorney No.	Appln.	Filed
100.	United States	00070.001	2750-0506P	60/145,276	7/26/99
101.	United States	00071.001	2750-0509P	60/145,913	7/27/99
102.	United States	00072.001	2750-0510P	60/145,951	7/28/99
103.	United States	00073.001	2750-0513P	60/146,386	8/2/99
104.	United States	00074.001	2750-0514P	60/147,038	8/3/99
105.	United States	00076.001	2750-0515P	60/147,204	8/4/99
106.	United States	00077.001	2750-0518P	60/147,260	8/5/99
107.	United States	00079.001	2750-0520P	60/147,416	8/6/99
108.	United States	00080.001	2750-0521P	60/147,493	8/9/99
109.	United States	00081.001	2750-0524P	60/148,319	8/11/99
110.	United States	00082.001	2750-0530P	60/148,341	8/12/99
111.	United States	00083.001	2750-0529P	60/148,565	8/13/99
112.	United States	00084.001	2750-0537P	60/149,175	8/17/99
113.	United States	00085.001	2750-0538P	60/149,426	8/18/99
114.	United States	00086.001	2750-0539P	60/149,722	8/20/99
115.	United States	00087.001	2750-0542P	60/149,723	8/20/99
116.	United States	00088.001	2750-0543P	60/149,902	8/23/99
117.	United States	00089.001	2750-0544P	60/150,566	8/25/99
118.	United States	00090.001	2750-0547P	60/150,884	8/26/99
119.	United States	00091.001	2750-0548P	60/151,080	8/27/99
120.	United States	00092.001	2750-0549P	60/151,303	8/30/99
121.	United States	00093.001	2750-0552P	60/151,438	8/31/99
122.	United States	00094.001	2750-0553P	60/151,930	9/1/99
123.	United States	00095.001	2750-0554P	60/152,363	9/7/99
124.	United States	00096.001	2750-0555P	60/153,070	9/10/99
125.	United States	00098.001	2750-0556P	60/153,758	9/13/99
126.	United States	00099.001	2750-0557P	60/154,018	9/15/99
127.	United States	00101.001	2750-0558P	60/154,039	9/16/99
128.	United States	00102.001	2750-0559P	60/154,779	9/20/99
129.	United States	00103.001	2750-0560P	60/155,139	9/22/99
130.	United States	00104.001	2750-0561P	60/155,486	9/23/99
131.	United States	00105.001	2750-0562P	60/155,659	9/24/99
132.	United States	00106.001	2750-0563P	60/156,458	9/28/99
133.	United States	00107.001	2750-0564P	60/156,596	9/29/99
134.	United States	00108.001	2750-0570P	60/157,117	10/4/99
135.	United States	00109.001	2750-0571P	60/157,753	10/5/99
136.	United States	00110.001	2750-0572P	60/157,865	10/6/99
137.	United States	00111.001	2750-0575P	60/158,029	10/7/99
138.	United States	00112.001	2750-0576P	60/158,232	10/8/99
139.	United States	00113.001	2750-0577P	60/158,369	10/12/99
140.	United States	00116.001	2750-0584P	60/159,584	10/18/99
141.	United States	00119.001	2750-0588P	60/160,741	10/21/99
142.	United States	00118.001	2750-0585P	60/160,815	10/21/99
143.	United States	00120.001	2750-0591P	60/160,980	10/22/99
144.	United States	00121.001	2750-0594P	60/161,405	10/25/99

	Country	Client No.	Attorney No.	Appln.	Filed
145.	United States	00122.001	2750-0597P	60/161,361	10/26/99
146.	United States	00123.001	2750-0601P	60/161,920	10/28/99
147.	United States	00124.001	2750-0604P	60/162,143	10/29/99
148.	United States	00125.001	2750-0607P	60/162,894	11/1/99
149.	United States	00126.001	2750-0610P	60/163,093	11/2/99
150.	United States	00127.001	2750-0613P	60/163,249	11/3/99
151.	United States	00128.001	2750-0616P	60/163,379	11/4/99
152.	United States	00129.001	2750-0619P	60/164,146	11/8/99
153.	United States	00131.001	2750-0628P	60/164,544	11/10/99
154.	United States	00133.001	2750-0634P	60/164,870	11/12/99
155.	United States	00132.001	2750-0631P	60/164,961	11/12/99
156.	United States	00134.001	2750-0637P	60/164,927	11/15/99
157.	United States	00135.001	2750-0640P	60/165,669	11/16/99
158.	United States	00136.001	2750-0643P	60/165,919	11/17/99
159.	United States	00137.001	2750-0646P	60/166,157	11/18/99
160.	United States	00139.001	2750-0649P	60/166,419	11/19/99
161.	United States	00140.001	2750-0652P	60/166,733	11/22/99
162.	United States	00141.001	2750-0656P	60/167,233	11/24/99
163.	United States	00142.001	2750-0659P	60/167,904	11/30/99
164.	United States	00143.001	2750-0663P	60/168,232	12/1/99
165.	United States	00144.001	2750-0666P	60/168,546	12/2/99
166.	United States	00145.001	2750-0669P	60/168,675	12/3/99
167.	United States	00147.001	2750-0672P	60/169,298	12/7/99
168.	United States	00149.001	2750-0677P	60/171,107	12/16/99
169.	United States	00153.001	2750-0690P	60/178,547	1/27/00
170.	United States	00155.001	2750-0692P	60/178,754	1/28/00
171.	United States	00157.001	2750-0695P	60/179,395	2/1/00
172.	United States	00158.001	2750-0697P	60/180,039	2/3/00
173.	United States	00159.001	2750-0699P	60/180,206	2/4/00
174.	United States	00160.001	2750-0701P	60/180,695	2/7/00
175.	United States	00161.001	2750-0703P	60/181,228	2/9/00
176.	United States	00162.001	2750-0705P	60/181,476	2/10/00
177.	United States	00163.001	2750-0707P	60/182,477	2/15/00
178.	United States	00164.001	2750-0712P	60/182,512	2/15/00
179.	United States	00165.001	2750-0714P	60/183,166	2/17/00
180.	United States	00167.001	2750-0716P	60/184,667	2/24/00
181.	United States	00168.001	2750-0719P	60/185,118	2/25/00
182.	United States	00169.001	2750-0722P	60/185,396	2/28/00
183.	United States	00170.001	2750-0725P	60/186,283	3/1/00
184.	United States	00172.001	2750-0729P	60/186,386	3/2/00
185.	United States	00171.001	2750-0711P	60/186,390	3/2/00
186.	United States	00173.001	2750-0732P	60/186,748	3/3/00
187.	United States	00174.001	2750-0734P	60/187,378	3/7/00
188.	United States	00175.001	2750-0736P	60/187,896	3/8/00
189.	United States	00177.001	2750-0739P	60/188,187	3/10/00

	Country	Client No.	Attorney No.	Appln.	Filed
190.	United States	00178.001	2750-0742P	60/188,185	3/10/00
191.	United States	00179.001	2750-0745P	60/189,080	3/14/00
192.	United States	00180.001	2750-0748P	60/189,461	3/15/00
193.	United States	00181.001	2750-0755P	60/189,953	3/16/00
194.	United States	00182.001	2750-0758P	60/190,069	3/20/00
195.	United States	00183.001	2750-0761P	60/190,545	3/20/00
196.	United States	00184.001	2750-0763P	60/191,084	3/22/00
197.	United States	00185.001	2750-0766P	60/191,543	3/23/00
198.	United States	00186.001	2750-0769P	60/191,823	3/24/00
199.	United States	00187.001	2750-0772P	60/192,421	3/27/00
200.	United States	00188.001	2750-0775P	60/192,940	3/29/00
201.	United States	00189.001	2750-0778P	60/193,244	3/30/00
202.	United States	00190.001	2750-0781P	60/193,453	3/31/00
203.	United States	00191.001	2750-0786P	60/194,404	4/4/00
204.	United States	00192.001	2750-0790P	60/194,683	4/5/00
205.	United States	00193.001	2750-0793P	60/194,874	4/6/00
206.	United States	00194.001	2750-0795P	60/194,885	4/6/00
207.	United States	00195.001	2750-0798P	60/195,283	4/7/00
208.	United States	00196.001	2750-0803P	60/196,169	4/11/00
209.	United States	00197.001	2750-0806P	60/196,487	4/12/00
210.	United States	00200.001	2750-0808P	60/196,485	4/12/00
211.	United States	00201.001	2750-0815P	60/197,687	4/17/00
212.	United States	00202.001	2750-0818P	60/198,133	4/17/00
213.	United States	00203.001	2750-0821P	60/198,386	4/19/00
214.	United States	00204.001	2750-0824P	60/198,619	4/20/00
215.	United States	00206.001	2750-0827P	60/198,767	4/21/00
216.	United States	00207.001	2750-0830P	60/199,124	4/24/00
217.	United States	00208.001	2750-0834P	60/199,828	4/26/00
218.	United States	00210.001	2750-0836P	60/200,103	4/27/00
219.	United States	00211.001	2750-0838P	60/201,275	5/2/00
220.	United States	00212.001	2750-0857P	60/201,740	5/4/00
221.	United States	00213.001	2750-0860P	60/202,112	5/5/00
222.	United States	00214.001	2750-0862P	60/202,914	5/9/00
223.	United States	00215.001	2750-0865P	60/202,919	5/9/00
224.	United States	00216.001	2750-0878P	60/202,968	5/10/00
225.	United States	00217.001	2750-0881P	60/203,457	5/11/00
226.	United States	00219.001	2750-0884P	60/203,916	5/12/00
227.	United States	00220.001	2750-0887P	60/204,388	5/15/00
228.	United States	00221.001	2750-0891P	60/204,568	5/16/00
229.	United States	00222.001	2750-0893P	60/204,830	5/17/00
230.	United States	00223.001	2750-0895P	60/205,201	5/18/00
231.	United States	00224.001	2750-0897P	60/205,242	5/19/00
232.	United States	00225.001	2750-0900P	60/205,572	5/22/00
233.	United States	00226.001	2750-0902P	60/206,316	5/23/00
234.	United States	00227.001	2750-0904P	60/206,553	5/24/00

	Country	Client No.	Attorney No.	Appln.	Filed
235.	United States	00228.001	2750-0907P	60/207,367	5/26/00
236.	United States	00229.001	2750-0910P	60/207,239	5/26/00
237.	United States	00230.001	2750-0913P	60/207,452	5/30/00
238.	United States	00231.001	2750-0920P	60/208,329	6/1/00
239.	United States	00232.001	2750-0923P	60/208,910	6/5/00
240.	United States	00233.001	2750-0926P	60/208,921	6/5/00
241.	United States	00234.001	2750-0930P	60/210,012	6/8/00
242.	United States	00235.001	2750-0932P	60/210,670	6/9/00
243.	United States	00237.001	2750-0935P	60/211,213	6/13/00
244.	United States	80274.001	2750-0939P	60/211,540	6/15/00
245.	United States	80275.001	2750-0957P	60/212,649	6/19/00
246.	United States	80276.001	2750-0960P	60/212,713	6/20/00
247.	United States	80276.001	2750-0960P	60/212,713	6/20/00
248.	United States	80278.001	2750-0966P	60/213,220	6/22/00
249.	United States	00242.001	2750-0962P	60/213,271	6/22/00
250.	United States	00248.001	2750-1035P	60/214,534	6/27/00
251.	United States	80279.001	2750-0969P	60/214,762	6/27/00
252.	United States	00249.001	2750-1038P	60/214,800	6/28/00
253.	United States	00250.001	2750-1040P	60/215,775	6/30/00
254.	United States	00252.001	2750-1042P	60/216,361	7/5/00
255.	United States	00253.001	2750-1045P	60/217,476	7/11/00
256.	United States	00254.001	2750-1056P	60/219,004	7/18/00
257.	United States	00255.001	2750-1059P	60/220,647	7/25/00
258.	United States	00256.001	2750-1080P	60/220,484	7/25/00
259.	United States	80298.001	2750-1082P	60/224,517	8/14/00
260.	United States	80300.001	2750-1084P	60/225,303	8/15/00
261.	United States	80301.001	2750-1086P	60/226,452	8/21/00
262.	United States	80307.001	2750-1162P	60/227,024	8/23/00
263.	United States	80308.001	2750-1225P	60/228,898	8/30/00
264.	United States	80309.001	2750-1227P	60/230,430	9/6/00
265.	United States	80310.001	2750-1229P	60/232,044	9/13/00
266.	United States	80311.001	2750-1231P	60/232,858	9/15/00
267.	United States	80312.001	2750-1233P	60/233,621	9/18/00
268.	United States	80313.001	2750-1253P	60/234,179	9/20/00
269.	United States	80314.001	2750-1259P	60/234,233	9/21/00
270.	United States	80315.001	2750-1262P	60/234,968	9/25/00
271.	United States	80316.001	2750-1264P	60/234,974	9/25/00
272.	United States	80317.001	2750-1266P	60/234,949	9/26/00
273.	United States	80318.001	2750-1270P	60/236,732	10/2/00
274.	United States	80319.001	2750-1272P	60/237,379	10/4/00
275.	United States	80320.001	2750-1274P	60/237,686	10/5/00
276.	United States	80321.001	2750-1275P	60/238,473	10/10/00
277.	United States	80322.001	2750-1277P	60/238,456	10/10/00
278.	United States	80323.001	2750-1279P	60/239,091	10/11/00
279.	United States	80324.001	2750-1281P	60/240,862	10/17/00

	Country	Client No.	Attorney No.	Appln.	Filed
280.	United States	80325.001	2750-1283P	60/241,368	10/19/00
281.	United States	80331.001	2750-1304P	60/241,751	10/20/00
282.	United States	80332.001	2750-1306P	60/242,065	10/23/00
283.	United States	80334.001	2750-1320P	60/242,686	10/24/00
284.	United States	80335.001	2750-1321P	60/242,705	10/25/00
285.	United States	80336.001	2750-1323P	60/243,289	10/26/00
286.	United States	80337.001	2750-1325P	60/243,398	10/27/00
287.	United States	80338.001	2750-1327P	60/243,723	10/30/00
288.	United States	80339.001	2750-1341P	60/244,691	11/1/00
289.	United States	80340.001	2750-1343P	60/244,923	11/2/00
290.	United States	80341.001	2750-1345P	60/245,164	11/3/00
291.	United States	80342.001	2750-1359P	60/245,676	11/6/00
292.	United States	80343.001	2750-1244P	60/246,732	11/9/00
293.	United States	80344.001	2750-1245P	60/247,010	11/13/00
294.	United States	80346.001	2750-1247P	60/247,050	11/13/00
295.	United States	80347.001	2750-1348P	60/248,198	11/15/00
296.	United States	80348.001	2750-1351P	60/249,256	11/17/00
297.	United States	80349.001	2750-1353P	60/249,454	11/20/00
298.	United States	80350.001	2750-1356P	60/252,464	11/22/00
299.	United States	80351.001	2750-1358P	60/252,598	11/24/00
300.	United States	80352.001	2750-1363P	60/253,722	11/29/00
301.	United States	80353.001	2750-1368P	60/251,504	12/7/00
302.	United States	80354.001	2750-1370P	60/251,853	12/8/00
303.	United States	80355.001	2750-1372P	60/254,174	12/11/00
304.	United States	80356.001	2750-1375P	60/256,503	12/15/00
305.	United States	80357.001	2750-1377P	60/255,891	12/18/00
306.	United States	80359.001	2750-1384P	60/258,880	1/2/01
307.	United States	80362.001	2750-1388P	60/262,389	1/19/01
308.	United States	80363.001	2750-1391P	60/264,026	1/26/01
309.	United States	80364.001	2750-1393P	60/264,282	1/29/01
310.	United States	3001-55300-US- P-30946.01	2750-1402P	60/266,468	2/6/01
311.	United States	3001-55300-US- P-31053.01	2750-1406P	60/267,425	2/9/01
312.	United States	3001-55300-US- P-31070.01	2750-1409P	60/267,707	2/12/01
313.	United States	3001-55300-US- P-31112.01	2750-1414P	60/269,890	2/21/01
314.	United States	3001-55300-US- P-31130.01	2750-1416P	60/269,892	2/21/01
315.	United States	3001-55300-US- P-31162.01	2750-1424P	60/271,724	2/28/01
316.	United States	00170.002	2750-1422P	09/795,347	3/1/01
317.	United States	3001-55300-US- P-31197.01	2750-1430P	60/273,553	3/7/01

	Country	Client No.	Attorney No.	Appln.	Filed
318.	United States	00191.002	2750-1435P	09/824,882	4/4/01
319.	United States	00211.002	2750-1441P	09/845,206	5/1/01
320.	United States	00252.002	2750-1455P	09/898,064	7/5/01
321.	United States	80298.002	2750-1471P	09/928,372	8/14/01

Number 49

Application No. 10/340,820 (attorney no. 2750-1543P) listed above is a continuation of Application No. 10/132,287 (Attorney No. 2750-1517P), filed on April 26, 2002, the entire contents of which are hereby incorporated by reference.

Application No. 10/132,287 (Attorney No. 2750-1517P) is a continuation-in-part of the following nonprovisional applications, to which the present application claims priority under 35 U.S.C. §120, the entire contents of which are hereby incorporated by reference:

	G.	H.	Attorney	Appln.	Filed	Status
1.	United States	91022.002	2750-1419P	09/790,663	2/23/01	Pending at the time of filing 10/132.287
2.	United States	91025.002	2750-1423P	09/795,359	3/1/01	Pending at the time of filing 10/132.287
3.	United States	91042.002	2750-1434P	09/824,790	4/4/01	Pending at the time of filing 10/132.287
4.	United States	91055.002	2750-1442P	09/845,311	5/1/01	Pending at the time of filing 10/132.287
5.	United States	91068.002	2750-1449P	09/870,476	6/1/01	Pending at the time of filing 10/132.287
6.	United States	91072.002	2750-1453P	09/878,974	6/13/01	Pending at the time of filing 10/132.287
7.	United States	91081.003	2750-1507P	10/123,222	4/17/02	Pending at the time of filing 10/132.287

Through the seven applications listed above, the present application also claims priority under 35 USC §119(e) of the following applications, the entire contents of which are hereby incorporated by reference:

1. Appln. No. 09/790,663 (Attorney No. 2750-1419P) filed 2/23/01 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
a)	United States	60/185,140	2750-0718P	2/25/00
b)	United States	60/185,398	2750-0721P	2/28/00
c)	United States	60/185,750	2750-0724P	2/29/00

2. Appln. No. 09/795,359 (Attorney No. 2750-1423P) filed 3/1/01 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
a)	United States	60/186,277	2750-0727P	3/1/00
b)	United States	60/186,670	2750-0731P	3/3/00
c)	United States	60/187,379	2750-0735P	3/7/00
d)	United States	60/187,985	2750-0738P	3/9/00
e)	United States	60/188,174	2750-0741P	3/10/00
f)	United States	60/188,687	2750-0744P	3/13/00
g)	United States	60/189,460	2750-0747P	3/15/00
h)	United States	60/189,958	2750-0754P	3/16/00
i)	United States	60/189,965	2750-0757P	3/17/00
j)	United States	60/190,090	2750-0760P	3/20/00
k)	United States	60/191,549	2750-0765P	3/23/00
l)	United States	60/191,826	2750-0768P	3/24/00
m)	United States	60/192,420	2750-0771P	3/27/00
n)	United States	60/192,855	2750-0774P	3/29/00
o)	United States	60/193,243	2750-0777P	3/30/00
p)	United States	60/193,469	2750-0780P	3/31/00

3. Appln. No. 09/824,790 (Attorney No. 2750-1434P) filed 4/4/01 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
a)	United States	60/194,385	2750-0785P	4/4/00
b)	United States	60/194,682	2750-0789P	4/5/00
c)	United States	60/194,698	2750-0792P	4/5/00
d)	United States	60/194,884	2750-0784P	4/6/00
e)	United States	60/195,258	2750-0797P	4/7/00
f)	United States	60/196,168	2750-0802P	4/11/00
g)	United States	60/196,483	2750-0805P	4/12/00
h)	United States	60/197,397	2750-0814P	4/14/00
i)	United States	60/198,268	2750-0817P	4/17/00
j)	United States	60/198,400	2750-0820P	4/19/00
k)	United States	60/198,629	2750-0823P	4/20/00
l)	United States	60/198,765	2750-0826P	4/21/00

m)	United States	60/199,123	2750-0829P	4/24/00
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4. Appln. No. 09/845,311 (Attorney No. 2750-1442P) filed 5/1/01 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
a)	United States	60/200,885	2750-0840P	5/1/00
b)	United States	60/201,279	2750-0849P	5/2/00
c)	United States	60/201,751	2750-0856P	5/4/00
d)	United States	60/202,178	2750-0859P	5/5/00
e)	United States	60/202,915	2750-0864P	5/9/00
f)	United States	60/202,969	2750-0877P	5/10/00
g)	United States	60/203,458	2750-0880P	5/11/00
h)	United States	60/203,911	2750-0883P	5/12/00
i)	United States	60/204,395	2750-0886P	5/15/00
j)	United States	60/205,574	2750-0899P	5/22/00
k)	United States	60/206,988	2750-0906P	5/25/00
l)	United States	60/207,242	2750-0909P	5/26/00
m)	United States	60/207,291	2750-0912P	5/30/00

5. Appln. No. 09/870,476 (Attorney No. 2750-1449P) filed 6/1/01 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
a)	United States	60/208,324	2750-0919P	6/1/00
b)	United States	60/208,919	2750-0922P	6/5/00
c)	United States	60/208,917	2750-0925P	6/5/00
d)	United States	60/210,008	2750-0929P	6/8/00

6. Appln. No. 09/878,974 (Attorney No. 2750-1453P) filed 6/13/01 claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
a)	United States	60/211,210	2750-0937P	6/13/00
b)	United States	60/211,539	2750-0938P	6/15/00
c)	United States	60/212,414	2750-0956P	6/19/00
d)	United States	60/212,677	2750-0959P	6/20/00
e)	United States	60/212,713	2750-0960P	6/20/00
f)	United States	60/213,195	2750-0964P	6/22/00
g)	United States	60/213,221	2750-0965P	6/22/00
h)	United States	60/214,760	2750-0968P	6/27/00

7. Appln. No. 10/123,222 (Attorney No. 2750-1507P) filed 4/17/02 is a continuation of Appln No. 09/902,093 (Attorney No. 2750-1456P) filed 7/11/01 and claims priority under 35 USC §119(e) of the following provisional applications:

	Country	Appln. No.	Attorney No.	Filing Date
a)	United States	60/217,385	2750-1044P	7/11/00
b)	United States	60/219,021	2750-1055P	7/18/00
c)	United States	60/220,814	2750-1058P	7/25/00
d)	United States	60/224,516	2750-1083P	8/14/00
e)	United States	60/225,302	2750-1085P	8/15/00
f)	United States	60/226,725	2750-1087P	8/21/00
g)	United States	60/227,026	2750-1163P	8/23/00
h)	United States	60/228,897	2750-1226P	8/30/00

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Application No. 50 (attorney no. 2750-1568P) listed above is a continuation of Application No. 10/281,347 (attorney no. 2750-1534P), filed on October 28, 2002, the entire contents of which are hereby incorporated by reference.

Through Application No. 10/281,347, the present application also claims priority of US Application No. 09/935,631 (attorney no. 2750-1482P) filed on August 24, 2001, the entire contents of which are hereby incorporated by reference:

Through Application No. 09/935,631, the present application claims priority under 35 USC §119(e) of the following application, the entire contents of which are hereby incorporated by reference:

Country	Filed	Attorney No.	Application No.
United States	August 25, 2000	2750-2115P	60/237,363

The entire contents of the applications listed in the table above are expressly incorporated herein by reference.

This application contains thirty-six (36) CDRs submitted in duplicate (totaling 72 CDs), the entire contents of which are hereby incorporated by reference. The CDR contains the following files:

FILE CREATE DATE	FILE SIZE	FILE NAME	CD#1
08/14/03 11:23a	16,397	2750-0990P Table 1.txt	
08/14/03 11:38a	13,742	2750-1000P Table 1.txt	
08/14/03 11:44a	76,309	2750-1014P Table 1.txt	
08/14/03 11:17a	63,621	2750-1022P Table 1.txt	
08/14/03 11:15a	36,229	2750-1024P Table 1.txt	
08/14/03 11:12a	37,293	2750-1026P Table 1.txt	
08/14/03 11:06a	24,431	2750-1032P Table 1.txt	
08/14/03 11:09a	125,843	2750-1033P Table 1.txt	
08/14/03 12:29p	29,397	2750-1309P Table 1.txt	
08/14/03 12:02p	37,896	2750-1330P Table 1.txt	
09/26/02 05:02p	970,635	2750-1434P Table 1.txt	
08/14/03 11:41a	81,391	2750-1539P.txt	
08/15/03 11:11a	12,306,911	2750-1067P Table 1.txt	
08/15/03 11:12a	20,082,158	2750-1067P Table 2.txt	
09/26/02 07:59p	2,282,461	010103 Protein Domain Table.txt	
09/26/02 07:59p	1,027,504	Linkage Table.txt	
09/26/02 07:59p	16,291,710	Reference table 1-1.txt	
09/26/02 07:59p	415,379	Reference table 1-10.txt	
09/26/02 07:59p	326,402	Reference table 1-11.txt	
09/26/02 07:59p	240,743	Reference table 1-12.txt	
09/26/02 07:59p	404,923	Reference table 1-13a.txt	
09/26/02 07:59p	293,706	Reference table 1-14.txt	
09/26/02 07:59p	17,970,104	Reference table 1-2.txt	
09/26/02 07:59p	368,382	Reference table 1-15.txt	
09/26/02 07:59p	353,705	Reference table 1-16.txt	
09/26/02 07:59p	343,729	Reference table 1-17.txt	
09/26/02 07:59p	213,461	Reference table 1-18.txt	
09/26/02 07:59p	21,214,300	Reference table 1-3.txt	
09/26/02 07:59p	19,917,620	Reference table 1-4.txt	
09/26/02 07:59p	19,445,025	Reference table 1-5.txt	
09/26/02 07:59p	19,966,407	Reference table 1-6.txt	
09/26/02 07:59p	20,715,021	Reference table 1-7.txt	
09/26/02 07:59p	19,910,834	Reference table 1-8.txt	
09/26/02 07:59p	13,614,514	Reference table 1-9.txt	
09/26/02 07:59p	19,109,376	Sequence table 2-1.txt	
09/26/02 07:59p	3,227,432	Sequence table 2-10.txt	
09/26/02 07:59p	3,163,686	Sequence table 2-11.txt	
09/26/02 07:59p	3,306,298	Sequence table 2-12.txt	
09/26/02 07:59p	4,138,687	Sequence table 2-13.txt	
09/26/02 07:59p	3,798,626	Sequence table 2-14.txt	
09/26/02 07:59p	3,545,192	Sequence table 2-15.txt	
09/26/02 07:59p	2,972,792	Sequence table 2-16.txt	
09/26/02 07:59p	3,036,865	Sequence table 2-17.txt	
08/05/03 01:29p	0	NE03~1	
09/26/02 07:59p	1,843,822	Sequence table 2-18.txt	
09/26/02 07:59p	24,249,248	Sequence table 2-2.txt	
09/26/02 07:59p	43,222,912	Sequence table 2-3.txt	
09/26/02 07:59p	37,592,742	Sequence table 2-4.txt	
09/26/02 07:59p	36,235,456	Sequence table 2-5.txt	
09/26/02 08:00p	38,936,898	Sequence table 2-6.txt	
09/26/02 08:00p	36,922,994	Sequence table 2-7.txt	
09/26/02 08:00p	36,253,009	Sequence table 2-8.txt	
09/26/02 08:00p	24,426,947	Sequence table 2-9.txt	
09/26/02 08:00p	5,823,003	Table 1.txt	
09/26/02 08:17p	2,159,160	001018 Protein Domain Table.txt	
09/26/02 08:17p	12,553,156	2750-1383P Reference Table 1-1.txt.txt	
09/26/02 08:17p	5,095,131	2750-1383P Reference Table 1-2.txt	

FILE CREATE DATE	FILE SIZE	FILE NAME	CD#1
09/26/02 08:17p	11,149,192	2750-1383P Reference Table 1-3.txt	
09/26/02 08:17p	3,653,294	2750-1383P Reference Table 1-4.txt	
09/26/02 08:17p	10,308,774	2750-1383P Reference Table 1-5.txt	
09/26/02 08:17p	640,480	2750-1383P Reference Table 1-6.txt	
09/26/02 08:17p	631,956	2750-1383P Reference Table 1-7.txt	
09/26/02 08:17p	524,287	2750-1383P reference table 1-8.txt	
09/26/02 08:17p	187,382	2750-1383P reference table 1-9.txt	
09/26/02 08:17p	16,939,937	2750-1383P Sequence Table 2-1.txt.txt	
09/26/02 08:17p	5,542,701	2750-1383P Sequence Table 2-2.txt	
09/26/02 08:17p	20,453,906	2750-1383P Sequence Table 2-3.txt	
09/26/02 08:17p	6,726,925	2750-1383P Sequence Table 2-4.txt	
09/26/02 08:17p	7,242,795	2750-1383P Sequence Table 2-5.txt	
09/26/02 08:17p	3,464,934	2750-1383P Sequence Table 2-6.txt	
09/26/02 08:17p	4,001,618	2750-1383P Sequence Table 2-7.txt	
09/26/02 08:17p	3,170,298	2750-1383P sequence table 2-8.txt	
09/26/02 08:17p	1,033,609	2750-1383P sequence table 2-9.txt	
09/26/02 04:44p	2,752,459	010809 Protein Domain Table.txt	
09/26/02 04:44p	4,820,849	Aragen_Table 1.txt	
09/26/02 04:44p	4,810,511	Aragen_Table 2.txt	
09/26/02 04:44p	1,678,120	Aragen_Table 3.txt	
09/26/02 04:44p	31,033	Ockham_Table 1.txt	
09/26/02 04:45p	9,677,321	2750-1250P Sequence Table 2-2.txt	
09/26/02 04:45p	2,620,647	2750-1250P Reference Table 1-1.txt	
09/26/02 04:45p	1,441,278	2750-1250P Reference Table 1-2.txt	
09/26/02 04:45p	11,618,052	2750-1250P Sequence Table 2-1.txt	
09/26/02 04:45p	2,159,160	001018 Protein Domain Table.txt	
09/26/02 04:45p	2,752,459	010809 Protein Domain Table.txt	
09/26/02 04:45p	1,125,500	Aragen_Table 1.txt	
09/26/02 04:45p	655,638	Ockham_Table 1.txt	
08/14/03 01:11p	8,349,820	2750-1572P Table 2.txt	
08/14/03 01:10p	1,871,818	2750-1572P Table 1.txt	
09/26/02 04:45p	2,752,459	010809 Protein Domain Table.txt	

File Create Date	File Size	File Name	CD#2
08/14/03 12:54p	30,304,534	2750-0709P Reference Table 1.txt	
08/14/03 12:55p	1,679,290	2750-0709P Reference Table 2.txt	
08/14/03 12:57p	144,192,876	2750-0709P Sequence Table 1.txt	
08/14/03 01:00p	12,085,979	2750-0709P Sequence table 2.txt	
09/26/02 05:58p	2,129,953	2750-1243P Reference Table 1-4.txt	
09/26/02 05:58p	2,990,524	2750-1243P Reference Table 1-2.txt	
09/26/02 05:58p	1,888,794	2750-1243P Reference Table 1-3.txt	
09/26/02 05:58p	10,066,163	2750-1243P Reference Table 1-1.txt	
09/26/02 05:58p	4,915,563	2750-1243P Reference Table 1-5.txt	
09/26/02 05:58p	3,838,034	2750-1243P Reference Table 1-6.txt	
09/26/02 05:58p	1,693,772	2750-1243P Reference Table 1-7.txt	
09/26/02 05:58p	1,397,767	2750-1243P Reference Table 1-8.txt	
09/26/02 05:58p	81,613,286	2750-1243P Sequence Table 2-1.txt	
09/26/02 05:58p	40,709,536	2750-1243P Sequence Table 2-2.txt	
09/26/02 05:58p	6,886,798	2750-1243P Sequence Table 2-3.txt	
09/26/02 05:58p	9,151,726	2750-1243P Sequence Table 2-8.txt	
09/26/02 05:58p	25,453,987	2750-1243P Sequence Table 2-5.txt	
09/26/02 05:58p	26,524,617	2750-1243P Sequence Table 2-6.txt	
09/26/02 05:58p	8,232,431	2750-1243P Sequence Table 2-7.txt	
09/26/02 05:58p	10,217,391	2750-1243P Sequence Table 2-4.txt	
09/26/02 08:17p	641,811	reference table 1-1.txt	
09/26/02 08:17p	587,405	reference table 1-10.txt	
09/26/02 08:17p	146,916	reference table 1-11.txt	
09/26/02 08:17p	809,200	reference table 1-12.txt	
09/26/02 08:17p	770,850	reference table 1-13.txt	

File Create Date	File Size	File Name	CD#2
09/26/02 08:17p	742,436	reference table 1-14.txt	
09/26/02 08:17p	845,060	reference table 1-15.txt	
09/26/02 08:17p	834,735	reference table 1-16.txt	
09/26/02 08:17p	920,456	reference table 1-17.txt	
09/26/02 08:17p	860,758	reference table 1-18.txt	
09/26/02 08:17p	899,236	reference table 1-19.txt	
09/26/02 08:17p	549,072	reference table 1-2.txt	
09/26/02 08:17p	618,299	reference table 1-20.txt	
09/26/02 08:17p	779,148	reference table 1-21.txt	
09/26/02 08:17p	475,429	reference table 1-22.txt	
09/26/02 08:17p	940,392	reference table 1-3.txt	
09/26/02 08:17p	384,546	reference table 1-4.txt	
09/26/02 08:17p	579,915	reference table 1-5.txt	
09/26/02 08:17p	631,478	reference table 1-6.txt	
09/26/02 08:17p	526,981	reference table 1-7.txt	
09/26/02 08:17p	141,293	reference table 1-8.txt	
09/26/02 08:17p	530,763	reference table 1-9.txt	
09/26/02 08:17p	4,991,567	sequence table 2-1.txt	
09/26/02 08:17p	4,238,212	sequence table 2-10.txt	
09/26/02 08:17p	898,672	sequence table 2-11.txt	
09/26/02 08:17p	4,292,250	sequence table 2-12.txt	
09/26/02 08:17p	3,984,641	sequence table 2-13.txt	
09/26/02 08:17p	4,146,908	sequence table 2-14.txt	
09/26/02 08:17p	4,537,900	sequence table 2-15.txt	
09/26/02 08:17p	4,392,445	sequence table 2-16.txt	
09/26/02 08:17p	4,701,080	sequence table 2-17.txt	
09/26/02 08:17p	4,623,958	sequence table 2-18.txt	
09/26/02 08:17p	4,604,021	sequence table 2-19.txt	
09/26/02 08:17p	3,150,768	sequence table 2-2.txt	
09/26/02 08:17p	3,104,710	sequence table 2-20.txt	
09/26/02 08:17p	4,034,065	sequence table 2-21.txt	
09/26/02 08:17p	2,620,664	sequence table 2-22.txt	
09/26/02 08:17p	4,865,790	sequence table 2-3.txt	
09/26/02 08:17p	2,062,952	sequence table 2-4.txt	
09/26/02 08:17p	3,062,616	sequence table 2-5.txt	
09/26/02 08:17p	3,367,387	sequence table 2-6.txt	
09/26/02 08:17p	2,754,090	sequence table 2-7.txt	
09/26/02 08:17p	744,260	sequence table 2-8.txt	
09/26/02 08:17p	2,962,293	sequence table 2-9.txt	
08/23/01 03:09p	674,259	2750-1481P Sequence Table 2-19.txt	
08/23/01 03:04p	34,099	2750-1481P AFLP_Diff Table 10.txt	
08/23/01 02:35p	8,947	2750-1481P AFLP_Diff Table 2.txt	
08/23/01 02:39p	4,193	2750-1481P AFLP_Diff Table 3.txt	
08/23/01 02:40p	8,040	2750-1481P AFLP_Diff Table 4.txt	
08/23/01 02:48p	27,843	2750-1481P AFLP_Diff Table 5.txt	
08/23/01 02:49p	24,909	2750-1481P AFLP_Diff Table 6.txt	
08/23/01 02:49p	19,232	2750-1481P AFLP_Diff Table 7.txt	
08/23/01 02:49p	37,256	2750-1481P AFLP_Diff Table 8.txt	
08/23/01 03:03p	17,382	2750-1481P AFLP_Diff Table 9.txt	
08/23/01 02:41p	6,838,002	2750-1481P AFLP_Int Table 1.txt	
08/23/01 02:43p	9,018,420	2750-1481P AFLP_Int Table 2.txt	
08/23/01 02:35p	1,431,495	2750-1481P GA Reference Table 1-05.txt	
08/23/01 02:36p	2,831,388	2750-1481P GA Reference Table 1-06.txt	
08/23/01 02:36p	16,259	2750-1481P GA Reference Table 1-07.txt	
08/23/01 02:37p	23,269	2750-1481P GA Reference Table 1-08.txt	
08/23/01 02:37p	2,228,027	2750-1481P GA Sequence Table 2-05.txt	
08/23/01 02:38p	5,140,356	2750-1481P GA Sequence Table 2-06.txt	
08/23/01 02:38p	146,210	2750-1481P GA Sequence Table 2-07.txt	
08/23/01 02:39p	198,226	2750-1481P GA Sequence Table 2-08.txt	
08/23/01 02:28p	4,637,946	2750-1481P Nitrogen Reference Table 1-01.txt	
08/23/01 02:29p	2,949,689	2750-1481P Nitrogen Reference Table 1-02.txt	
08/23/01 02:30p	45,050	2750-1481P Nitrogen Reference Table 1-03.txt	
08/23/01 02:30p	27,722	2750-1481P Nitrogen Reference Table 1-04.txt	
08/23/01 02:31p	6,614,978	2750-1481P Nitrogen Sequence Table 2-01.txt	
08/23/01 02:32p	4,698,688	2750-1481P Nitrogen Sequence Table 2-02.txt	
08/23/01 02:33p	414,051	2750-1481P Nitrogen Sequence Table 2-03.txt	
08/23/01 02:33p	220,703	2750-1481P Nitrogen Sequence Table 2-04.txt	

File Create Date	File Size	File Name	CD#2
08/23/01 02:59p	6,458,302	2750-1481P Reference Table 1-13.txt	
08/23/01 02:59p	9,489,750	2750-1481P Reference Table 1-14.txt	
08/23/01 03:00p	74,951	2750-1481P Reference Table 1-15.txt	
08/23/01 03:00p	98,566	2750-1481P Reference Table 1-16.txt	
08/23/01 03:05p	6,256,208	2750-1481P Reference Table 1-17.txt	
08/23/01 03:06p	9,058,233	2750-1481P Reference Table 1-18.txt	
08/23/01 03:07p	54,534	2750-1481P Reference Table 1-19.txt	
08/23/01 03:07p	115,376	2750-1481P Reference Table 1-20.txt	
08/23/01 02:44p	8,271,553	2750-1481P SA Reference Table 1-09.txt	
08/23/01 02:45p	7,643,610	2750-1481P SA Reference Table 1-10.txt	
08/23/01 02:45p	105,942	2750-1481P SA Reference Table 1-11.txt	
08/23/01 02:46p	109,452	2750-1481P SA Reference Table 1-12.txt	
08/23/01 02:46p	13,253,894	2750-1481P SA Sequence Table 2-09.txt	
08/23/01 02:47p	11,287,488	2750-1481P SA Sequence Table 2-10.txt	
08/23/01 02:47p	877,943	2750-1481P SA Sequence Table 2-11.txt	
08/23/01 02:48p	933,024	2750-1481P SA Sequence Table 2-12.txt	
08/23/01 03:01p	11,183,177	2750-1481P Sequence Table 2-13.txt	
08/23/01 03:02p	14,646,870	2750-1481P Sequence Table 2-14.txt	
08/23/01 03:02p	861,039	2750-1481P Sequence Table 2-15.txt	
08/23/01 03:03p	820,148	2750-1481P Sequence Table 2-16.txt	
08/23/01 03:08p	12,886,010	2750-1481P Sequence Table 2-17.txt	
08/23/01 03:09p	12,281,310	2750-1481P Sequence Table 2-18.txt	
08/23/01 02:34p	15,074	2750-1481P AFLP_Diff Table 1.txt	
08/23/01 03:10p	892,250	2750-1481P Sequence Table 2-20.txt	
09/26/02 04:36p	8,135,801	2750-0954P Seq Table 1.txt	
09/26/02 04:36p	8,246,903	2750-0954P Ref Table 1.txt	
09/26/02 04:36p	2,289,314	010214 Protein Domain Table.txt	
09/26/02 04:44p	2,752,459	010809 Protein Domain Table.txt	
09/26/02 04:44p	633,971	Ockham_Table 1.txt	
09/26/02 04:46p	91,002	Cluster Functions and Utilities 02.txt	
09/26/02 04:46p	6,256	Cluster Functions and Utilities 03.txt	
09/26/02 04:46p	6,292	Cluster Functions and Utilities 04.txt	
09/26/02 04:46p	37,345	Cluster Functions and Utilities 05.txt	
09/26/02 04:46p	96,535	Cluster Functions and Utilities 06.txt	
09/26/02 04:46p	8,447	Cluster Functions and Utilities 07.txt	
09/26/02 04:46p	17,087	Cluster Functions and Utilities 08.txt	
09/26/02 04:46p	1,232	docket_80090_101_cdna_map_II_delta	
09/26/02 04:45p	28,516	Ockham_Table 1.txt	
09/26/02 04:45p	1,172,396	Aragen_Table 1.txt	
09/26/02 04:45p	414,332	Aragen_Table 2.txt	
09/26/02 04:45p	2,752,459	010809 Protein Domain Table.txt	
07/29/03 10:17a	148,957	2750-1569P Table 1.txt	
07/29/03 10:18a	960,943	2750-1569P Table 2.txt	
09/26/02 04:45p	2,752,459	010809 Protein Domain Table.txt	

File Create Date	File Size	File Name	CD#3
09/26/02 04:59p	12,684	Cluster Functions and Utilities 01.txt	
09/26/02 04:59p	91,002	Cluster Functions and Utilities 02.txt	
09/26/02 04:59p	6,256	Cluster Functions and Utilities 03.txt	
09/26/02 04:59p	6,292	Cluster Functions and Utilities 04.txt	
09/26/02 04:59p	37,345	Cluster Functions and Utilities 05.txt	
09/26/02 04:59p	96,535	Cluster Functions and Utilities 06.txt	
09/26/02 04:59p	8,447	Cluster Functions and Utilities 07.txt	
09/26/02 04:59p	17,087	Cluster Functions and Utilities 08.txt	
09/26/02 04:59p	1,090,292	gb_only_peptides_II.fasta	
09/26/02 04:59p	6,947	KNOCK-IN_01.txt	
09/26/02 04:59p	11,374	KNOCK-IN_02.txt	
09/26/02 04:59p	1,645,031	knock_out_01	
09/26/02 04:59p	2,752,459	Protein Domain Table.txt	
09/26/02 04:59p	19,858,561	protein_group.001	
09/26/02 04:59p	10,115,454	protein_group.002	
09/26/02 04:59p	20,971,520	protein_group_matrix.001	
09/26/02 04:59p	20,971,520	protein_group_matrix.002	

File Create Date	File Size	File Name	CD#3
09/26/02 04:59p	20,971,520	protein_group_matrix.003	
09/26/02 04:59p	20,971,520	protein_group_matrix.004	
09/26/02 04:59p	20,971,520	protein_group_matrix.005	
09/26/02 04:59p	20,971,520	protein_group_matrix.006	
09/26/02 04:59p	20,971,520	protein_group_matrix.007	
09/26/02 04:59p	20,971,520	protein_group_matrix.008	
09/26/02 04:59p	20,971,520	protein_group_matrix.009	
09/26/02 04:59p	20,971,520	protein_group_matrix.010	
09/26/02 04:59p	20,971,520	protein_group_matrix.011	
09/26/02 05:00p	101,007	Table A.txt	
09/26/02 04:59p	12,595,677	protein_group_matrix.012	
09/26/02 04:59p	24,200	reference.311987.710-0004-55300-US-U-31949.01_0a_1	
09/26/02 04:59p	1,789,210	reference.311987.710-0004-55300-US-U-31949.01_1	
09/26/02 04:59p	6,241	reference.311988.710-0004-55300-US-U-31949.01_1	
09/26/02 04:59p	39,017	reference.3769.710-0004-55300-US-U-31949.01_0a_1	
09/26/02 04:59p	5,306,421	reference.3769.710-0004-55300-US-U-31949.01_1	
09/26/02 04:59p	23,116	reference.3847.710-0004-55300-US-U-31949.01_0a_1	
09/26/02 04:59p	685,251	reference.3847.710-0004-55300-US-U-31949.01_1	
09/26/02 04:59p	136,815	sequences.311987.710-0004-55300-US-U-31949.01_0a_1	
09/26/02 04:59p	1,130,823	sequences.311987.710-0004-55300-US-U-31949.01_1	
09/26/02 04:59p	3,492	sequences.311988.710-0004-55300-US-U-31949.01_1	
09/26/02 04:59p	373,913	sequences.3769.710-0004-55300-US-U-31949.01_0a_1	
09/26/02 04:59p	9,436,931	sequences.3769.710-0004-55300-US-U-31949.01_1	
09/26/02 04:59p	524,416	sequences.3847.710-0004-55300-US-U-31949.01_1	
09/26/02 04:59p	129,541	sequences.3847.710-0004-55300-US-U-31949.01_0a_1	
09/26/02 04:35p	2,282,461	010103 Protein Domain Table.txt	
09/26/02 04:35p	2,659,137	2750-1387P Reference Table 1-1.txt	
09/26/02 04:35p	5,547,575	2750-1387P Reference Table 1-2.txt	
09/26/02 04:36p	1,023,813	2750-1387P Reference Table 1-3.txt	
09/26/02 04:36p	3,360,505	2750-1387P Reference Table 1-4.txt	
09/26/02 04:36p	8,269,532	2750-1387P Reference Table 1-5.txt	
09/26/02 04:36p	1,010,271	2750-1387P Reference Table 1-6.txt	
09/26/02 04:36p	15,141,732	2750-1387P Sequence Table 2-1.txt	
09/26/02 04:36p	29,045,309	2750-1387P Sequence Table 2-2.txt	
09/26/02 04:36p	5,973,892	2750-1387P Sequence Table 2-3.txt	
09/26/02 04:36p	15,288,450	2750-1387P Sequence Table 2-4.txt	
09/26/02 04:36p	47,699,502	2750-1387P Sequence Table 2-5.txt	
09/26/02 04:36p	4,790,691	2750-1387P Sequence Table 2-6.txt	
09/26/02 04:36p	614,728	2750-1387P Sequence Table 2-7.txt	
09/26/02 04:44p	2,752,459	010809 Protein Domain Table.txt	
09/26/02 04:44p	6,652,180	2750-1252P Reference Table 1-001.txt	
09/26/02 04:44p	2,032,841	2750-1252P Reference Table 1-002.txt	
09/26/02 04:44p	5,220,297	2750-1252P Reference Table 1-003.txt	
09/26/02 04:44p	5,160,707	2750-1252P Reference Table 1-004.txt	
09/26/02 04:44p	4,574,052	2750-1252P Reference Table 1-005.txt	
09/26/02 04:44p	5,409,324	2750-1252P Reference Table 1-006.txt	
09/26/02 04:44p	5,030,974	2750-1252P Reference Table 1-007.txt	
09/26/02 04:44p	5,793,139	2750-1252P Reference Table 1-008.txt	
09/26/02 04:44p	6,005,613	2750-1252P Reference Table 1-009.txt	
09/26/02 04:44p	4,313,369	2750-1252P Reference Table 1-010.txt	
09/26/02 04:44p	4,448,300	2750-1252P Reference Table 1-011.txt	
09/26/02 04:44p	5,494,573	2750-1252P Reference Table 1-012.txt	
09/26/02 04:44p	5,340,296	2750-1252P Reference Table 1-013.txt	
09/26/02 04:44p	6,149,154	2750-1252P Reference Table 1-014.txt	
09/26/02 04:44p	2,116,257	2750-1252P Reference Table 1-015.txt	
09/26/02 04:44p	43,111	2750-1252P Reference Table 1-016.txt	
09/26/02 04:44p	7,230	2750-1252P Reference Table 1-017.txt	
09/26/02 04:44p	175,569	2750-1252P Reference Table 1-018.txt	
09/26/02 04:44p	164,674	2750-1252P Reference Table 1-019.txt	
09/26/02 04:44p	193,412	2750-1252P Reference Table 1-020.txt	
09/26/02 04:44p	133,821	2750-1252P Reference Table 1-021.txt	
09/26/02 04:44p	173,694	2750-1252P Reference Table 1-022.txt	
09/26/02 04:44p	129,711	2750-1252P Reference Table 1-023.txt	
09/26/02 04:44p	158,225	2750-1252P Reference Table 1-024.txt	
09/26/02 04:44p	151,019	2750-1252P Reference Table 1-025.txt	
09/26/02 04:44p	203,108	2750-1252P Reference Table 1-026.txt	
09/26/02 04:44p	132,151	2750-1252P Reference Table 1-027.txt	

File Create Date	File Size	File Name	CD#3
09/26/02 04:44p	157,413	2750-1252P Reference Table 1-028.txt	
09/26/02 04:44p	177,452	2750-1252P Reference Table 1-029.txt	
09/26/02 04:44p	51,045	2750-1252P Reference Table 1-030.txt	
09/26/02 04:44p	5,736,649	2750-1252P Sequence Table 2-001.txt	
09/26/02 04:44p	1,643,051	2750-1252P Sequence Table 2-002.txt	
09/26/02 04:44p	6,020,021	2750-1252P Sequence Table 2-003.txt	
09/26/02 04:44p	5,418,841	2750-1252P Sequence Table 2-004.txt	
09/26/02 04:44p	5,154,091	2750-1252P Sequence Table 2-005.txt	
09/26/02 04:44p	6,516,087	2750-1252P Sequence Table 2-006.txt	
09/26/02 04:44p	6,252,730	2750-1252P Sequence Table 2-007.txt	
09/26/02 04:44p	7,359,295	2750-1252P Sequence Table 2-008.txt	
09/26/02 04:44p	7,601,548	2750-1252P Sequence Table 2-009.txt	
09/26/02 04:44p	5,848,429	2750-1252P Sequence Table 2-010.txt	
09/26/02 04:44p	5,157,539	2750-1252P Sequence Table 2-011.txt	
09/26/02 04:44p	6,534,180	2750-1252P Sequence Table 2-012.txt	
09/26/02 04:44p	6,488,455	2750-1252P Sequence Table 2-013.txt	
09/26/02 04:44p	7,656,741	2750-1252P Sequence Table 2-014.txt	
09/26/02 04:44p	2,625,572	2750-1252P Sequence Table 2-015.txt	
09/26/02 04:44p	275,991	2750-1252P Sequence Table 2-016.txt	
09/26/02 04:44p	42,826	2750-1252P Sequence Table 2-017.txt	
09/26/02 04:44p	1,131,139	2750-1252P Sequence Table 2-018.txt	
09/26/02 04:44p	1,011,301	2750-1252P Sequence Table 2-019.txt	
09/26/02 04:44p	1,207,032	2750-1252P Sequence Table 2-020.txt	
09/26/02 04:44p	987,564	2750-1252P Sequence Table 2-021.txt	
09/26/02 04:44p	1,222,215	2750-1252P Sequence Table 2-022.txt	
09/26/02 04:44p	1,007,444	2750-1252P Sequence Table 2-023.txt	
09/26/02 04:44p	1,016,011	2750-1252P Sequence Table 2-024.txt	
09/26/02 04:44p	882,796	2750-1252P Sequence Table 2-025.txt	
09/26/02 04:44p	1,050,724	2750-1252P Sequence Table 2-026.txt	
09/26/02 04:44p	1,027,314	2750-1252P Sequence Table 2-027.txt	
09/26/02 04:44p	1,095,754	2750-1252P Sequence Table 2-028.txt	
09/26/02 04:44p	1,014,547	2750-1252P Sequence Table 2-029.txt	
09/26/02 04:44p	316,520	2750-1252P Sequence Table 2-030.txt	
02/05/03 05:24p	24,266,857	2750-1545P CD as filed.zip.pgp	
02/05/03 05:19p	24,683,951	2750-1545P CD as filed.zip	
09/26/02 04:44p	2,752,459	010809 Protein Domain Table.txt	
09/26/02 04:44p	44,396	Table 1.txt	
05/05/03 11:43a	1,504,078	2000-07-21 2750-1070P Protein Domain Table.txt	
05/05/03 11:55a	24,444,077	2750-1070P Table 1.txt	
05/05/03 11:56a	9,845,287	2750-1070P Table 2.txt	
07/15/03 01:30p	1,321,027	2750-1567P Table 1.txt	
07/15/03 01:31p	4,773,627	2750-1567P Table 2.txt	
09/26/02 04:45p	2,752,459	010809 Protein Domain Table.txt	
09/26/02 04:45p	2,752,459	010809 Protein Domain Table.txt	
08/04/03 12:30p	4,909,844	2750-1570P Table 2.txt	
08/04/03 12:29p	4,093,059	2750-1570P Table 1.txt	

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08/14/03 01:12p	3,816,673	2750-1063P Table 1.txt	
08/14/03 01:13p	16,086,510	2750-1063P Table 2.txt	
08/14/03 01:13p	2,048,453	2750-1064P Table 1.txt	
08/14/03 01:14p	9,105,798	2750-1064P Table 2.txt	
08/14/03 01:14p	837,468	2750-1242P TABLE 1.txt	
08/14/03 01:14p	5,292,389	2750-1242P TABLE 2.txt	
12/13/02 03:05p	161,899	reference.311987.710-0004-55300-US-U-33929.01_0a_1	
12/13/02 03:05p	4,482,839	reference.4565.710-0004-55300-US-U-33929.01_1	
12/13/02 03:05p	187,136	reference.4565.710-0004-55300-US-U-33929.01_0a_2	
12/13/02 03:05p	204,932	reference.4565.710-0004-55300-US-U-33929.01_0a_1	
12/13/02 03:05p	516,185	reference.39946.710-0004-55300-US-U-33929.01_1	
12/13/02 03:05p	13	reference.39946.710-0004-55300-US-U-33929.01_0a_1	
12/13/02 03:05p	1,461,495	reference.3847.710-0004-55300-US-U-33929.01_2	
12/13/02 03:05p	5,196,105	reference.3847.710-0004-55300-US-U-33929.01_1	

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12/13/02 03:05p	171,276	reference.3847.710-0004-55300-US-U-33929.01_0a_2	
12/13/02 03:05p	157,744	reference.3847.710-0004-55300-US-U-33929.01_0a_1	
12/13/02 03:05p	903,438	reference.3769.710-0004-55300-US-U-33929.01_3	
12/13/02 03:05p	6,702,929	reference.3769.710-0004-55300-US-U-33929.01_2	
12/13/02 03:05p	7,557,218	reference.3769.710-0004-55300-US-U-33929.01_1	
12/13/02 03:05p	4,728	reference.3769.710-0004-55300-US-U-33929.01_0a_3	
12/13/02 03:05p	80,880	reference.3769.710-0004-55300-US-U-33929.01_0a_2	
12/13/02 03:05p	53,003	reference.3769.710-0004-55300-US-U-33929.01_0a_1	
12/13/02 03:05p	1,378,487	reference.3708.710-0004-55300-US-U-33929.01_1	
12/13/02 03:05p	3,631	reference.3708.710-0004-55300-US-U-33929.01_0a_1	
12/13/02 03:05p	646,509	reference.311988.710-0004-55300-US-U-33929.01_1	
12/13/02 03:05p	13	reference.311988.710-0004-55300-US-U-33929.01_0a_1	
12/13/02 03:05p	2,423,462	reference.311987.710-0004-55300-US-U-33929.01_5	
12/13/02 03:05p	3,162,883	reference.311987.710-0004-55300-US-U-33929.01_4	
12/13/02 03:05p	5,018,727	reference.311987.710-0004-55300-US-U-33929.01_3	
12/13/02 03:05p	5,473,154	reference.311987.710-0004-55300-US-U-33929.01_2	
12/13/02 03:05p	5,612,668	reference.311987.710-0004-55300-US-U-33929.01_1	
12/13/02 03:05p	247,901	reference.311987.710-0004-55300-US-U-33929.01_0a_5	
12/13/02 03:05p	235,001	reference.311987.710-0004-55300-US-U-33929.01_0a_4	
12/13/02 03:05p	159,034	reference.311987.710-0004-55300-US-U-33929.01_0a_3	
12/13/02 03:05p	139,652	reference.311987.710-0004-55300-US-U-33929.01_0a_2	
12/13/02 03:05p	1,704,454	reference.4565.710-0004-55300-US-U-33929.01_2	
12/13/02 03:06p	1,818,166	sequences.4565.710-0004-55300-US-U-33929.01_2	
12/13/02 03:06p	4,817,405	sequences.4565.710-0004-55300-US-U-33929.01_1	
12/13/02 03:06p	1,063,406	sequences.4565.710-0004-55300-US-U-33929.01_0a_2	
12/13/02 03:06p	1,214,525	sequences.4565.710-0004-55300-US-U-33929.01_0a_1	
12/13/02 03:06p	559,071	sequences.39946.710-0004-55300-US-U-33929.01_1	
12/13/02 03:06p	13	sequences.39946.710-0004-55300-US-U-33929.01_0a_1	
12/13/02 03:06p	1,381,068	sequences.3847.710-0004-55300-US-U-33929.01_2	
12/13/02 03:06p	5,490,732	sequences.3847.710-0004-55300-US-U-33929.01_1	
12/13/02 03:06p	881,765	sequences.3847.710-0004-55300-US-U-33929.01_0a_2	
12/13/02 03:06p	879,313	sequences.3847.710-0004-55300-US-U-33929.01_0a_1	
12/13/02 03:06p	1,085,601	sequences.3769.710-0004-55300-US-U-33929.01_3	
12/13/02 03:06p	10,411,525	sequences.3769.710-0004-55300-US-U-33929.01_2	
12/13/02 03:06p	11,658,521	sequences.3769.710-0004-55300-US-U-33929.01_1	
12/13/02 03:06p	21,229	sequences.3769.710-0004-55300-US-U-33929.01_0a_3	
12/13/02 03:06p	633,533	sequences.3769.710-0004-55300-US-U-33929.01_0a_2	
12/13/02 03:06p	585,466	sequences.3769.710-0004-55300-US-U-33929.01_0a_1	
12/13/02 03:06p	1,260,011	sequences.3708.710-0004-55300-US-U-33929.01_1	
12/13/02 03:06p	27,070	sequences.3708.710-0004-55300-US-U-33929.01_0a_1	
12/13/02 03:06p	727,497	sequences.311988.710-0004-55300-US-U-33929.01_1	
12/13/02 03:06p	13	sequences.311988.710-0004-55300-US-U-33929.01_0a_1	
12/13/02 03:06p	2,435,263	sequences.311987.710-0004-55300-US-U-33929.01_5	
12/13/02 03:06p	2,672,012	sequences.311987.710-0004-55300-US-U-33929.01_4	
12/13/02 03:06p	6,219,995	sequences.311987.710-0004-55300-US-U-33929.01_3	
12/13/02 03:06p	8,126,428	sequences.311987.710-0004-55300-US-U-33929.01_2	
12/13/02 03:06p	1,290,515	sequences.311987.710-0004-55300-US-U-33929.01_0a_1	
12/13/02 03:06p	1,352,466	sequences.311987.710-0004-55300-US-U-33929.01_0a_5	
12/13/02 03:06p	1,117,762	sequences.311987.710-0004-55300-US-U-33929.01_0a_4	
12/13/02 03:06p	990,150	sequences.311987.710-0004-55300-US-U-33929.01_0a_3	
12/13/02 03:06p	1,080,713	sequences.311987.710-0004-55300-US-U-33929.01_0a_2	
12/13/02 03:06p	7,904,030	sequences.311987.710-0004-55300-US-U-33929.01_1	
09/26/02 04:45p	2,752,459	010809 Protein Domain Table.txt	
09/26/02 04:45p	34,876	2750-1478P ABA MA_Diff Table 13.txt	
09/26/02 04:45p	8,114,623	2750-1478P ABA Reference Table 1-033.txt	
09/26/02 04:45p	235,643	2750-1478P ABA Reference Table 1-034.txt	
09/26/02 04:45p	11,264,007	2750-1478P ABA Sequence Table 2-033.txt	
09/26/02 04:45p	1,479,355	2750-1478P ABA Sequence Table 2-034.txt	
09/26/02 04:45p	12,602	2750-1478P BA MA_Diff Table 14.txt	
09/26/02 04:45p	3,146,661	2750-1478P BA Reference Table 1-035.txt	
09/26/02 04:45p	79,951	2750-1478P BA Reference Table 1-036.txt	
09/26/02 04:45p	5,175,695	2750-1478P BA Sequence Table 2-035.txt	
09/26/02 04:45p	491,022	2750-1478P BA Sequence Table 2-036.txt	
09/26/02 04:45p	39,229	2750-1478P Cold MA_Diff Table 15.txt	
09/26/02 04:45p	9,980,136	2750-1478P Cold Reference Table 1-037.txt	
09/26/02 04:45p	323,833	2750-1478P Cold Reference Table 1-038.txt	
09/26/02 04:45p	14,155,715	2750-1478P Cold Sequence Table 2-037.txt	

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09/26/02	04:45p		12,429,909	2750-1478P Drought Reference Table 1-001.txt	
09/26/02	04:45p		5,957,204	2750-1478P Drought Reference Table 1-002.txt	
09/26/02	04:45p		329,244	2750-1478P Drought Reference Table 1-003.txt	
09/26/02	04:45p		163,094	2750-1478P Drought Reference Table 1-004.txt	
09/26/02	04:45p		18,830,064	2750-1478P Drought Sequence Table 2-001.txt	
09/26/02	04:45p		6,962,292	2750-1478P Drought Sequence Table 2-002.txt	
09/26/02	04:45p		2,340,574	2750-1478P Drought Sequence Table 2-003.txt	
09/26/02	04:45p		1,006,980	2750-1478P Drought Sequence Table 2-004.txt	
09/26/02	04:45p		5,852	2750-1478P Epi-Brass MA Diff Table 2.txt	
09/26/02	04:45p		1,493,135	2750-1478P Epi-Brass Reference Table 1-005.txt	
09/26/02	04:45p		38,191	2750-1478P Epi-Brass Reference Table 1-006.txt	
09/26/02	04:45p		2,093,327	2750-1478P Epi-Brass Sequence Table 2-005.txt	
09/26/02	04:45p		211,384	2750-1478P Epi-Brass Sequence Table 2-006.txt	
09/26/02	04:45p		2,731	2750-1478P GA3 MA Diff Table 3.txt	
09/26/02	04:45p		613,053	2750-1478P GA3 Reference Table 1-007.txt	
09/26/02	04:45p		20,963	2750-1478P GA3 Reference Table 1-008.txt	
09/26/02	04:45p		879,816	2750-1478P GA3 Sequence Table 2-007.txt	
09/26/02	04:45p		115,208	2750-1478P GA3 Sequence Table 2-008.txt	
09/26/02	04:45p		17,139	2750-1478P H2O2 MA Diff Table 7.txt	
09/26/02	04:45p		4,217,783	2750-1478P H2O2 Reference Table 1-017.txt	
09/26/02	04:45p		135,138	2750-1478P H2O2 Reference Table 1-018.txt	
09/26/02	04:45p		6,275,832	2750-1478P H2O2 Sequence Table 2-017.txt	
09/26/02	04:45p		861,090	2750-1478P H2O2 Sequence Table 2-018.txt	
09/26/02	04:45p		58,453	2750-1478P Heat MA Diff Table 8.txt	
09/26/02	04:45p		13,157,320	2750-1478P Heat Reference Table 1-019.txt	
09/26/02	04:45p		328,512	2750-1478P Heat Reference Table 1-020.txt	
09/26/02	04:45p		396,083	2750-1478P Heat Reference Table 1-021.txt	
09/26/02	04:45p		17,895	2750-1478P Heat Reference Table 1-022.txt	
09/26/02	04:45p		18,383,397	2750-1478P Heat Sequence Table 2-019.txt	
09/26/02	04:45p		357,785	2750-1478P Heat Sequence Table 2-020.txt	
09/26/02	04:45p		2,492,505	2750-1478P Heat Sequence Table 2-021.txt	
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09/26/02	04:45p		55,902	2750-1478P Ler-pi MA Diff Table 16.txt	
09/26/02	04:45p		11,727,933	2750-1478P Ler-pi Reference Table 1-039.txt	
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09/26/02	04:45p		384,228	2750-1478P Ler-pi Reference Table 1-041.txt	
09/26/02	04:45p		215,696	2750-1478P Ler-pi Reference Table 1-042.txt	
09/26/02	04:45p		18,008,803	2750-1478P Ler-pi Sequence Table 2-039.txt	
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09/26/02	04:46p		2,542,236	2750-1478P Ler-pi Sequence Table 2-041.txt	
09/26/02	04:46p		1,340,428	2750-1478P Ler-pi Sequence Table 2-042.txt	
09/26/02	04:46p		13,714	2750-1478P Ler-rhl MA Diff Table 17.txt	
09/26/02	04:46p		4,710,765	2750-1478P Ler-rhl Reference Table 1-043.txt	
09/26/02	04:46p		112,402	2750-1478P Ler-rhl Reference Table 1-044.txt	
09/26/02	04:46p		6,485,459	2750-1478P Ler-rhl Sequence Table 2-043.txt	
09/26/02	04:46p		698,619	2750-1478P Ler-rhl Sequence Table 2-044.txt	
09/26/02	04:46p		38,642	2750-1478P MeJA MA Diff Table 4.txt	
09/26/02	04:46p		9,687,270	2750-1478P MeJA Reference Table 1-009.txt	
09/26/02	04:46p		291,044	2750-1478P MeJA Reference Table 1-010.txt	
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09/26/02	04:46p		1,807,003	2750-1478P MeJA Sequence Table 2-010.txt	
09/26/02	04:46p		22,901	2750-1478P NAA MA Diff Table 5.txt	
09/26/02	04:46p		5,717,128	2750-1478P NAA Reference Table 1-011.txt	
09/26/02	04:46p		169,894	2750-1478P NAA Reference Table 1-012.txt	
09/26/02	04:46p		8,853,422	2750-1478P NAA Sequence Table 2-011.txt	
09/26/02	04:46p		1,269,525	2750-1478P NAA Sequence Table 2-012.txt	
09/26/02	04:46p		61,724	2750-1478P NANP MA Diff Table 6.txt	
09/26/02	04:46p		12,897,001	2750-1478P NANP Reference Table 1-013.txt	
09/26/02	04:46p		1,305,165	2750-1478P NANP Reference Table 1-014.txt	
09/26/02	04:46p		389,963	2750-1478P NANP Reference Table 1-015.txt	
09/26/02	04:46p		38,170	2750-1478P NANP Reference Table 1-016.txt	
09/26/02	04:46p		19,379,277	2750-1478P NANP Sequence Table 2-013.txt	
09/26/02	04:46p		1,485,555	2750-1478P NANP Sequence Table 2-014.txt	
09/26/02	04:46p		2,659,706	2750-1478P NANP Sequence Table 2-015.txt	
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09/26/02 04:46p	1,589,615	2750-1478P Nitrogen Reference Table 1-025.txt	
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09/26/02 04:46p	30,665	2750-1478P PEG MA_Diff Table 11.txt	
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09/26/02 04:46p	228,347	2750-1478P PEG Reference Table 1-028.txt	
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09/26/02 04:46p	1,474,301	2750-1478P PEG Sequence Table 2-028.txt	
09/26/02 04:46p	57,061	2750-1478P SA MA_Diff Table 12.txt	
09/26/02 04:46p	13,586,897	2750-1478P SA Reference Table 1-029.txt	
09/26/02 04:46p	224,149	2750-1478P SA Reference Table 1-030.txt	
09/26/02 04:46p	392,414	2750-1478P SA Reference Table 1-031.txt	
09/26/02 04:46p	10,984	2750-1478P SA Reference Table 1-032.txt	
09/26/02 04:46p	19,677,158	2750-1478P SA Sequence Table 2-029.txt	
09/26/02 04:46p	219,958	2750-1478P SA Sequence Table 2-030.txt	
09/26/02 04:46p	2,655,768	2750-1478P SA Sequence Table 2-031.txt	
09/26/02 04:46p	41,051	2750-1478P SA Sequence Table 2-032.txt	
09/26/02 04:46p	14,931	2750-1478P Wounding MA_Diff Table 18.txt	
09/26/02 04:46p	3,476,687	2750-1478P Wounding Reference Table 1-045.txt	
09/26/02 04:46p	93,814	2750-1478P Wounding Reference Table 1-046.txt	
09/26/02 04:46p	4,893,522	2750-1478P Wounding Sequence Table 2-045.txt	
09/26/02 04:46p	605,811	2750-1478P Wounding Sequence Table 2-046.txt	
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08/24/01 01:27p	12,083,955	2750-1482P Reference Table 1-02.txt	
08/24/01 01:31p	509,511	2750-1482P Reference Table 1-03.txt	
08/24/01 01:32p	226,209	2750-1482P Reference Table 1-04.txt	
08/24/01 01:36p	19,614,187	2750-1482P Sequence Table 2-01.txt	
08/24/01 01:40p	14,114,973	2750-1482P Sequence Table 2-02.txt	
08/12/03 04:57p	0	NE04-1	
08/24/01 01:41p	4,176,568	2750-1482P Sequence Table 2-03.txt	
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09/26/02 08:24p	3,887,554	orthologs.710-0004-55300-US-U-32792_10	
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09/26/02 08:24p	3,709,763	orthologs.710-0004-55300-US-U-32792_12	
09/26/02 08:24p	3,709,648	orthologs.710-0004-55300-US-U-32792_13	
09/26/02 08:24p	3,574,485	orthologs.710-0004-55300-US-U-32792_14	
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09/26/02 08:24p	3,650,891	orthologs.710-0004-55300-US-U-32792_17	
09/26/02 08:24p	3,420,198	orthologs.710-0004-55300-US-U-32792_18	
09/26/02 08:24p	3,493,649	orthologs.710-0004-55300-US-U-32792_19	
09/26/02 08:24p	3,812,707	orthologs.710-0004-55300-US-U-32792_2	
09/26/02 08:24p	3,514,236	orthologs.710-0004-55300-US-U-32792_20	
09/26/02 08:24p	3,627,651	orthologs.710-0004-55300-US-U-32792_21	
09/26/02 08:24p	3,484,322	orthologs.710-0004-55300-US-U-32792_22	
09/26/02 08:24p	3,409,930	orthologs.710-0004-55300-US-U-32792_23	
09/26/02 08:24p	3,391,808	orthologs.710-0004-55300-US-U-32792_24	
09/26/02 08:24p	3,622,761	orthologs.710-0004-55300-US-U-32792_25	
09/26/02 08:24p	3,675,893	orthologs.710-0004-55300-US-U-32792_26	
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09/26/02 08:24p	3,905,502	orthologs.710-0004-55300-US-U-32792_3	
09/26/02 08:24p	5,116,383	orthologs.710-0004-55300-US-U-32792_30	
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09/26/02 08:24p	5,880,889	orthologs.710-0004-55300-US-U-32792_32	
09/26/02 08:24p	5,826,198	orthologs.710-0004-55300-US-U-32792_33	
09/26/02 08:24p	5,919,050	orthologs.710-0004-55300-US-U-32792_34	
09/26/02 08:24p	5,886,020	orthologs.710-0004-55300-US-U-32792_35	
09/26/02 08:24p	5,700,570	orthologs.710-0004-55300-US-U-32792_36	
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09/26/02 08:24p	3,679,820	orthologs.710-0004-55300-US-U-32792_6	
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09/26/02 08:24p	565,708	reference.311988.710-0004-55300-US-U-32792.01_0a_4	
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32792.01_0a_8.txt			
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09/26/02 08:24p	1,498,061	reference.311988.710-0004-55300-US-U-32792.01_3	
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09/26/02 08:24p	2,866,471	reference.311988.710-0004-55300-US-U-32792.01_6	
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09/26/02 08:24p	419,032	reference.39946.710-0004-55300-US-U-32792.01_0a_26	
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09/26/02 08:24p	183,806	reference.39946.710-0004-55300-US-U-32792.01_0a_3	
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09/26/02	08:24p	4,518,438	reference.39946.710-0004-55300-US-U-32792.01_17	
09/26/02	08:24p	4,144,438	reference.39946.710-0004-55300-US-U-32792.01_18	
09/26/02	08:24p	4,259,798	reference.39946.710-0004-55300-US-U-32792.01_19	
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09/26/02	08:24p	4,146,239	reference.39946.710-0004-55300-US-U-32792.01_20	
09/26/02	08:24p	4,250,134	reference.39946.710-0004-55300-US-U-32792.01_21	
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09/26/02	08:24p	1,503,579	reference.39946.710-0004-55300-US-U-32792.01_24	
09/26/02	08:24p	1,205,697	reference.39946.710-0004-55300-US-U-32792.01_25	
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09/26/02	08:25p	223,493	reference.39946.710-0004-55300-US-U-32792.01_30	
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09/26/02	08:25p	4,229,924	reference.39946.710-0004-55300-US-U-32792.01_5	
09/26/02	08:25p	4,296,895	reference.39946.710-0004-55300-US-U-32792.01_6	
09/26/02	08:25p	4,342,863	reference.39946.710-0004-55300-US-U-32792.01_7	
09/26/02	08:25p	4,260,131	reference.39946.710-0004-55300-US-U-32792.01_8	
09/26/02	08:25p	4,178,089	reference.39946.710-0004-55300-US-U-32792.01_9	
09/26/02	08:25p	3,653,891	sequences.311988.710-0004-55300-US-U-32792.01_0a_1	
09/26/02	08:25p	1,167,672	sequences.311988.710-0004-55300-US-U-	
09/26/02	08:25p		32792.01_0a_10	
09/26/02	08:25p	4,775,014	sequences.311988.710-0004-55300-US-U-32792.01_0a_2	
09/26/02	08:25p	4,740,883	sequences.311988.710-0004-55300-US-U-32792.01_0a_3	
09/26/02	08:25p	4,510,006	sequences.311988.710-0004-55300-US-U-32792.01_0a_4	
09/26/02	08:25p	4,525,717	sequences.311988.710-0004-55300-US-U-32792.01_0a_5	
09/26/02	08:25p	2,962,193	sequences.311988.710-0004-55300-US-U-32792.01_0a_6	
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09/26/02	08:25p	1,567,360	sequences.311988.710-0004-55300-US-U-32792.01_0a_9	
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09/26/02	08:25p	4,704,757	sequences.311988.710-0004-55300-US-U-32792.01_2	
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09/26/02	08:25p	4,189,865	sequences.311988.710-0004-55300-US-U-32792.01_4	
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09/26/02	08:25p	7,717,443	sequences.311988.710-0004-55300-US-U-32792.01_7	
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09/26/02	08:25p	1,462,469	sequences.39946.710-0004-55300-US-U-32792.01_0a_10	
09/26/02	08:25p	7,198,873	sequences.39946.710-0004-55300-US-U-32792.01_1	
09/26/02	08:25p	1,480,567	sequences.39946.710-0004-55300-US-U-32792.01_0a_11	
09/26/02	08:25p	1,698,423	sequences.39946.710-0004-55300-US-U-32792.01_0a_12	
09/26/02	08:25p	1,470,343	sequences.39946.710-0004-55300-US-U-32792.01_0a_13	
09/26/02	08:25p	1,360,526	sequences.39946.710-0004-55300-US-U-32792.01_0a_14	
09/26/02	08:25p	1,828,886	sequences.39946.710-0004-55300-US-U-32792.01_0a_15	
09/26/02	08:25p	1,554,501	sequences.39946.710-0004-55300-US-U-32792.01_0a_16	
09/26/02	08:25p	1,423,535	sequences.39946.710-0004-55300-US-U-32792.01_0a_17	
09/26/02	08:25p	1,725,122	sequences.39946.710-0004-55300-US-U-32792.01_0a_18	
09/26/02	08:25p	1,592,888	sequences.39946.710-0004-55300-US-U-32792.01_0a_19	
09/26/02	08:25p	1,497,026	sequences.39946.710-0004-55300-US-U-32792.01_0a_2	
09/26/02	08:25p	1,729,271	sequences.39946.710-0004-55300-US-U-32792.01_0a_20	

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09/26/02 08:25p	4,399,193	sequences.39946.710-0004-55300-US-U-32792.01_0a_23	
09/26/02 08:25p	4,290,415	sequences.39946.710-0004-55300-US-U-32792.01_0a_24	
09/26/02 08:25p	4,130,566	sequences.39946.710-0004-55300-US-U-32792.01_0a_25	
09/26/02 08:25p	4,350,905	sequences.39946.710-0004-55300-US-U-32792.01_0a_26	
09/26/02 08:25p	4,326,357	sequences.39946.710-0004-55300-US-U-32792.01_0a_27	
09/26/02 08:25p	4,862,400	sequences.39946.710-0004-55300-US-U-32792.01_0a_28	
09/26/02 08:25p	4,147,664	sequences.39946.710-0004-55300-US-U-32792.01_0a_29	
09/26/02 08:25p	1,441,270	sequences.39946.710-0004-55300-US-U-32792.01_0a_3	
09/26/02 08:25p	556,615	sequences.39946.710-0004-55300-US-U-32792.01_0a_30	
09/26/02 08:25p	1,520,136	sequences.39946.710-0004-55300-US-U-32792.01_0a_4	
09/26/02 08:25p	1,393,707	sequences.39946.710-0004-55300-US-U-32792.01_0a_5	
09/26/02 08:25p	1,424,077	sequences.39946.710-0004-55300-US-U-32792.01_0a_6	
09/26/02 08:25p	1,484,994	sequences.39946.710-0004-55300-US-U-32792.01_0a_7	
09/26/02 08:25p	1,420,064	sequences.39946.710-0004-55300-US-U-32792.01_0a_8	
09/26/02 08:25p	1,539,402	sequences.39946.710-0004-55300-US-U-32792.01_0a_9	
09/26/02 08:25p	7,357,798	sequences.39946.710-0004-55300-US-U-32792.01_10	
09/26/02 08:25p	7,375,711	sequences.39946.710-0004-55300-US-U-32792.01_11	
09/26/02 08:25p	6,678,366	sequences.39946.710-0004-55300-US-U-32792.01_12	
09/26/02 08:26p	6,700,673	sequences.39946.710-0004-55300-US-U-32792.01_13	
09/26/02 08:26p	7,285,752	sequences.39946.710-0004-55300-US-U-32792.01_14	
09/26/02 08:26p	5,904,721	sequences.39946.710-0004-55300-US-U-32792.01_15	
09/26/02 08:26p	7,267,387	sequences.39946.710-0004-55300-US-U-32792.01_16	
09/26/02 08:26p	7,578,226	sequences.39946.710-0004-55300-US-U-32792.01_17	
09/26/02 08:26p	7,233,121	sequences.39946.710-0004-55300-US-U-32792.01_18	
09/26/02 08:26p	7,226,685	sequences.39946.710-0004-55300-US-U-32792.01_19	
09/26/02 08:26p	7,423,753	sequences.39946.710-0004-55300-US-U-32792.01_2	
09/26/02 08:26p	6,764,024	sequences.39946.710-0004-55300-US-U-32792.01_20	
09/26/02 08:26p	7,241,386	sequences.39946.710-0004-55300-US-U-32792.01_21	
09/26/02 08:26p	5,396,152	sequences.39946.710-0004-55300-US-U-32792.01_22	
09/26/02 08:26p	4,010,522	sequences.39946.710-0004-55300-US-U-32792.01_23	
09/26/02 08:26p	4,357,062	sequences.39946.710-0004-55300-US-U-32792.01_24	
09/26/02 08:26p	3,430,396	sequences.39946.710-0004-55300-US-U-32792.01_25	
09/26/02 08:26p	3,177,277	sequences.39946.710-0004-55300-US-U-32792.01_26	
09/26/02 08:26p	3,957,081	sequences.39946.710-0004-55300-US-U-32792.01_27	
09/26/02 08:26p	4,172,510	sequences.39946.710-0004-55300-US-U-32792.01_28	
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09/26/02 08:26p	560,320	sequences.39946.710-0004-55300-US-U-32792.01_30	
09/26/02 08:26p	6,777,554	sequences.39946.710-0004-55300-US-U-32792.01_4	
09/26/02 08:26p	7,375,829	sequences.39946.710-0004-55300-US-U-32792.01_5	
09/26/02 08:26p	7,168,961	sequences.39946.710-0004-55300-US-U-32792.01_6	
09/26/02 08:26p	7,064,843	sequences.39946.710-0004-55300-US-U-32792.01_7	
09/26/02 08:26p	7,029,455	sequences.39946.710-0004-55300-US-U-32792.01_8	
09/26/02 08:26p	6,865,084	sequences.39946.710-0004-55300-US-U-32792.01_9	

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09/26/02 05:00p	831,736	80090-004_knock_out	
09/26/02 05:00p	16,635,460	80090-004_ma_clusters	
09/26/02 05:00p	4,318,956	80090-004_ma_diff	
09/26/02 05:00p	2,752,459	80090-004_Protein Domain Table.txt	
09/26/02 05:00p	30,304,496	80090-004_Reference Table 1.txt	
09/26/02 05:00p	1,679,252	80090-004_Reference Table 2.txt	
09/26/02 05:00p	144,192,839	80090-004_Sequence Table 1.txt	
09/26/02 05:00p	4,052,876	cdna_clusters.txt	
09/26/02 05:00p	12,085,942	80090-004_Sequence Table 2.txt	
09/26/02 05:00p	35,153	Cluster Functions and Utilities (01).txt	
09/26/02 05:00p	40,447	Cluster Functions and Utilities (02).txt	
09/26/02 05:00p	4,473	Cluster Functions and Utilities (03).txt	

File Create Date	File Size	File Name	CD#6
09/26/02 05:00p	7,820	Cluster Functions and Utilities (04).txt	
09/26/02 05:00p	24,047	Cluster Functions and Utilities (05).txt	
09/26/02 05:00p	18,490	Cluster Functions and Utilities (06).txt	
09/26/02 05:00p	331,616	enhanced_amino.txt	
09/26/02 05:00p	36,273	Cluster functions and utilities (07).txt	
09/26/02 05:00p	33,962	Cluster Functions and Utilities (08).txt	
09/26/02 05:00p	23,000	Cluster functions and utilities (09).txt	
09/26/02 05:00p	2,691	Cluster functions and utilities (10).txt	
09/26/02 05:00p	2,290	Cluster functions and utilities (11).txt	
09/26/02 05:00p	23,740	Cluster Functions and Utilities (12).txt	
09/26/02 05:00p	296,887	docket_80090_101_cdna_map.txt	
09/26/02 05:00p	55,307	ma_diff Aluminum.txt	
09/26/02 05:00p	27,557	ma_diff Axel.txt	
09/26/02 05:00p	41,505	ma_diff Cadmium .txt	
09/26/02 05:00p	53,938	ma_diff Cauliflower .txt	
09/26/02 05:00p	98,775	ma_diff Chloroplast.txt	
09/26/02 05:00p	160,542	ma_diff Circadian 1-02.txt	
09/26/02 05:00p	127,498	ma_diff Circadian 1-03.txt	
09/26/02 05:00p	166,158	ma_diff Circadian 1-04.txt	
09/26/02 05:00p	141,971	ma_diff Circadian 1-01.txt	
09/26/02 05:00p	56,536	ma_diff Circadian 1-05.txt	
09/26/02 05:00p	121,178	ma_diff Circadian 1-06.txt	
09/26/02 05:00p	133,389	ma_diff Circadian 1-07.txt	
09/26/02 05:00p	259,096	ma_diff Circadian 1-08.txt	
09/26/02 05:00p	228,222	ma_diff Circadian 1-09.txt	
09/26/02 05:00p	54,526	ma_diff Circadian 1-10.txt	
09/26/02 05:00p	134,759	ma_diff CO2 1-1.txt	
09/26/02 05:00p	241,865	ma_diff CO2 1-2.txt	
09/26/02 05:00p	63,264	ma_diff CO2 1-3.txt	
09/26/02 05:00p	59,530	ma_diff CO2 1-4.txt	
09/26/02 05:00p	372,633	ma_diff CO2 1-5.txt	
09/26/02 05:00p	9,220	ma_diff Disease .txt	
09/26/02 05:00p	25,114	ma_diff H2O2 .txt	
09/26/02 05:00p	4,073	ma_diff Iol .txt	
09/26/02 05:00p	283,026	ma_diff Iron 1-1.txt	
09/26/02 05:00p	90,890	ma_diff Iron 1-2.txt	
09/26/02 05:00p	51,342	ma_diff Mitochondria-Electron Transp.txt	
09/26/02 05:00p	107,920	ma_diff NAA (Auxin) 1-1.txt	
09/26/02 05:00p	50,267	ma_diff NAA (Auxin) 1-2.txt	
09/26/02 05:00p	67,291	ma_diff Nitrogen.txt	
09/26/02 05:00p	6,441	ma_diff Phototropism 1-1.txt	
09/26/02 05:00p	45,620	ma_diff Shade.txt	
09/26/02 05:00p	22,229	ma_diff Phototropism 1-2.txt	
09/26/02 05:00p	28,270	ma_diff Phototropism 1-3.txt	
09/26/02 05:00p	73,438	ma_diff Sqn.txt	
09/26/02 05:00p	3,828	ma_diff Sulfur.txt	
09/26/02 05:00p	67,949	ma_diff Wounding.txt	
09/26/02 05:00p	30,836	ma_diff Zinc.txt	
09/26/02 05:00p	1,476	Single gene functions and utilities (1).txt	
09/26/02 05:00p	2,223	Single gene functions and utilities (2).txt	
09/26/02 05:00p	905	Single gene functions and utilities (3).txt	
09/26/02 05:00p	1,517	Single gene functions and utilities (4).txt	
09/26/02 05:00p	4,626	Single gene functions and utilities (5).txt	
09/26/02 05:00p	4,887	Single gene functions and utilities (6).txt	
09/26/02 05:00p	7,456	Single gene functions and utilities (7).txt	
09/26/02 05:00p	9,339	Single gene functions and utilities (8).txt	
09/26/02 05:00p	228,792	stanford_old_new_cdna_map.txt	
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09/26/02 08:27p	293,301	reference.311987.710-0004-55300-US-U-33017.01_0a_2	
09/26/02 08:27p	309,035	reference.311987.710-0004-55300-US-U-33017.01_0a_3	
09/26/02 08:27p	214,197	reference.311987.710-0004-55300-US-U-33017.01_0a_4	
09/26/02 08:27p	2,906,221	reference.311987.710-0004-55300-US-U-33017.01_1	
09/26/02 08:27p	2,022,776	reference.311987.710-0004-55300-US-U-33017.01_2	
09/26/02 08:27p	1,944,097	reference.311987.710-0004-55300-US-U-33017.01_3	
09/26/02 08:27p	1,365,420	reference.311987.710-0004-55300-US-U-33017.01_4	
09/26/02 08:27p	122,752	reference.3708.710-0004-55300-US-U-33017.01_0a_1	

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09/26/02 08:27p	125,714	reference.3708.710-0004-55300-US-U-33017.01_0a_4	
09/26/02 08:27p	149,921	reference.3708.710-0004-55300-US-U-33017.01_0a_5	
09/26/02 08:27p	227,954	reference.3708.710-0004-55300-US-U-33017.01_0a_6	
09/26/02 08:27p	240,651	reference.3708.710-0004-55300-US-U-33017.01_0a_7	
09/26/02 08:27p	222,409	reference.3708.710-0004-55300-US-U-33017.01_0a_8	
09/26/02 08:27p	61,285	reference.3708.710-0004-55300-US-U-33017.01_0a_9	
09/26/02 08:27p	4,143,408	reference.3708.710-0004-55300-US-U-33017.01_1	
09/26/02 08:27p	4,433,693	reference.3708.710-0004-55300-US-U-33017.01_2	
09/26/02 08:27p	4,740,980	reference.3708.710-0004-55300-US-U-33017.01_3	
09/26/02 08:27p	3,896,452	reference.3708.710-0004-55300-US-U-33017.01_4	
09/26/02 08:27p	3,423,953	reference.3708.710-0004-55300-US-U-33017.01_5	
09/26/02 08:27p	2,513,676	reference.3708.710-0004-55300-US-U-33017.01_6	
09/26/02 08:27p	2,200,354	reference.3708.710-0004-55300-US-U-33017.01_7	
09/26/02 08:27p	2,317,292	reference.3708.710-0004-55300-US-U-33017.01_8	
09/26/02 08:27p	798,150	reference.3708.710-0004-55300-US-U-33017.01_9	
09/26/02 08:27p	137,571	reference.3769.710-0004-55300-US-U-33017.01_0a_1	
09/26/02 08:27p	83,784	reference.3769.710-0004-55300-US-U-33017.01_0a_10	
09/26/02 08:27p	53,082	reference.3769.710-0004-55300-US-U-33017.01_0a_11	
09/26/02 08:27p	58,753	reference.3769.710-0004-55300-US-U-33017.01_0a_12	
09/26/02 08:27p	54,094	reference.3769.710-0004-55300-US-U-33017.01_0a_13	
09/26/02 08:27p	48,256	reference.3769.710-0004-55300-US-U-33017.01_0a_14	
09/26/02 08:27p	76,759	reference.3769.710-0004-55300-US-U-33017.01_0a_15	
09/26/02 08:27p	155,633	reference.3769.710-0004-55300-US-U-33017.01_0a_16	
09/26/02 08:27p	32,937	reference.3769.710-0004-55300-US-U-33017.01_0a_17	
09/26/02 08:27p	105,689	reference.3769.710-0004-55300-US-U-33017.01_0a_2	
09/26/02 08:27p	109,500	reference.3769.710-0004-55300-US-U-33017.01_0a_3	
09/26/02 08:27p	151,633	reference.3769.710-0004-55300-US-U-33017.01_0a_4	
09/26/02 08:27p	146,524	reference.3769.710-0004-55300-US-U-33017.01_0a_5	
09/26/02 08:27p	144,883	reference.3769.710-0004-55300-US-U-33017.01_0a_6	
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09/26/02	04:47p	6,292	Cluster Functions and Utilities 04.txt	
09/26/02	04:47p	37,345	Cluster Functions and Utilities 05.txt	
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09/26/02	04:47p	14,734,163	protein_group_matrix.002	
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09/26/02 04:32p	2,104,593	sequences.3847.710-0004-55300-US-U-31837.01_12	
09/26/02 04:32p	1,119,835	sequences.3847.710-0004-55300-US-U-31837.01_13	
09/26/02 04:32p	1,150,254	sequences.3847.710-0004-55300-US-U-31837.01_14	
09/26/02 04:32p	1,718,830	sequences.3847.710-0004-55300-US-U-31837.01_15	
09/26/02 04:32p	1,059,550	sequences.3847.710-0004-55300-US-U-31837.01_16	
09/26/02 04:32p	1,289,986	sequences.3847.710-0004-55300-US-U-31837.01_17	
09/26/02 04:32p	894,435	sequences.3847.710-0004-55300-US-U-31837.01_18	
09/26/02 04:32p	893,536	sequences.3847.710-0004-55300-US-U-31837.01_19	
09/26/02 04:33p	906,412	sequences.3847.710-0004-55300-US-U-31837.01_20	
09/26/02 04:33p	3,250,669	sequences.3847.710-0004-55300-US-U-31837.01_21	
09/26/02 04:33p	2,308,413	sequences.3847.710-0004-55300-US-U-31837.01_22	
09/26/02 04:33p	2,341,847	sequences.3847.710-0004-55300-US-U-31837.01_23	
09/26/02 04:33p	2,730,277	sequences.3847.710-0004-55300-US-U-31837.01_24	
09/26/02 04:33p	4,276,026	sequences.3847.710-0004-55300-US-U-31837.01_25	
09/26/02 04:33p	906,646	sequences.3847.710-0004-55300-US-U-31837.01_26	
09/26/02 04:47p	311,205	sequences.3847.710-0004-55300-US-U-31950.01_0a_1	
09/26/02 04:47p	111,913	sequences.3847.710-0004-55300-US-U-31950.01_1	
09/26/02 04:32p	1,075,842	sequences.3847.710-0004-55300-US-U-31837.01_0a_25	
09/26/02 04:32p	298,443	sequences.3847.710-0004-55300-US-U-31837.01_0a_26	
09/26/02 04:32p	2,114,850	sequences.3847.710-0004-55300-US-U-31837.01_10	
09/26/02 04:32p	1,392,995	sequences.3847.710-0004-55300-US-U-31837.01_11	
09/26/02 04:32p	2,104,593	sequences.3847.710-0004-55300-US-U-31837.01_12	
09/26/02 04:32p	1,119,835	sequences.3847.710-0004-55300-US-U-31837.01_13	
09/26/02 04:32p	1,150,254	sequences.3847.710-0004-55300-US-U-31837.01_14	
09/26/02 04:32p	1,718,830	sequences.3847.710-0004-55300-US-U-31837.01_15	
09/26/02 04:32p	1,059,550	sequences.3847.710-0004-55300-US-U-31837.01_16	
09/26/02 04:32p	1,289,986	sequences.3847.710-0004-55300-US-U-31837.01_17	
09/26/02 04:32p	894,435	sequences.3847.710-0004-55300-US-U-31837.01_18	
09/26/02 04:32p	893,536	sequences.3847.710-0004-55300-US-U-31837.01_19	
09/26/02 04:33p	906,412	sequences.3847.710-0004-55300-US-U-31837.01_20	

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09/26/02 04:32p	1,150,254	sequences.3847.710-0004-55300-US-U-31837.01_14	
09/26/02 04:32p	1,718,830	sequences.3847.710-0004-55300-US-U-31837.01_15	
09/26/02 04:32p	1,059,550	sequences.3847.710-0004-55300-US-U-31837.01_16	
09/26/02 04:32p	1,289,986	sequences.3847.710-0004-55300-US-U-31837.01_17	
09/26/02 04:32p	894,435	sequences.3847.710-0004-55300-US-U-31837.01_18	
09/26/02 04:32p	893,536	sequences.3847.710-0004-55300-US-U-31837.01_19	
09/26/02 04:33p	906,412	sequences.3847.710-0004-55300-US-U-31837.01_20	
09/26/02 04:33p	3,250,669	sequences.3847.710-0004-55300-US-U-31837.01_21	
09/26/02 04:33p	2,308,413	sequences.3847.710-0004-55300-US-U-31837.01_22	
09/26/02 04:33p	2,341,847	sequences.3847.710-0004-55300-US-U-31837.01_23	
09/26/02 04:33p	2,730,277	sequences.3847.710-0004-55300-US-U-31837.01_24	
09/26/02 04:33p	4,276,026	sequences.3847.710-0004-55300-US-U-31837.01_25	
09/26/02 04:33p	906,646	sequences.3847.710-0004-55300-US-U-31837.01_26	
09/26/02 04:47p	311,205	sequences.3847.710-0004-55300-US-U-31950.01_0a_1	
09/26/02 04:47p	111,913	sequences.3847.710-0004-55300-US-U-31950.01_1	
09/26/02 04:32p	1,075,842	sequences.3847.710-0004-55300-US-U-31837.01_0a_25	
09/26/02 04:32p	298,443	sequences.3847.710-0004-55300-US-U-31837.01_0a_26	
09/26/02 04:32p	2,114,850	sequences.3847.710-0004-55300-US-U-31837.01_10	
09/26/02 04:32p	1,392,995	sequences.3847.710-0004-55300-US-U-31837.01_11	
09/26/02 04:32p	2,104,593	sequences.3847.710-0004-55300-US-U-31837.01_12	
09/26/02 04:32p	1,119,835	sequences.3847.710-0004-55300-US-U-31837.01_13	
09/26/02 04:32p	1,150,254	sequences.3847.710-0004-55300-US-U-31837.01_14	
09/26/02 04:32p	1,718,830	sequences.3847.710-0004-55300-US-U-31837.01_15	
09/26/02 04:32p	1,059,550	sequences.3847.710-0004-55300-US-U-31837.01_16	
09/26/02 04:32p	1,289,986	sequences.3847.710-0004-55300-US-U-31837.01_17	
09/26/02 04:32p	894,435	sequences.3847.710-0004-55300-US-U-31837.01_18	
09/26/02 04:32p	893,536	sequences.3847.710-0004-55300-US-U-31837.01_19	
09/26/02 04:33p	906,412	sequences.3847.710-0004-55300-US-U-31837.01_20	
09/26/02 04:33p	3,250,669	sequences.3847.710-0004-55300-US-U-31837.01_21	
09/26/02 04:33p	2,308,413	sequences.3847.710-0004-55300-US-U-31837.01_22	
09/26/02 04:33p	2,341,847	sequences.3847.710-0004-55300-US-U-31837.01_23	
09/26/02 04:33p	2,730,277	sequences.3847.710-0004-55300-US-U-31837.01_24	
09/26/02 04:33p	4,276,026	sequences.3847.710-0004-55300-US-U-31837.01_25	
09/26/02 04:33p	906,646	sequences.3847.710-0004-55300-US-U-31837.01_26	
09/26/02 04:47p	311,205	sequences.3847.710-0004-55300-US-U-31950.01_0a_1	
09/26/02 04:47p	111,913	sequences.3847.710-0004-55300-US-U-31950.01_1	
09/26/02 04:32p	1,075,842	sequences.3847.710-0004-55300-US-U-31837.01_0a_25	
09/26/02 04:32p	298,443	sequences.3847.710-0004-55300-US-U-31837.01_0a_26	
09/26/02 04:32p	2,114,850	sequences.3847.710-0004-55300-US-U-31837.01_10	
09/26/02 04:32p	1,392,995	sequences.3847.710-0004-55300-US-U-31837.01_11	
09/26/02 04:32p	2,104,593	sequences.3847.710-0004-55300-US-U-31837.01_12	
09/26/02 04:32p	1,119,835	sequences.3847.710-0004-55300-US-U-31837.01_13	
09/26/02 04:32p	1,150,254	sequences.3847.710-0004-55300-US-U-31837.01_14	
09/26/02 04:32p	1,718,830	sequences.3847.710-0004-55300-US-U-31837.01_15	

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09/26/02 04:32p	894,435	sequences.3847.710-0004-55300-US-U-31837.01_18	
09/26/02 04:32p	893,536	sequences.3847.710-0004-55300-US-U-31837.01_19	
09/26/02 04:33p	906,412	sequences.3847.710-0004-55300-US-U-31837.01_20	
09/26/02 04:33p	3,250,669	sequences.3847.710-0004-55300-US-U-31837.01_21	
09/26/02 04:33p	2,308,413	sequences.3847.710-0004-55300-US-U-31837.01_22	
09/26/02 04:33p	2,341,847	sequences.3847.710-0004-55300-US-U-31837.01_23	
09/26/02 04:33p	2,730,277	sequences.3847.710-0004-55300-US-U-31837.01_24	
09/26/02 04:33p	4,276,026	sequences.3847.710-0004-55300-US-U-31837.01_25	
09/26/02 04:33p	906,646	sequences.3847.710-0004-55300-US-U-31837.01_26	
09/26/02 04:47p	311,205	sequences.3847.710-0004-55300-US-U-31950.01_0a_1	
09/26/02 04:47p	111,913	sequences.3847.710-0004-55300-US-U-31950.01_1	
09/26/02 04:32p	1,075,842	sequences.3847.710-0004-55300-US-U-31837.01_0a_25	
09/26/02 04:32p	298,443	sequences.3847.710-0004-55300-US-U-31837.01_0a_26	
09/26/02 04:32p	2,114,850	sequences.3847.710-0004-55300-US-U-31837.01_10	
09/26/02 04:32p	1,392,995	sequences.3847.710-0004-55300-US-U-31837.01_11	

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09/26/02 08:09p	3,610,169	2750-1251 Reference Table 1-288.txt	
09/26/02 08:09p	2,637,092	2750-1251 Reference Table 1-289.txt	
09/26/02 08:09p	2,606,136	2750-1251 Reference Table 1-290.txt	
09/26/02 08:09p	2,998,153	2750-1251 Reference Table 1-291.txt	
09/26/02 08:09p	2,538,058	2750-1251 Reference Table 1-292.txt	
09/26/02 08:09p	2,672,187	2750-1251 Reference Table 1-293.txt	
09/26/02 08:09p	3,372,656	2750-1251 Reference Table 1-294.txt	
09/26/02 08:09p	3,167,370	2750-1251 Reference Table 1-295.txt	
09/26/02 08:09p	216,379	2750-1251 Reference Table 1-296.txt	
09/26/02 08:09p	208,179	2750-1251 Reference Table 1-297.txt	
09/26/02 08:09p	234,316	2750-1251 Reference Table 1-298.txt	
09/26/02 08:09p	250,849	2750-1251 Reference Table 1-299.txt	
09/26/02 08:09p	244,022	2750-1251 Reference Table 1-300.txt	
09/26/02 08:09p	238,332	2750-1251 Reference Table 1-301.txt	
09/26/02 08:09p	228,072	2750-1251 Reference Table 1-302.txt	
09/26/02 08:09p	205,197	2750-1251 Reference Table 1-303.txt	
09/26/02 08:09p	235,546	2750-1251 Reference Table 1-304.txt	
09/26/02 08:09p	227,302	2750-1251 Reference Table 1-305.txt	
09/26/02 08:09p	238,797	2750-1251 Reference Table 1-306.txt	
09/26/02 08:09p	209,881	2750-1251 Reference Table 1-307.txt	
09/26/02 08:09p	228,869	2750-1251 Reference Table 1-308.txt	
09/26/02 08:09p	181,324	2750-1251 Reference Table 1-309.txt	
09/26/02 08:09p	213,900	2750-1251 Reference Table 1-310.txt	
09/26/02 08:09p	193,674	2750-1251 Reference Table 1-311.txt	
09/26/02 08:09p	226,186	2750-1251 Reference Table 1-312.txt	
09/26/02 08:09p	267,411	2750-1251 Reference Table 1-313.txt	
09/26/02 08:09p	172,199	2750-1251 Reference Table 1-314.txt	
09/26/02 08:09p	248,401	2750-1251 Reference Table 1-315.txt	
09/26/02 08:09p	221,959	2750-1251 Reference Table 1-316.txt	
09/26/02 08:09p	161,812	2750-1251 Reference Table 1-317.txt	
09/26/02 08:09p	186,817	2750-1251 Reference Table 1-318.txt	
09/26/02 08:09p	205,361	2750-1251 Reference Table 1-319.txt	
09/26/02 08:09p	199,344	2750-1251 Reference Table 1-320.txt	
09/26/02 08:09p	182,946	2750-1251 Reference Table 1-321.txt	
09/26/02 08:09p	233,388	2750-1251 Reference Table 1-322.txt	
09/26/02 08:09p	153,619	2750-1251 Reference Table 1-323.txt	
09/26/02 08:09p	181,447	2750-1251 Reference Table 1-324.txt	
09/26/02 08:09p	204,625	2750-1251 Reference Table 1-325.txt	
09/26/02 08:09p	211,076	2750-1251 Reference Table 1-326.txt	
09/26/02 08:09p	207,879	2750-1251 Reference Table 1-327.txt	
09/26/02 08:09p	210,688	2750-1251 Reference Table 1-328.txt	
09/26/02 08:09p	216,815	2750-1251 Reference Table 1-329.txt	

File	Create	Date	File	Size	File	Name	CD#10
09/26/02	08:09p		219,186	2750-1251	Reference	Table 1-330.txt	
09/26/02	08:09p		295,210	2750-1251	Reference	Table 1-331.txt	
09/26/02	08:09p		277,806	2750-1251	Reference	Table 1-332.txt	
09/26/02	08:09p		205,559	2750-1251	Reference	Table 1-333.txt	
09/26/02	08:09p		294,216	2750-1251	Reference	Table 1-334.txt	
09/26/02	08:09p		279,922	2750-1251	Reference	Table 1-335.txt	
09/26/02	08:09p		297,442	2750-1251	Reference	Table 1-336.txt	
09/26/02	08:09p		240,639	2750-1251	Reference	Table 1-337.txt	
09/26/02	08:09p		3,218,234	2750-1251	Reference	Table 1-338.txt	
09/26/02	08:09p		3,228,645	2750-1251	Reference	Table 1-339.txt	
09/26/02	08:09p		3,457,565	2750-1251	Reference	Table 1-340.txt	
09/26/02	08:09p		3,559,935	2750-1251	Reference	Table 1-341.txt	
09/26/02	08:09p		3,677,604	2750-1251	Reference	Table 1-342.txt	
09/26/02	08:09p		3,313,986	2750-1251	Reference	Table 1-343.txt	
09/26/02	08:09p		3,921,955	2750-1251	Reference	Table 1-344.txt	
09/26/02	08:09p		3,510,701	2750-1251	Reference	Table 1-345.txt	
09/26/02	08:09p		2,610,192	2750-1251	Reference	Table 1-346.txt	
09/26/02	08:09p		4,848,573	2750-1251	Reference	Table 1-347.txt	
09/26/02	08:09p		3,713,403	2750-1251	Reference	Table 1-348.txt	
09/26/02	08:09p		3,034,616	2750-1251	Reference	Table 1-349.txt	
09/26/02	08:09p		4,329,286	2750-1251	Reference	Table 1-350.txt	
09/26/02	08:09p		4,417,020	2750-1251	Reference	Table 1-351.txt	
09/26/02	08:09p		3,977,476	2750-1251	Reference	Table 1-352.txt	
09/26/02	08:09p		4,362,329	2750-1251	Reference	Table 1-353.txt	
09/26/02	08:09p		4,289,050	2750-1251	Reference	Table 1-354.txt	
09/26/02	08:09p		3,177,265	2750-1251	Reference	Table 1-355.txt	
09/26/02	08:09p		4,056,791	2750-1251	Reference	Table 1-356.txt	
09/26/02	08:09p		3,915,567	2750-1251	Reference	Table 1-357.txt	
09/26/02	08:09p		3,093,974	2750-1251	Reference	Table 1-358.txt	
09/26/02	08:09p		3,713,815	2750-1251	Reference	Table 1-359.txt	
09/26/02	08:09p		3,342,786	2750-1251	Reference	Table 1-360.txt	
09/26/02	08:09p		3,210,495	2750-1251	Reference	Table 1-361.txt	
09/26/02	08:09p		2,908,038	2750-1251	Reference	Table 1-362.txt	
09/26/02	08:09p		3,613,291	2750-1251	Reference	Table 1-363.txt	
09/26/02	08:09p		2,786,967	2750-1251	Reference	Table 1-364.txt	
09/26/02	08:09p		3,046,660	2750-1251	Reference	Table 1-365.txt	
09/26/02	08:09p		3,232,541	2750-1251	Reference	Table 1-366.txt	
09/26/02	08:09p		2,012,578	2750-1251	Reference	Table 1-367.txt	
09/26/02	08:09p		1,898,394	2750-1251	Reference	Table 1-368.txt	
09/26/02	08:09p		1,777,406	2750-1251	Reference	Table 1-369.txt	
09/26/02	08:09p		1,514,572	2750-1251	Reference	Table 1-370.txt	
09/26/02	08:09p		3,027,319	2750-1251	Reference	Table 1-371.txt	
09/26/02	08:09p		3,061,923	2750-1251	Reference	Table 1-372.txt	
09/26/02	08:09p		3,250,110	2750-1251	Reference	Table 1-373.txt	
09/26/02	08:09p		2,972,358	2750-1251	Reference	Table 1-374.txt	
09/26/02	08:09p		2,774,127	2750-1251	Reference	Table 1-375.txt	
09/26/02	08:09p		3,200,706	2750-1251	Reference	Table 1-376.txt	
09/26/02	08:09p		3,388,713	2750-1251	Reference	Table 1-377.txt	
09/26/02	08:09p		2,608,705	2750-1251	Reference	Table 1-378.txt	
09/26/02	08:09p		3,372,747	2750-1251	Reference	Table 1-379.txt	
09/26/02	08:09p		236,700	2750-1251	Reference	Table 1-380.txt	
09/26/02	08:09p		232,688	2750-1251	Reference	Table 1-381.txt	
09/26/02	08:09p		229,889	2750-1251	Reference	Table 1-382.txt	
09/26/02	08:09p		246,097	2750-1251	Reference	Table 1-383.txt	
09/26/02	08:09p		271,621	2750-1251	Reference	Table 1-384.txt	
09/26/02	08:09p		226,445	2750-1251	Reference	Table 1-385.txt	
09/26/02	08:09p		227,632	2750-1251	Reference	Table 1-386.txt	
09/26/02	08:09p		272,621	2750-1251	Reference	Table 1-387.txt	
09/26/02	08:09p		223,814	2750-1251	Reference	Table 1-388.txt	
09/26/02	08:09p		201,897	2750-1251	Reference	Table 1-389.txt	
09/26/02	08:09p		300,094	2750-1251	Reference	Table 1-390.txt	
09/26/02	08:09p		252,819	2750-1251	Reference	Table 1-391.txt	
09/26/02	08:09p		214,587	2750-1251	Reference	Table 1-392.txt	
09/26/02	08:09p		265,622	2750-1251	Reference	Table 1-393.txt	
09/26/02	08:09p		243,580	2750-1251	Reference	Table 1-394.txt	
09/26/02	08:09p		266,635	2750-1251	Reference	Table 1-395.txt	
09/26/02	08:09p		289,793	2750-1251	Reference	Table 1-396.txt	

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09/26/02	08:09p		264,755	2750-1251	Reference	Table 1-398.txt	
09/26/02	08:09p		278,869	2750-1251	Reference	Table 1-399.txt	
09/26/02	08:09p		295,602	2750-1251	Reference	Table 1-400.txt	
09/26/02	08:09p		162,033	2750-1251	Reference	Table 1-401.txt	
09/26/02	08:09p		184,978	2750-1251	Reference	Table 1-402.txt	
09/26/02	08:09p		195,660	2750-1251	Reference	Table 1-403.txt	
09/26/02	08:09p		228,798	2750-1251	Reference	Table 1-404.txt	
09/26/02	08:09p		225,795	2750-1251	Reference	Table 1-405.txt	
09/26/02	08:09p		308,647	2750-1251	Reference	Table 1-406.txt	
09/26/02	08:09p		305,230	2750-1251	Reference	Table 1-407.txt	
09/26/02	08:09p		330,275	2750-1251	Reference	Table 1-408.txt	
09/26/02	08:09p		379,558	2750-1251	Reference	Table 1-409.txt	
09/26/02	08:09p		389,488	2750-1251	Reference	Table 1-410.txt	
09/26/02	08:09p		369,267	2750-1251	Reference	Table 1-411.txt	
09/26/02	08:10p		309,224	2750-1251	Reference	Table 1-412.txt	
09/26/02	08:10p		354,209	2750-1251	Reference	Table 1-413.txt	
09/26/02	08:10p		379,098	2750-1251	Reference	Table 1-414.txt	
09/26/02	08:10p		286,274	2750-1251	Reference	Table 1-415.txt	
09/26/02	08:10p		269,818	2750-1251	Reference	Table 1-416.txt	
09/26/02	08:10p		294,831	2750-1251	Reference	Table 1-417.txt	
09/26/02	08:10p		321,437	2750-1251	Reference	Table 1-418.txt	
09/26/02	08:10p		321,961	2750-1251	Reference	Table 1-419.txt	
09/26/02	08:10p		369,688	2750-1251	Reference	Table 1-420.txt	
09/26/02	08:10p		424,679	2750-1251	Reference	Table 1-421.txt	
09/26/02	08:10p		427,758	2750-1251	Reference	Table 1-422.txt	
09/26/02	08:10p		407,943	2750-1251	Reference	Table 1-423.txt	
09/26/02	08:10p		410,954	2750-1251	Reference	Table 1-424.txt	
09/26/02	08:10p		60,741	2750-1251	Reference	Table 1-425.txt	
09/26/02	08:10p		3,667,254	2750-1251	Reference	Table 1-426.txt	
09/26/02	08:10p		2,845,368	2750-1251	Reference	Table 1-427.txt	
09/26/02	08:10p		3,119,015	2750-1251	Reference	Table 1-428.txt	
09/26/02	08:10p		3,464,214	2750-1251	Reference	Table 1-429.txt	
09/26/02	08:10p		2,802,609	2750-1251	Reference	Table 1-430.txt	
09/26/02	08:10p		3,056,250	2750-1251	Reference	Table 1-431.txt	
09/26/02	08:10p		2,687,652	2750-1251	Reference	Table 1-432.txt	
09/26/02	08:10p		2,369,602	2750-1251	Reference	Table 1-433.txt	
09/26/02	08:10p		2,718,396	2750-1251	Reference	Table 1-434.txt	
09/26/02	08:10p		2,836,056	2750-1251	Reference	Table 1-435.txt	
09/26/02	08:10p		2,612,114	2750-1251	Reference	Table 1-436.txt	
09/26/02	08:10p		2,532,079	2750-1251	Reference	Table 1-437.txt	
09/26/02	08:10p		4,338,459	2750-1251	Reference	Table 1-438.txt	
09/26/02	08:10p		3,881,960	2750-1251	Reference	Table 1-439.txt	
09/26/02	08:10p		3,620,683	2750-1251	Reference	Table 1-440.txt	
09/26/02	08:10p		3,412,464	2750-1251	Reference	Table 1-441.txt	
09/26/02	08:10p		3,479,885	2750-1251	Reference	Table 1-442.txt	
09/26/02	08:10p		2,475,543	2750-1251	Reference	Table 1-443.txt	
09/26/02	08:10p		2,248,600	2750-1251	Reference	Table 1-444.txt	
09/26/02	08:10p		2,437,877	2750-1251	Reference	Table 1-445.txt	
09/26/02	08:10p		1,699,180	2750-1251	Reference	Table 1-446.txt	
09/26/02	08:10p		1,608,941	2750-1251	Reference	Table 1-447.txt	
09/26/02	08:10p		1,826,664	2750-1251	Reference	Table 1-448.txt	
09/26/02	08:10p		2,802,708	2750-1251	Reference	Table 1-449.txt	
09/26/02	08:10p		1,998,576	2750-1251	Reference	Table 1-450.txt	
09/26/02	08:10p		1,817,492	2750-1251	Reference	Table 1-451.txt	
09/26/02	08:10p		2,809,047	2750-1251	Reference	Table 1-452.txt	
09/26/02	08:10p		2,757,103	2750-1251	Reference	Table 1-453.txt	
09/26/02	08:10p		2,299,691	2750-1251	Reference	Table 1-454.txt	
09/26/02	08:10p		1,833,347	2750-1251	Reference	Table 1-455.txt	
09/26/02	08:10p		1,969,345	2750-1251	Reference	Table 1-456.txt	
09/26/02	08:10p		1,637,888	2750-1251	Reference	Table 1-457.txt	
09/26/02	08:10p		1,089,035	2750-1251	Reference	Table 1-458.txt	
09/26/02	08:10p		993,499	2750-1251	Reference	Table 1-459.txt	
09/26/02	08:10p		1,203,457	2750-1251	Reference	Table 1-460.txt	
09/26/02	08:10p		1,211,627	2750-1251	Reference	Table 1-461.txt	
09/26/02	08:10p		200,454	2750-1251	Reference	Table 1-462.txt	

File Create Date		File Size	File Name	CD#11
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09/26/02	08:10p	1,657,360	2750-1251P Sequence Table 2-03.txt	
09/26/02	08:10p	1,698,147	2750-1251P Sequence Table 2-04.txt	
09/26/02	08:10p	4,162,790	2750-1251P Sequence Table 2-05.txt	
09/26/02	08:10p	4,614,923	2750-1251P Sequence Table 2-06.txt	
09/26/02	08:10p	3,792,793	2750-1251P Sequence Table 2-07.txt	
09/26/02	08:10p	273	desktop.ini	
09/26/02	08:10p	3,874,904	2750-1251P Sequence Table 2-08.txt	
09/26/02	08:10p	4,925,916	2750-1251P Sequence Table 2-09.txt	
09/26/02	08:10p	1,660,538	2750-1251P Sequence Table 2-10.txt	
09/26/02	08:10p	1,504,564	2750-1251P Sequence Table 2-11.txt	
09/26/02	08:10p	1,701,082	2750-1251P Sequence Table 2-12.txt	
09/26/02	08:10p	1,765,355	2750-1251P Sequence Table 2-13.txt	
09/26/02	08:10p	1,930,595	2750-1251P Sequence Table 2-14.txt	
09/26/02	08:10p	1,752,872	2750-1251P Sequence Table 2-15.txt	
09/26/02	08:10p	1,950,729	2750-1251P Sequence Table 2-16.txt	
09/26/02	08:10p	1,715,656	2750-1251P Sequence Table 2-17.txt	
09/26/02	08:10p	1,807,680	2750-1251P Sequence Table 2-18.txt	
09/26/02	08:10p	1,841,424	2750-1251P Sequence Table 2-19.txt	
09/26/02	08:10p	1,793,563	2750-1251P Sequence Table 2-20.txt	
09/26/02	08:10p	1,489,266	2750-1251P Sequence Table 2-21.txt	
09/26/02	08:10p	1,639,834	2750-1251P Sequence Table 2-22.txt	
09/26/02	08:10p	1,823,227	2750-1251P Sequence Table 2-23.txt	
09/26/02	08:10p	1,675,137	2750-1251P Sequence Table 2-24.txt	
09/26/02	08:10p	1,714,599	2750-1251P Sequence Table 2-25.txt	
09/26/02	08:10p	1,656,327	2750-1251P Sequence Table 2-26.txt	
09/26/02	08:10p	1,554,473	2750-1251P Sequence Table 2-27.txt	
09/26/02	08:10p	1,784,745	2750-1251P Sequence Table 2-28.txt	
09/26/02	08:10p	2,043,076	2750-1251P Sequence Table 2-29.txt	
09/26/02	08:10p	1,768,767	2750-1251P Sequence Table 2-30.txt	
09/26/02	08:10p	1,920,121	2750-1251P Sequence Table 2-31.txt	
09/26/02	08:10p	1,578,209	2750-1251P Sequence Table 2-32.txt	
09/26/02	08:10p	1,569,804	2750-1251P Sequence Table 2-33.txt	
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09/26/02	08:10p	1,569,021	2750-1251P Sequence Table 2-35.txt	
09/26/02	08:10p	1,821,161	2750-1251P Sequence Table 2-36.txt	
09/26/02	08:10p	1,743,922	2750-1251P Sequence Table 2-37.txt	
09/26/02	08:10p	1,695,535	2750-1251P Sequence Table 2-38.txt	
09/26/02	08:10p	1,341,765	2750-1251P Sequence Table 2-39.txt	
09/26/02	08:10p	1,270,364	2750-1251P Sequence Table 2-40.txt	
09/26/02	08:10p	1,161,441	2750-1251P Sequence Table 2-41.txt	
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09/26/02	08:10p	5,286,926	2750-1251P Sequence Table 2-47.txt	
09/26/02	08:10p	6,291,073	2750-1251P Sequence Table 2-48.txt	
09/26/02	08:10p	4,279,766	2750-1251P Sequence Table 2-49.txt	
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09/26/02	08:10p	6,320,733	2750-1251P Sequence Table 2-54.txt	
09/26/02	08:10p	5,410,260	2750-1251P Sequence Table 2-55.txt	
09/26/02	08:10p	2,244,531	2750-1251P Sequence Table 2-56.txt	
09/26/02	08:10p	2,182,682	2750-1251P Sequence Table 2-57.txt	
09/26/02	08:10p	3,894,074	2750-1251P Sequence Table 2-58.txt	
09/26/02	08:10p	3,854,986	2750-1251P Sequence Table 2-59.txt	
09/26/02	08:10p	4,900,131	2750-1251P Sequence Table 2-60.txt	
09/26/02	08:10p	2,883,354	2750-1251P Sequence Table 2-61.txt	
09/26/02	08:10p	3,359,337	2750-1251P Sequence Table 2-62.txt	

File	Create Date	File Size	File Name	CD#11
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09/26/02	08:10p	5,021,467	2750-1251P Sequence Table 2-65.txt	
09/26/02	08:10p	2,779,104	2750-1251P Sequence Table 2-66.txt	
09/26/02	08:10p	2,277,254	2750-1251P Sequence Table 2-67.txt	
09/26/02	08:10p	2,428,011	2750-1251P Sequence Table 2-68.txt	
09/26/02	08:10p	2,555,544	2750-1251P Sequence Table 2-69.txt	
09/26/02	08:10p	2,403,691	2750-1251P Sequence Table 2-70.txt	
09/26/02	08:10p	2,623,087	2750-1251P Sequence Table 2-71.txt	
09/26/02	08:10p	1,917,948	2750-1251P Sequence Table 2-72.txt	
09/26/02	08:10p	1,485,239	2750-1251P Sequence Table 2-73.txt	
09/26/02	08:10p	855,857	2750-1251P Sequence Table 2-74.txt	
09/26/02	08:10p	5,711,238	2750-1251P Sequence Table 2-75.txt	
09/26/02	08:10p	5,673,560	2750-1251P Sequence Table 2-76.txt	
09/26/02	08:10p	6,917,903	2750-1251P Sequence Table 2-77.txt	
09/26/02	08:10p	6,422,494	2750-1251P Sequence Table 2-78.txt	
09/26/02	08:10p	6,687,789	2750-1251P Sequence Table 2-79.txt	
09/26/02	08:10p	6,049,957	2750-1251P Sequence Table 2-80.txt	
09/26/02	08:10p	6,765,446	2750-1251P Sequence Table 2-81.txt	
09/26/02	08:10p	273	desktop.ini	
09/26/02	08:10p	6,651,228	2750-1251P Sequence Table 2-82.txt	
09/26/02	08:10p	1,306,973	2750-1251P Sequence Table 2-83.txt	
09/26/02	08:10p	1,616,973	2750-1251P Sequence Table 2-84.txt	
09/26/02	08:10p	1,966,670	2750-1251P Sequence Table 2-85.txt	
09/26/02	08:10p	2,007,901	2750-1251P Sequence Table 2-86.txt	
09/26/02	08:10p	1,749,945	2750-1251P Sequence Table 2-87.txt	
09/26/02	08:10p	1,875,661	2750-1251P Sequence Table 2-88.txt	
09/26/02	08:10p	2,021,866	2750-1251P Sequence Table 2-89.txt	
09/26/02	08:10p	1,838,953	2750-1251P Sequence Table 2-90.txt	
09/26/02	08:10p	1,801,647	2750-1251P Sequence Table 2-91.txt	
09/26/02	08:10p	281,163	2750-1251P Sequence Table 2-92.txt	
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09/26/02	08:10p	2,423,202	2750-1251P Sequence Table 2-101.txt	
09/26/02	08:10p	897,746	2750-1251P Sequence Table 2-102.txt	
09/26/02	08:10p	924,573	2750-1251P Sequence Table 2-103.txt	
09/26/02	08:10p	915,997	2750-1251P Sequence Table 2-104.txt	
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09/26/02	08:11p	273	desktop.ini	
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09/26/02	08:10p	607,711	2750-1251P Sequence Table 2-108.txt	
09/26/02	08:10p	966,009	2750-1251P Sequence Table 2-109.txt	
09/26/02	08:10p	785,714	2750-1251P Sequence Table 2-110.txt	
09/26/02	08:10p	995,227	2750-1251P Sequence Table 2-111.txt	
09/26/02	08:10p	1,019,275	2750-1251P Sequence Table 2-112.txt	
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09/26/02	08:10p	974,367	2750-1251P Sequence Table 2-114.txt	
09/26/02	08:10p	978,475	2750-1251P Sequence Table 2-115.txt	
09/26/02	08:10p	1,105,834	2750-1251P Sequence Table 2-116.txt	
09/26/02	08:10p	1,042,354	2750-1251P Sequence Table 2-117.txt	
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09/26/02	08:10p	1,563,393	2750-1251P Sequence Table 2-119.txt	
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09/26/02	08:10p	1,088,907	2750-1251P Sequence Table 2-121.txt	
09/26/02	08:10p	955,411	2750-1251P Sequence Table 2-122.txt	
09/26/02	08:10p	1,012,863	2750-1251P Sequence Table 2-123.txt	
09/26/02	08:10p	332,900	2750-1251P Sequence Table 2-124.txt	
09/26/02	08:10p	2,245,436	2750-1251P Sequence Table 2-125.txt	
09/26/02	08:10p	2,062,700	2750-1251P Sequence Table 2-126.txt	
09/26/02	08:10p	2,200,806	2750-1251P Sequence Table 2-127.txt	
09/26/02	08:10p	2,198,487	2750-1251P Sequence Table 2-128.txt	
09/26/02	08:10p	2,193,488	2750-1251P Sequence Table 2-129.txt	
09/26/02	08:10p	2,236,417	2750-1251P Sequence Table 2-130.txt	
09/26/02	08:10p	2,400,482	2750-1251P Sequence Table 2-131.txt	
09/26/02	08:10p	2,926,305	2750-1251P Sequence Table 2-132.txt	
09/26/02	08:10p	3,218,588	2750-1251P Sequence Table 2-133.txt	
09/26/02	08:10p	2,698,797	2750-1251P Sequence Table 2-134.txt	

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09/26/02	08:11p	781,483	2750-1251P Sequence Table 2-138.txt	
09/26/02	08:11p	2,664,765	2750-1251P Sequence Table 2-93.txt	
09/26/02	08:11p	2,567,753	2750-1251P Sequence Table 2-94.txt	
09/26/02	08:11p	2,525,906	2750-1251P Sequence Table 2-95.txt	
09/26/02	08:11p	2,382,901	2750-1251P Sequence Table 2-96.txt	
09/26/02	08:11p	2,395,607	2750-1251P Sequence Table 2-97.txt	
09/26/02	08:11p	2,731,108	2750-1251P Sequence Table 2-98.txt	
09/26/02	08:11p	2,880,212	2750-1251P Sequence Table 2-99.txt	
09/26/02	08:11p	2,557,369	2750-1251P Sequence Table 2-139.txt	
09/26/02	08:11p	2,853,781	2750-1251P Sequence Table 2-140.txt	
09/26/02	08:11p	1,989,875	2750-1251P Sequence Table 2-141.txt	
09/26/02	08:11p	2,106,541	2750-1251P Sequence Table 2-142.txt	
09/26/02	08:11p	2,498,911	2750-1251P Sequence Table 2-143.txt	
09/26/02	08:11p	1,860,537	2750-1251P Sequence Table 2-144.txt	
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09/26/02	08:11p	1,125,327	2750-1251P Sequence Table 2-149.txt	
09/26/02	08:11p	1,120,749	2750-1251P Sequence Table 2-150.txt	
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09/26/02	08:11p	1,039,599	2750-1251P Sequence Table 2-154.txt	
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09/26/02	08:11p	894,922	2750-1251P Sequence Table 2-161.txt	
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09/26/02	08:11p	1,291,664	2750-1251P Sequence Table 2-165.txt	
09/26/02	08:11p	1,184,768	2750-1251P Sequence Table 2-166.txt	
09/26/02	08:11p	1,699,364	2750-1251P Sequence Table 2-167.txt	
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09/26/02	08:11p	1,397,366	2750-1251P Sequence Table 2-174.txt	
09/26/02	08:11p	767,040	2750-1251P Sequence Table 2-175.txt	
09/26/02	08:11p	789,783	2750-1251P Sequence Table 2-176.txt	
09/26/02	08:11p	912,240	2750-1251P Sequence Table 2-177.txt	
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09/26/02	08:11p	1,114,602	2750-1251P Sequence Table 2-179.txt	
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09/26/02	08:11p	1,155,964	2750-1251P Sequence Table 2-182.txt	
09/26/02	08:11p	1,579,837	2750-1251P Sequence Table 2-183.txt	
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09/26/02	08:11p	1,302,947	2750-1251P Sequence Table 2-187.txt	
09/26/02	08:11p	1,386,989	2750-1251P Sequence Table 2-188.txt	
09/26/02	08:11p	1,168,456	2750-1251P Sequence Table 2-189.txt	
09/26/02	08:11p	2,585,638	2750-1251P Sequence Table 2-190.txt	
09/26/02	08:11p	2,589,413	2750-1251P Sequence Table 2-191.txt	
09/26/02	08:11p	2,742,639	2750-1251P Sequence Table 2-192.txt	
09/26/02	08:11p	3,316,079	2750-1251P Sequence Table 2-193.txt	

File Create Date	File Size	File Name	CD#11
09/26/02 08:11p	2,721,831	2750-1251P Sequence Table 2-194.txt	
09/26/02 08:11p	2,460,485	2750-1251P Sequence Table 2-195.txt	
09/26/02 08:11p	3,712,199	2750-1251P Sequence Table 2-196.txt	
09/26/02 08:11p	3,062,135	2750-1251P Sequence Table 2-197.txt	
09/26/02 08:11p	2,324,748	2750-1251P Sequence Table 2-198.txt	
09/26/02 08:11p	5,805,417	2750-1251P Sequence Table 2-199.txt	
09/26/02 08:11p	4,484,190	2750-1251P Sequence Table 2-200.txt	
09/26/02 08:11p	2,886,756	2750-1251P Sequence Table 2-201.txt	
09/26/02 08:11p	3,152,805	2750-1251P Sequence Table 2-202.txt	
09/26/02 08:11p	4,113,648	2750-1251P Sequence Table 2-203.txt	
09/26/02 08:11p	4,539,820	2750-1251P Sequence Table 2-204.txt	
09/26/02 08:11p	5,279,187	2750-1251P Sequence Table 2-205.txt	
09/26/02 08:11p	5,282,318	2750-1251P Sequence Table 2-206.txt	
09/26/02 08:11p	3,875,494	2750-1251P Sequence Table 2-207.txt	
09/26/02 08:11p	3,227,215	2750-1251P Sequence Table 2-208.txt	
09/26/02 08:11p	2,542,116	2750-1251P Sequence Table 2-209.txt	
09/26/02 08:11p	2,154,442	2750-1251P Sequence Table 2-210.txt	
09/26/02 08:11p	3,040,311	2750-1251P Sequence Table 2-211.txt	
09/26/02 08:11p	2,843,279	2750-1251P Sequence Table 2-212.txt	
09/26/02 08:11p	2,679,715	2750-1251P Sequence Table 2-213.txt	
09/26/02 08:11p	2,069,892	2750-1251P Sequence Table 2-214.txt	
09/26/02 08:11p	2,774,060	2750-1251P Sequence Table 2-215.txt	
09/26/02 08:11p	2,395,440	2750-1251P Sequence Table 2-216.txt	
09/26/02 08:11p	2,484,149	2750-1251P Sequence Table 2-217.txt	
09/26/02 08:11p	2,314,135	2750-1251P Sequence Table 2-218.txt	
09/26/02 08:11p	1,572,173	2750-1251P Sequence Table 2-219.txt	
09/26/02 08:11p	1,483,612	2750-1251P Sequence Table 2-220.txt	
09/26/02 08:11p	1,341,529	2750-1251P Sequence Table 2-221.txt	
09/26/02 08:11p	1,255,155	2750-1251P Sequence Table 2-222.txt	
09/26/02 08:11p	2,484,999	2750-1251P Sequence Table 2-223.txt	
09/26/02 08:11p	2,545,172	2750-1251P Sequence Table 2-224.txt	
09/26/02 08:11p	2,611,886	2750-1251P Sequence Table 2-225.txt	
09/26/02 08:11p	2,482,720	2750-1251P Sequence Table 2-226.txt	
09/26/02 08:11p	2,295,734	2750-1251P Sequence Table 2-227.txt	
09/26/02 08:11p	2,579,591	2750-1251P Sequence Table 2-228.txt	
09/26/02 08:11p	2,640,839	2750-1251P Sequence Table 2-229.txt	
09/26/02 08:11p	266	desktop.ini	
09/26/02 08:11p	2,301,215	2750-1251P Sequence Table 2-230.txt	
09/26/02 08:11p	3,114,083	2750-1251P Sequence Table 2-231.txt	
09/26/02 08:11p	1,171,364	2750-1251P Sequence Table 2-232.txt	
09/26/02 08:11p	1,156,815	2750-1251P Sequence Table 2-233.txt	
09/26/02 08:11p	1,130,529	2750-1251P Sequence Table 2-234.txt	
09/26/02 08:11p	1,267,508	2750-1251P Sequence Table 2-235.txt	
09/26/02 08:11p	1,367,809	2750-1251P Sequence Table 2-236.txt	
09/26/02 08:11p	1,122,628	2750-1251P Sequence Table 2-237.txt	
09/26/02 08:11p	1,135,394	2750-1251P Sequence Table 2-238.txt	
09/26/02 08:11p	1,371,082	2750-1251P Sequence Table 2-239.txt	
09/26/02 08:11p	1,261,144	2750-1251P Sequence Table 2-240.txt	
09/26/02 08:11p	1,178,241	2750-1251P Sequence Table 2-241.txt	
09/26/02 08:11p	1,739,014	2750-1251P Sequence Table 2-242.txt	
09/26/02 08:11p	1,307,555	2750-1251P Sequence Table 2-243.txt	
09/26/02 08:11p	1,034,671	2750-1251P Sequence Table 2-244.txt	
09/26/02 08:11p	1,459,913	2750-1251P Sequence Table 2-245.txt	
09/26/02 08:11p	1,274,639	2750-1251P Sequence Table 2-246.txt	
09/26/02 08:11p	1,358,712	2750-1251P Sequence Table 2-247.txt	
09/26/02 08:11p	1,446,767	2750-1251P Sequence Table 2-248.txt	
09/26/02 08:11p	1,599,682	2750-1251P Sequence Table 2-249.txt	
09/26/02 08:11p	1,443,866	2750-1251P Sequence Table 2-250.txt	
09/26/02 08:11p	1,431,278	2750-1251P Sequence Table 2-251.txt	
09/26/02 08:11p	1,522,875	2750-1251P Sequence Table 2-252.txt	
09/26/02 08:11p	801,857	2750-1251P Sequence Table 2-253.txt	
09/26/02 08:11p	922,371	2750-1251P Sequence Table 2-254.txt	
09/26/02 08:11p	979,530	2750-1251P Sequence Table 2-255.txt	
09/26/02 08:11p	1,137,713	2750-1251P Sequence Table 2-256.txt	
09/26/02 08:11p	1,139,016	2750-1251P Sequence Table 2-257.txt	
09/26/02 08:11p	1,615,047	2750-1251P Sequence Table 2-258.txt	
09/26/02 08:11p	1,606,539	2750-1251P Sequence Table 2-259.txt	

File Create Date	File Size	File Name	CD#11
09/26/02 08:11p	1,857,291	2750-1251P Sequence Table 2-260.txt	
09/26/02 08:11p	2,186,164	2750-1251P Sequence Table 2-261.txt	
09/26/02 08:11p	2,162,287	2750-1251P Sequence Table 2-262.txt	
09/26/02 08:11p	2,074,224	2750-1251P Sequence Table 2-263.txt	
09/26/02 08:11p	1,673,177	2750-1251P Sequence Table 2-264.txt	
09/26/02 08:11p	1,997,716	2750-1251P Sequence Table 2-265.txt	
09/26/02 08:11p	2,038,387	2750-1251P Sequence Table 2-266.txt	
09/26/02 08:11p	1,421,339	2750-1251P Sequence Table 2-267.txt	
09/26/02 08:11p	1,358,029	2750-1251P Sequence Table 2-268.txt	
09/26/02 08:11p	1,510,770	2750-1251P Sequence Table 2-269.txt	
09/26/02 08:11p	1,638,917	2750-1251P Sequence Table 2-270.txt	
09/26/02 08:11p	1,585,428	2750-1251P Sequence Table 2-271.txt	
09/26/02 08:11p	1,804,287	2750-1251P Sequence Table 2-272.txt	
09/26/02 08:11p	2,058,480	2750-1251P Sequence Table 2-273.txt	
09/26/02 08:11p	2,140,569	2750-1251P Sequence Table 2-274.txt	
09/26/02 08:11p	2,006,620	2750-1251P Sequence Table 2-275.txt	
09/26/02 08:11p	2,004,807	2750-1251P Sequence Table 2-276.txt	
09/26/02 08:11p	281,295	2750-1251P Sequence Table 2-277.txt	
09/26/02 08:11p	3,519,408	2750-1251P Sequence Table 2-278.txt	
09/26/02 08:11p	2,892,616	2750-1251P Sequence Table 2-279.txt	
09/26/02 08:11p	2,537,900	2750-1251P Sequence Table 2-280.txt	
09/26/02 08:11p	2,742,562	2750-1251P Sequence Table 2-281.txt	
09/26/02 08:11p	2,674,740	2750-1251P Sequence Table 2-282.txt	
09/26/02 08:11p	2,662,157	2750-1251P Sequence Table 2-283.txt	
09/26/02 08:11p	2,260,140	2750-1251P Sequence Table 2-284.txt	
09/26/02 08:11p	2,053,431	2750-1251P Sequence Table 2-285.txt	
09/26/02 08:11p	2,666,877	2750-1251P Sequence Table 2-286.txt	
09/26/02 08:11p	2,668,943	2750-1251P Sequence Table 2-287.txt	
09/26/02 08:11p	2,179,544	2750-1251P Sequence Table 2-288.txt	
09/26/02 08:11p	2,159,998	2750-1251P Sequence Table 2-289.txt	
09/26/02 08:11p	3,148,049	2750-1251P Sequence Table 2-290.txt	
09/26/02 08:11p	2,910,241	2750-1251P Sequence Table 2-291.txt	
09/26/02 08:11p	2,842,608	2750-1251P Sequence Table 2-292.txt	
09/26/02 08:11p	2,655,523	2750-1251P Sequence Table 2-293.txt	
09/26/02 08:11p	2,779,284	2750-1251P Sequence Table 2-294.txt	
09/26/02 08:11p	2,381,391	2750-1251P Sequence Table 2-295.txt	
09/26/02 08:11p	2,355,845	2750-1251P Sequence Table 2-296.txt	
09/26/02 08:11p	2,355,901	2750-1251P Sequence Table 2-297.txt	
09/26/02 08:11p	1,879,327	2750-1251P Sequence Table 2-298.txt	
09/26/02 08:11p	1,710,956	2750-1251P Sequence Table 2-299.txt	
09/26/02 08:11p	1,878,989	2750-1251P Sequence Table 2-300.txt	
09/26/02 08:11p	2,372,963	2750-1251P Sequence Table 2-301.txt	
09/26/02 08:11p	2,100,984	2750-1251P Sequence Table 2-302.txt	
09/26/02 08:11p	1,689,858	2750-1251P Sequence Table 2-303.txt	
09/26/02 08:11p	2,069,970	2750-1251P Sequence Table 2-304.txt	
09/26/02 08:11p	2,184,675	2750-1251P Sequence Table 2-305.txt	
09/26/02 08:11p	1,902,854	2750-1251P Sequence Table 2-306.txt	
09/26/02 08:11p	1,651,456	2750-1251P Sequence Table 2-307.txt	
09/26/02 08:11p	1,706,938	2750-1251P Sequence Table 2-308.txt	
09/26/02 08:11p	1,378,700	2750-1251P Sequence Table 2-309.txt	
09/26/02 08:11p	1,038,131	2750-1251P Sequence Table 2-310.txt	
09/26/02 08:11p	994,540	2750-1251P Sequence Table 2-311.txt	
09/26/02 08:11p	1,085,850	2750-1251P Sequence Table 2-312.txt	
09/26/02 08:11p	1,057,364	2750-1251P Sequence Table 2-313.txt	
09/26/02 08:11p	195,057	2750-1251P Sequence Table 2-314.txt	

File Create Date	File Size	File Name	CD#12
09/26/02 08:12p	6,498,586	2750-1251P Sequence Table 2-315.txt	
09/26/02 08:12p	10,199,072	2750-1251P Sequence Table 2-316.txt	
09/26/02 08:12p	12,036,630	2750-1251P Sequence Table 2-317.txt	
09/26/02 08:12p	11,752,397	2750-1251P Sequence Table 2-318.txt	
09/26/02 08:12p	11,328,855	2750-1251P Sequence Table 2-319.txt	
09/26/02 08:12p	6,099,008	2750-1251P Sequence Table 2-320.txt	

File	Create	Date	File	Size	File	Name	CD#12
09/26/02	08:12p		6,341,448	2750-1251P	Sequence	Table 2-321.txt	
09/26/02	08:12p		7,813,361	2750-1251P	Sequence	Table 2-322.txt	
09/26/02	08:12p		7,462,370	2750-1251P	Sequence	Table 2-323.txt	
09/26/02	08:12p		7,320,568	2750-1251P	Sequence	Table 2-324.txt	
09/26/02	08:12p		7,260,488	2750-1251P	Sequence	Table 2-325.txt	
09/26/02	08:12p		7,218,559	2750-1251P	Sequence	Table 2-326.txt	
09/26/02	08:12p		9,879,422	2750-1251P	Sequence	Table 2-327.txt	
09/26/02	08:12p		11,133,682	2750-1251P	Sequence	Table 2-328.txt	
09/26/02	08:12p		11,786,619	2750-1251P	Sequence	Table 2-329.txt	
09/26/02	08:12p		11,165,230	2750-1251P	Sequence	Table 2-330.txt	
09/26/02	08:12p		8,972,274	2750-1251P	Sequence	Table 2-331.txt	
09/26/02	08:12p		2,780,653	2750-1251P	Sequence	Table 2-332.txt	
09/26/02	08:12p		8,615,635	2750-1251P	Sequence	Table 2-333.txt	
09/26/02	08:12p		8,523,103	2750-1251P	Sequence	Table 2-334.txt	
09/26/02	08:12p		9,422,642	2750-1251P	Sequence	Table 2-335.txt	
09/26/02	08:12p		9,389,088	2750-1251P	Sequence	Table 2-336.txt	
09/26/02	08:12p		9,612,247	2750-1251P	Sequence	Table 2-337.txt	
09/26/02	08:12p		9,885,866	2750-1251P	Sequence	Table 2-338.txt	
09/26/02	08:12p		7,757,608	2750-1251P	Sequence	Table 2-339.txt	
09/26/02	08:12p		10,006,125	2750-1251P	Sequence	Table 2-340.txt	
09/26/02	08:12p		2,238,454	2750-1251P	Sequence	Table 2-341.txt	
09/26/02	08:12p		2,341,096	2750-1251P	Sequence	Table 2-342.txt	
09/26/02	08:12p		4,662,049	2750-1251P	Sequence	Table 2-343.txt	
09/26/02	08:12p		7,548,211	2750-1251P	Sequence	Table 2-344.txt	
09/26/02	08:12p		8,492,475	2750-1251P	Sequence	Table 2-345.txt	
09/26/02	08:12p		8,606,480	2750-1251P	Sequence	Table 2-346.txt	
09/26/02	08:12p		8,529,685	2750-1251P	Sequence	Table 2-347.txt	
09/26/02	08:12p		9,307,111	2750-1251P	Sequence	Table 2-348.txt	
09/26/02	08:12p		9,475,512	2750-1251P	Sequence	Table 2-349.txt	
09/26/02	08:12p		10,925,483	2750-1251P	Sequence	Table 2-350.txt	
09/26/02	08:12p		9,549,730	2750-1251P	Sequence	Table 2-351.txt	
09/26/02	08:13p		9,420,696	2750-1251P	Sequence	Table 2-352.txt	
09/26/02	08:13p		9,796,536	2750-1251P	Sequence	Table 2-353.txt	
09/26/02	08:13p		9,446,273	2750-1251P	Sequence	Table 2-354.txt	
09/26/02	08:13p		9,676,816	2750-1251P	Sequence	Table 2-355.txt	
09/26/02	08:13p		11,072,001	2750-1251P	Sequence	Table 2-356.txt	
09/26/02	08:13p		9,579,990	2750-1251P	Sequence	Table 2-357.txt	
09/26/02	08:13p		8,310,594	2750-1251P	Sequence	Table 2-358.txt	
09/26/02	08:13p		11,611,950	2750-1251P	Sequence	Table 2-359.txt	
09/26/02	08:13p		9,124,788	2750-1251P	Sequence	Table 2-360.txt	
09/26/02	08:13p		10,561,261	2750-1251P	Sequence	Table 2-361.txt	
09/26/02	08:13p		7,867,957	2750-1251P	Sequence	Table 2-362.txt	
09/26/02	08:13p		6,719,514	2750-1251P	Sequence	Table 2-363.txt	
09/26/02	08:13p		8,289,686	2750-1251P	Sequence	Table 2-364.txt	
09/26/02	08:13p		5,982,487	2750-1251P	Sequence	Table 2-365.txt	
09/26/02	08:13p		11,770,382	2750-1251P	Sequence	Table 2-366.txt	
09/26/02	08:13p		11,500,131	2750-1251P	Sequence	Table 2-367.txt	
09/26/02	08:13p		11,697,796	2750-1251P	Sequence	Table 2-368.txt	
09/26/02	08:13p		12,537,239	2750-1251P	Sequence	Table 2-369.txt	
09/26/02	08:13p		12,060,873	2750-1251P	Sequence	Table 2-370.txt	
09/26/02	08:13p		11,377,116	2750-1251P	Sequence	Table 2-371.txt	
09/26/02	08:13p		12,409,974	2750-1251P	Sequence	Table 2-372.txt	
09/26/02	08:13p		11,590,344	2750-1251P	Sequence	Table 2-373.txt	
09/26/02	08:13p		12,793,977	2750-1251P	Sequence	Table 2-374.txt	
09/26/02	08:13p		11,148,530	2750-1251P	Sequence	Table 2-375.txt	
09/26/02	08:13p		11,844,914	2750-1251P	Sequence	Table 2-376.txt	
09/26/02	08:13p		11,297,588	2750-1251P	Sequence	Table 2-377.txt	
09/26/02	08:13p		10,940,286	2750-1251P	Sequence	Table 2-378.txt	
09/26/02	08:13p		11,538,574	2750-1251P	Sequence	Table 2-379.txt	
09/26/02	08:13p		12,086,002	2750-1251P	Sequence	Table 2-380.txt	
09/26/02	08:13p		12,893,746	2750-1251P	Sequence	Table 2-381.txt	
09/26/02	08:14p		11,115,866	2750-1251P	Sequence	Table 2-382.txt	
09/26/02	08:14p		12,062,481	2750-1251P	Sequence	Table 2-383.txt	
09/26/02	08:14p		10,134,157	2750-1251P	Sequence	Table 2-384.txt	
09/26/02	08:14p		8,527,358	2750-1251P	Sequence	Table 2-385.txt	
09/26/02	08:14p		8,310,745	2750-1251P	Sequence	Table 2-386.txt	
09/26/02	08:14p		7,479,110	2750-1251P	Sequence	Table 2-387.txt	

File Create Date	File Size	File Name	CD#12
09/26/02 08:14p	3,429,936	2750-1251P Sequence Table 2-388.txt	
09/26/02 08:12p	7,320,568	sequences.3769.710-0004-55300-US-U-31610.01 10	

File Create Date	File Size	File Name	CD#13
08/21/01 02:28p	392,675	80090-004 knock_in.txt	
08/14/01 06:12p	831,736	80090-004 knock_out	
08/20/01 10:56a	16,635,460	80090-004 ma_clusters	
08/21/01 02:54p	4,318,956	80090-004 ma_diff	
08/10/01 02:06p	2,752,459	80090-004_Protein Domain Table.txt	
07/25/01 06:17p	30,304,496	80090-004_Reference Table 1.txt	
07/25/01 05:56p	1,679,252	80090-004_Reference Table 2.txt	
07/25/01 06:00p	144,192,839	80090-004_Sequence Table 1.txt	
08/17/01 03:48p	4,052,876	cdna_clusters.txt	
07/25/01 06:06p	12,085,942	80090-004_Sequence Table 2.txt	
08/22/01 04:03p	35,153	Cluster Functions and Utilities (01).txt	
08/22/01 04:04p	40,447	Cluster Functions and Utilities (02).txt	
08/22/01 04:04p	4,473	Cluster Functions and Utilities (03).txt	
08/22/01 04:05p	7,820	Cluster Functions and Utilities (04).txt	
08/22/01 04:05p	24,047	Cluster Functions and Utilities (05).txt	
08/22/01 04:06p	18,490	Cluster Functions and Utilities (06).txt	
08/22/01 02:14p	331,616	enhanced_amino.txt	
08/22/01 04:11p	36,273	Cluster functions and utilities (07).txt	
08/22/01 03:17p	33,962	Cluster Functions and Utilities (08).txt	
08/22/01 03:16p	23,000	Cluster functions and utilities (09).txt	
08/21/01 08:47p	2,691	Cluster functions and utilities (10).txt	
08/21/01 08:47p	2,290	Cluster functions and utilities (11).txt	
08/24/01 02:54p	12,684	Cluster Functions and Utilities 01.txt	
08/24/01 02:56p	91,002	Cluster Functions and Utilities 02.txt	
02/25/02 02:36p	10,512,576	group0.txt	
08/24/01 02:57p	6,256	Cluster Functions and Utilities 03.txt	
08/24/01 02:58p	6,292	Cluster Functions and Utilities 04.txt	
08/24/01 02:58p	37,345	Cluster Functions and Utilities 05.txt	
08/24/01 03:02p	96,535	Cluster Functions and Utilities 06.txt	
08/24/01 03:44p	8,447	Cluster Functions and Utilities 07.txt	
08/24/01 04:04p	17,087	Cluster Functions and Utilities 08.txt	
08/22/01 04:24p	23,740	Cluster Functions and Utilities (12).txt	
08/21/01 07:46a	296,887	docket_80090_101_cdna_map.txt	
08/24/01 02:10p	1,232	docket_80090_101_cdna_map_II_delta	
02/25/02 02:38p	10,493,605	group1.txt	
02/25/02 02:41p	10,489,244	group2.txt	
02/25/02 02:44p	10,687,170	group3.txt	
02/25/02 02:47p	10,732,414	group4.txt	
02/25/02 02:49p	10,727,807	group5.txt	
02/25/02 02:52p	10,616,591	group6.txt	
02/25/02 02:53p	6,065,227	group7.txt	
08/24/01 05:13p	6,947	Knock-in_02.txt	
08/24/01 05:14p	11,374	KNOCK-IN_01.txt	
08/24/01 03:12p	1,645,031	knock_out	
08/21/01 01:09p	55,307	ma_diff Aluminum.txt	
02/28/02 04:04p	3,733,718	titles	
08/21/01 01:10p	27,557	ma_diff Axel.txt	
08/21/01 01:13p	41,505	ma_diff Cadium .txt	
08/21/01 01:51p	53,938	ma_diff Cauliflower .txt	
08/21/01 01:50p	98,775	ma_diff Chloroplast.txt	
08/21/01 01:50p	160,542	ma_diff Circadian 1-02.txt	
08/21/01 01:50p	127,498	ma_diff Circadian 1-03.txt	
08/21/01 01:51p	166,158	ma_diff Circadian 1-04.txt	
08/21/01 01:50p	141,971	ma_diff Circadian 1-01.txt	
08/21/01 01:52p	56,536	ma_diff Circadian 1-05.txt	
08/21/01 01:52p	121,178	ma_diff Circadian 1-06.txt	
08/21/01 01:52p	133,389	ma_diff Circadian 1-07.txt	
08/21/01 01:52p	259,096	ma_diff Circadian 1-08.txt	
08/21/01 01:52p	228,222	ma_diff Circadian 1-09.txt	
08/21/01 01:53p	54,526	ma_diff Circadian 1-10.txt	

File Create Date	File Size	File Name	CD#13
08/21/01 01:53p	134,759	ma_diff CO2 1-1.txt	
08/21/01 01:53p	241,865	ma_diff CO2 1-2.txt	
08/21/01 01:54p	63,264	ma_diff CO2 1-3.txt	
08/21/01 01:54p	59,530	ma_diff CO2 1-4.txt	
08/21/01 01:54p	372,633	ma_diff CO2 1-5.txt	
08/21/01 01:54p	9,220	ma_diff Disease .txt	
08/21/01 01:54p	25,114	ma_diff H2O2 .txt	
08/21/01 01:55p	4,073	ma_diff Iol .txt	
08/21/01 01:55p	283,026	ma_diff Iron 1-1.txt	
08/21/01 01:55p	90,890	ma_diff Iron 1-2.txt	
08/21/01 01:55p	51,342	ma_diff Mitochondria-Electron Transp.txt	
08/21/01 01:55p	107,920	ma_diff NAA (Auxin) 1-1.txt	
08/21/01 01:55p	50,267	ma_diff NAA (Auxin) 1-2.txt	
08/21/01 01:55p	67,291	ma_diff Nitrogen.txt	
08/21/01 01:56p	6,441	ma_diff Phototropism 1-1.txt	
08/21/01 01:56p	45,620	ma_diff Shade.txt	
08/21/01 01:56p	22,229	ma_diff Phototropism 1-2.txt	
08/21/01 01:56p	28,270	ma_diff Phototropism 1-3.txt	
08/21/01 01:56p	73,438	ma_diff Sqn.txt	
08/21/01 01:56p	3,828	ma_diff Sulfur.txt	
08/21/01 01:56p	67,949	ma_diff Wounding.txt	
08/21/01 01:57p	30,836	ma_diff Zinc.txt	
08/10/01 03:06p	2,752,459	Protein Domain Table.txt	
02/21/02 05:54p	10,401,255	seqs.fasta.1	
02/21/02 05:54p	3,149,009	seqs.fasta.2	
08/22/01 04:01p	1,476	Single gene functions and utilities (1).txt	
08/22/01 04:01p	2,223	Single gene functions and utilities (2).txt	
08/22/01 04:02p	905	Single gene functions and utilities (3).txt	
08/22/01 04:03p	1,517	Single gene functions and utilities (4).txt	
08/22/01 04:07p	4,626	Single gene functions and utilities (5).txt	
08/22/01 03:57p	4,887	Single gene functions and utilities (6).txt	
08/22/01 03:57p	7,456	Single gene functions and utilities (7).txt	
08/22/01 04:06p	9,339	Single gene functions and utilities (8).txt	
08/20/01 02:33p	228,792	stanford_old_new_cdna_map.txt	

File Create Date	File Size	File Name	CD#14
02/27/02 04:27p	279,711,648	flib1	
02/27/02 04:22p	290,311,988	flib2	

File Create Date	File Size	File Name	CD#15
02/27/02 04:17p	209,849,751	flib3	
02/27/02 04:14p	226,030,922	flib4	
02/27/02 04:40p	174,831,246	flib5	

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08/12/01 12:28p	861,063	reference.311987.710-0004-55300-US-U-31837.01_01	
08/12/01 12:28p	1,031,558	reference.311987.710-0004-55300-US-U-31837.01_02	
08/12/01 12:27p	923,000	reference.311987.710-0004-55300-US-U-31837.01_03	
08/12/01 12:27p	1,295,643	reference.311987.710-0004-55300-US-U-31837.01_04	
08/12/01 12:27p	1,235,936	reference.311987.710-0004-55300-US-U-31837.01_05	
08/12/01 12:27p	1,290,154	reference.311987.710-0004-55300-US-U-31837.01_06	
08/12/01 12:27p	1,408,509	reference.311987.710-0004-55300-US-U-31837.01_07	
08/12/01 12:27p	1,155,221	reference.311987.710-0004-55300-US-U-31837.01_08	
08/12/01 12:27p	1,519,100	reference.311987.710-0004-55300-US-U-31837.01_09	
08/12/01 12:28p	429,628	reference.311987.710-0004-55300-US-U-	

File Create Date	File Size	File Name	CD#16
31837.01_0a_01			
08/12/01 12:28p	401,809	reference.311987.710-0004-55300-US-U-	
31837.01_0a_02			
08/12/01 12:27p	427,694	reference.311987.710-0004-55300-US-U-	
31837.01_0a_03			
08/12/01 12:27p	432,251	reference.311987.710-0004-55300-US-U-	
31837.01_0a_04			
08/12/01 12:27p	413,138	reference.311987.710-0004-55300-US-U-	
31837.01_0a_05			
08/12/01 12:27p	451,105	reference.311987.710-0004-55300-US-U-	
31837.01_0a_06			
08/12/01 12:27p	379,667	reference.311987.710-0004-55300-US-U-	
31837.01_0a_07			
08/12/01 12:27p	417,795	reference.311987.710-0004-55300-US-U-	
31837.01_0a_08			
08/12/01 12:27p	413,350	reference.311987.710-0004-55300-US-U-	
31837.01_0a_09			
08/12/01 12:27p	410,249	reference.311987.710-0004-55300-US-U-	
31837.01_0a_10			
08/12/01 12:26p	436,240	reference.311987.710-0004-55300-US-U-	
31837.01_0a_11			
08/12/01 12:26p	429,548	reference.311987.710-0004-55300-US-U-	
31837.01_0a_12			
08/12/01 12:26p	398,666	reference.311987.710-0004-55300-US-U-	
31837.01_0a_13			
08/12/01 12:26p	384,878	reference.311987.710-0004-55300-US-U-	
31837.01_0a_14			
08/12/01 12:26p	426,874	reference.311987.710-0004-55300-US-U-	
31837.01_0a_15			
08/12/01 12:26p	407,594	reference.311987.710-0004-55300-US-U-	
31837.01_0a_16			
08/12/01 12:26p	406,573	reference.311987.710-0004-55300-US-U-	
31837.01_0a_17			
08/12/01 12:26p	390,856	reference.311987.710-0004-55300-US-U-	
31837.01_0a_18			
08/12/01 12:25p	389,559	reference.311987.710-0004-55300-US-U-	
31837.01_0a_19			
08/12/01 12:25p	386,358	reference.311987.710-0004-55300-US-U-	
31837.01_0a_20			
08/12/01 12:25p	233,121	reference.311987.710-0004-55300-US-U-	
31837.01_0a_21			
08/12/01 12:25p	257,016	reference.311987.710-0004-55300-US-U-	
31837.01_0a_22			
08/12/01 12:27p	1,214,164	reference.311987.710-0004-55300-US-U-31837.01_10	
08/12/01 12:26p	880,728	reference.311987.710-0004-55300-US-U-31837.01_11	
08/12/01 12:26p	1,243,734	reference.311987.710-0004-55300-US-U-31837.01_12	
08/12/01 12:26p	1,172,494	reference.311987.710-0004-55300-US-U-31837.01_13	
08/12/01 12:26p	1,410,540	reference.311987.710-0004-55300-US-U-31837.01_14	
08/12/01 12:26p	1,284,893	reference.311987.710-0004-55300-US-U-31837.01_15	
08/12/01 12:26p	1,238,139	reference.311987.710-0004-55300-US-U-31837.01_16	
08/12/01 12:26p	1,123,370	reference.311987.710-0004-55300-US-U-31837.01_17	
08/12/01 12:26p	1,383,948	reference.311987.710-0004-55300-US-U-31837.01_18	
08/12/01 12:26p	1,334,757	reference.311987.710-0004-55300-US-U-31837.01_19	
08/12/01 12:25p	1,262,149	reference.311987.710-0004-55300-US-U-31837.01_20	
08/12/01 12:25p	3,141,453	reference.311987.710-0004-55300-US-U-31837.01_21	
08/12/01 12:25p	2,268,453	reference.311987.710-0004-55300-US-U-31837.01_22	
08/12/01 12:25p	1,311,040	reference.311988.710-0004-55300-US-U-31837.01_01	
08/12/01 12:25p	1,315,168	reference.311988.710-0004-55300-US-U-31837.01_02	
08/12/01 12:25p	1,422,465	reference.311988.710-0004-55300-US-U-31837.01_03	
08/12/01 12:25p	1,362,078	reference.311988.710-0004-55300-US-U-31837.01_04	
08/12/01 12:24p	1,796,701	reference.311988.710-0004-55300-US-U-31837.01_05	
08/12/01 12:59p	443,305	reference.311988.710-0004-55300-US-U-31837.01_06	
08/12/01 12:25p	454,861	reference.311988.710-0004-55300-US-U-	
31837.01_0a_01			
08/12/01 12:25p	498,999	reference.311988.710-0004-55300-US-U-	
31837.01_0a_02			
08/12/01 12:25p	462,050	reference.311988.710-0004-55300-US-U-	

File Create Date	File Size	File Name	CD#16
31837.01_0a_03			
08/12/01 12:25p	481,049	reference.311988.710-0004-55300-US-U-	
31837.01_0a_04			
08/12/01 12:24p	442,638	reference.311988.710-0004-55300-US-U-	
31837.01_0a_05			
08/12/01 12:59p	108,273	reference.311988.710-0004-55300-US-U-	
31837.01_0a_06			
08/12/01 12:40p	1,162,616	reference.3708.710-0004-55300-US-U-31837.01_01	
08/12/01 12:40p	1,265,127	reference.3708.710-0004-55300-US-U-31837.01_02	
08/12/01 12:40p	1,064,503	reference.3708.710-0004-55300-US-U-31837.01_03	
08/12/01 12:39p	1,107,300	reference.3708.710-0004-55300-US-U-31837.01_04	
08/12/01 12:39p	1,033,733	reference.3708.710-0004-55300-US-U-31837.01_05	
08/12/01 12:39p	1,062,213	reference.3708.710-0004-55300-US-U-31837.01_06	
08/12/01 12:39p	1,051,659	reference.3708.710-0004-55300-US-U-31837.01_07	
08/12/01 12:39p	333,169	reference.3708.710-0004-55300-US-U-31837.01_08	
08/12/01 12:40p	354,429	reference.3708.710-0004-55300-US-U-31837.01_0a_01	
08/12/01 12:40p	343,086	reference.3708.710-0004-55300-US-U-31837.01_0a_02	
08/12/01 12:39p	306,206	reference.3708.710-0004-55300-US-U-31837.01_0a_03	
08/12/01 12:39p	303,772	reference.3708.710-0004-55300-US-U-31837.01_0a_04	
08/12/01 12:39p	349,121	reference.3708.710-0004-55300-US-U-31837.01_0a_05	
08/12/01 12:39p	378,008	reference.3708.710-0004-55300-US-U-31837.01_0a_06	
08/12/01 12:39p	319,039	reference.3708.710-0004-55300-US-U-31837.01_0a_07	
08/12/01 12:39p	13,652	reference.3708.710-0004-55300-US-U-31837.01_0a_08	
08/12/01 12:39p	2,960,662	reference.3769.710-0004-55300-US-U-31837.01_01	
08/12/01 12:39p	3,928,944	reference.3769.710-0004-55300-US-U-31837.01_02	
08/12/01 12:39p	1,143,746	reference.3769.710-0004-55300-US-U-31837.01_03	
08/12/01 12:38p	1,850,674	reference.3769.710-0004-55300-US-U-31837.01_04	
08/12/01 12:38p	1,491,681	reference.3769.710-0004-55300-US-U-31837.01_05	
08/12/01 12:38p	2,151,104	reference.3769.710-0004-55300-US-U-31837.01_06	
08/12/01 12:38p	3,456,519	reference.3769.710-0004-55300-US-U-31837.01_07	
08/12/01 12:38p	2,605,573	reference.3769.710-0004-55300-US-U-31837.01_08	
08/12/01 12:38p	2,031,088	reference.3769.710-0004-55300-US-U-31837.01_09	
08/12/01 12:39p	204,712	reference.3769.710-0004-55300-US-U-31837.01_0a_01	
08/12/01 12:39p	259,843	reference.3769.710-0004-55300-US-U-31837.01_0a_02	
08/12/01 12:39p	481,705	reference.3769.710-0004-55300-US-U-31837.01_0a_03	
08/12/01 12:38p	431,423	reference.3769.710-0004-55300-US-U-31837.01_0a_04	
08/12/01 12:38p	447,907	reference.3769.710-0004-55300-US-U-31837.01_0a_05	
08/12/01 12:38p	397,490	reference.3769.710-0004-55300-US-U-31837.01_0a_06	
08/12/01 12:38p	307,188	reference.3769.710-0004-55300-US-U-31837.01_0a_07	
08/12/01 12:38p	242,156	reference.3769.710-0004-55300-US-U-31837.01_0a_08	
08/12/01 12:38p	239,017	reference.3769.710-0004-55300-US-U-31837.01_0a_09	
08/12/01 12:37p	329,822	reference.3769.710-0004-55300-US-U-31837.01_0a_10	
08/12/01 12:37p	315,287	reference.3769.710-0004-55300-US-U-31837.01_0a_11	
08/12/01 12:37p	321,237	reference.3769.710-0004-55300-US-U-31837.01_0a_12	
08/12/01 12:37p	231,415	reference.3769.710-0004-55300-US-U-31837.01_0a_13	
08/12/01 12:37p	207,085	reference.3769.710-0004-55300-US-U-31837.01_0a_14	
08/12/01 12:37p	373,324	reference.3769.710-0004-55300-US-U-31837.01_0a_15	
08/12/01 12:37p	404,723	reference.3769.710-0004-55300-US-U-31837.01_0a_16	
08/12/01 12:37p	353,390	reference.3769.710-0004-55300-US-U-31837.01_0a_17	
08/12/01 12:36p	297,987	reference.3769.710-0004-55300-US-U-31837.01_0a_18	
08/12/01 12:36p	288,433	reference.3769.710-0004-55300-US-U-31837.01_0a_19	
08/12/01 12:36p	278,112	reference.3769.710-0004-55300-US-U-31837.01_0a_20	
08/12/01 12:36p	315,185	reference.3769.710-0004-55300-US-U-31837.01_0a_21	
08/12/01 12:36p	313,774	reference.3769.710-0004-55300-US-U-31837.01_0a_22	
08/12/01 12:36p	241,504	reference.3769.710-0004-55300-US-U-31837.01_0a_23	
08/12/01 12:35p	209,582	reference.3769.710-0004-55300-US-U-31837.01_0a_24	
08/12/01 12:35p	234,527	reference.3769.710-0004-55300-US-U-31837.01_0a_25	
08/12/01 12:35p	253,047	reference.3769.710-0004-55300-US-U-31837.01_0a_26	
08/12/01 12:35p	251,628	reference.3769.710-0004-55300-US-U-31837.01_0a_27	
08/12/01 12:34p	237,104	reference.3769.710-0004-55300-US-U-31837.01_0a_28	
08/12/01 12:34p	218,825	reference.3769.710-0004-55300-US-U-31837.01_0a_29	
08/12/01 12:34p	191,898	reference.3769.710-0004-55300-US-U-31837.01_0a_30	
08/12/01 12:37p	2,745,034	reference.3769.710-0004-55300-US-U-31837.01_10	
08/12/01 12:37p	3,086,810	reference.3769.710-0004-55300-US-U-31837.01_11	
08/12/01 12:37p	2,483,988	reference.3769.710-0004-55300-US-U-31837.01_12	
08/12/01 12:37p	1,180,798	reference.3769.710-0004-55300-US-U-31837.01_13	
08/12/01 12:37p	784,550	reference.3769.710-0004-55300-US-U-31837.01_14	

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08/12/01 12:37p	2,952,817	reference.3769.710-0004-55300-US-U-31837.01_17	
08/12/01 12:36p	3,144,171	reference.3769.710-0004-55300-US-U-31837.01_18	
08/12/01 12:36p	3,532,194	reference.3769.710-0004-55300-US-U-31837.01_19	
08/12/01 12:36p	3,273,553	reference.3769.710-0004-55300-US-U-31837.01_20	
08/12/01 12:36p	3,198,889	reference.3769.710-0004-55300-US-U-31837.01_21	
08/12/01 12:36p	1,817,401	reference.3769.710-0004-55300-US-U-31837.01_22	
08/12/01 12:36p	4,090,789	reference.3769.710-0004-55300-US-U-31837.01_23	
08/12/01 12:35p	4,384,924	reference.3769.710-0004-55300-US-U-31837.01_24	
08/12/01 12:35p	4,165,383	reference.3769.710-0004-55300-US-U-31837.01_25	
08/12/01 12:35p	3,649,910	reference.3769.710-0004-55300-US-U-31837.01_26	
08/12/01 12:35p	3,850,452	reference.3769.710-0004-55300-US-U-31837.01_27	
08/12/01 12:34p	4,244,058	reference.3769.710-0004-55300-US-U-31837.01_28	
08/12/01 12:34p	4,465,585	reference.3769.710-0004-55300-US-U-31837.01_29	
08/12/01 12:34p	3,700,210	reference.3769.710-0004-55300-US-U-31837.01_30	
08/12/01 12:34p	1,827,982	reference.3847.710-0004-55300-US-U-31837.01_01	
08/12/01 12:34p	1,457,336	reference.3847.710-0004-55300-US-U-31837.01_02	
08/12/01 12:34p	1,346,895	reference.3847.710-0004-55300-US-U-31837.01_03	
08/12/01 12:33p	1,215,086	reference.3847.710-0004-55300-US-U-31837.01_04	
08/12/01 12:33p	1,543,146	reference.3847.710-0004-55300-US-U-31837.01_05	
08/12/01 12:33p	1,446,159	reference.3847.710-0004-55300-US-U-31837.01_06	
08/12/01 12:33p	1,455,614	reference.3847.710-0004-55300-US-U-31837.01_07	
08/12/01 12:33p	1,478,382	reference.3847.710-0004-55300-US-U-31837.01_08	
08/12/01 12:33p	1,325,423	reference.3847.710-0004-55300-US-U-31837.01_09	
08/12/01 12:34p	294,242	reference.3847.710-0004-55300-US-U-31837.01_0a_01	
08/12/01 12:34p	296,876	reference.3847.710-0004-55300-US-U-31837.01_0a_02	
08/12/01 12:34p	330,461	reference.3847.710-0004-55300-US-U-31837.01_0a_03	
08/12/01 12:33p	308,192	reference.3847.710-0004-55300-US-U-31837.01_0a_04	
08/12/01 12:33p	325,967	reference.3847.710-0004-55300-US-U-31837.01_0a_05	
08/12/01 12:33p	345,975	reference.3847.710-0004-55300-US-U-31837.01_0a_06	
08/12/01 12:33p	336,577	reference.3847.710-0004-55300-US-U-31837.01_0a_07	
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08/12/01 12:33p	347,209	reference.3847.710-0004-55300-US-U-31837.01_0a_09	
08/12/01 12:33p	374,396	reference.3847.710-0004-55300-US-U-31837.01_0a_10	
08/12/01 12:33p	334,996	reference.3847.710-0004-55300-US-U-31837.01_0a_11	
08/12/01 12:33p	387,158	reference.3847.710-0004-55300-US-U-31837.01_0a_12	
08/12/01 12:32p	320,680	reference.3847.710-0004-55300-US-U-31837.01_0a_13	
08/12/01 12:32p	324,002	reference.3847.710-0004-55300-US-U-31837.01_0a_14	
08/12/01 12:32p	297,822	reference.3847.710-0004-55300-US-U-31837.01_0a_15	
08/12/01 12:32p	322,104	reference.3847.710-0004-55300-US-U-31837.01_0a_16	
08/12/01 12:32p	405,974	reference.3847.710-0004-55300-US-U-31837.01_0a_17	
08/12/01 12:32p	373,820	reference.3847.710-0004-55300-US-U-31837.01_0a_18	
08/12/01 12:32p	357,846	reference.3847.710-0004-55300-US-U-31837.01_0a_19	
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08/12/01 12:34p	1,453,337	sequences.3769.710-0004-55300-US-U-31837.01_0a_29	
08/12/01 12:34p	1,040,431	sequences.3769.710-0004-55300-US-U-31837.01_0a_30	
08/12/01 12:38p	6,322,437	sequences.3769.710-0004-55300-US-U-31837.01_10	
08/12/01 12:37p	7,229,469	sequences.3769.710-0004-55300-US-U-31837.01_11	
08/12/01 12:37p	5,856,227	sequences.3769.710-0004-55300-US-U-31837.01_12	

File Create Date	File Size	File Name	CD#16
08/12/01 12:37p	1,871,619	sequences.3769.710-0004-55300-US-U-31837.01_13	
08/12/01 12:37p	1,068,100	sequences.3769.710-0004-55300-US-U-31837.01_14	
08/12/01 12:37p	4,230,930	sequences.3769.710-0004-55300-US-U-31837.01_15	
08/12/01 12:37p	5,038,862	sequences.3769.710-0004-55300-US-U-31837.01_16	
08/12/01 12:37p	7,361,421	sequences.3769.710-0004-55300-US-U-31837.01_17	
08/12/01 12:37p	6,746,843	sequences.3769.710-0004-55300-US-U-31837.01_18	
08/12/01 12:36p	8,093,383	sequences.3769.710-0004-55300-US-U-31837.01_19	
08/12/01 12:36p	7,542,448	sequences.3769.710-0004-55300-US-U-31837.01_20	
08/12/01 12:36p	7,203,991	sequences.3769.710-0004-55300-US-U-31837.01_21	
08/12/01 12:36p	3,418,395	sequences.3769.710-0004-55300-US-U-31837.01_22	
08/12/01 12:36p	9,731,566	sequences.3769.710-0004-55300-US-U-31837.01_23	
08/12/01 12:35p	10,233,786	sequences.3769.710-0004-55300-US-U-31837.01_24	
08/12/01 12:35p	9,444,719	sequences.3769.710-0004-55300-US-U-31837.01_25	
08/12/01 12:35p	9,697,820	sequences.3769.710-0004-55300-US-U-31837.01_26	
08/12/01 12:35p	9,008,720	sequences.3769.710-0004-55300-US-U-31837.01_27	
08/12/01 12:35p	10,480,641	sequences.3769.710-0004-55300-US-U-31837.01_28	
08/12/01 12:34p	7,417,362	sequences.3769.710-0004-55300-US-U-31837.01_29	
08/12/01 12:34p	4,676,436	sequences.3769.710-0004-55300-US-U-31837.01_30	
08/12/01 12:34p	1,708,595	sequences.3847.710-0004-55300-US-U-31837.01_01	
08/12/01 12:34p	1,273,283	sequences.3847.710-0004-55300-US-U-31837.01_02	
08/12/01 12:34p	1,325,142	sequences.3847.710-0004-55300-US-U-31837.01_03	
08/12/01 12:34p	1,000,132	sequences.3847.710-0004-55300-US-U-31837.01_04	
08/12/01 12:33p	1,350,824	sequences.3847.710-0004-55300-US-U-31837.01_05	
08/12/01 12:33p	1,391,293	sequences.3847.710-0004-55300-US-U-31837.01_06	
08/12/01 12:33p	1,565,355	sequences.3847.710-0004-55300-US-U-31837.01_07	
08/12/01 12:33p	1,335,459	sequences.3847.710-0004-55300-US-U-31837.01_08	
08/12/01 12:33p	1,217,484	sequences.3847.710-0004-55300-US-U-31837.01_09	
08/12/01 12:34p	1,602,384	sequences.3847.710-0004-55300-US-U-31837.01_0a_01	
08/12/01 12:34p	1,397,192	sequences.3847.710-0004-55300-US-U-31837.01_0a_02	
08/12/01 12:34p	1,790,919	sequences.3847.710-0004-55300-US-U-31837.01_0a_03	
08/12/01 12:33p	1,375,977	sequences.3847.710-0004-55300-US-U-31837.01_0a_04	
08/12/01 12:33p	1,625,752	sequences.3847.710-0004-55300-US-U-31837.01_0a_05	
08/12/01 12:33p	1,826,869	sequences.3847.710-0004-55300-US-U-31837.01_0a_06	
08/12/01 12:33p	1,760,973	sequences.3847.710-0004-55300-US-U-31837.01_0a_07	
08/12/01 12:33p	1,673,425	sequences.3847.710-0004-55300-US-U-31837.01_0a_08	
08/12/01 12:33p	1,641,398	sequences.3847.710-0004-55300-US-U-31837.01_0a_09	
08/12/01 12:33p	2,207,438	sequences.3847.710-0004-55300-US-U-31837.01_0a_10	
08/12/01 12:33p	1,557,981	sequences.3847.710-0004-55300-US-U-31837.01_0a_11	
08/12/01 12:33p	2,377,538	sequences.3847.710-0004-55300-US-U-31837.01_0a_12	
08/12/01 12:32p	1,448,464	sequences.3847.710-0004-55300-US-U-31837.01_0a_13	
08/12/01 12:32p	1,463,852	sequences.3847.710-0004-55300-US-U-31837.01_0a_14	
08/12/01 12:32p	1,598,669	sequences.3847.710-0004-55300-US-U-31837.01_0a_15	
08/12/01 12:32p	1,469,314	sequences.3847.710-0004-55300-US-U-31837.01_0a_16	
08/12/01 12:32p	2,123,438	sequences.3847.710-0004-55300-US-U-31837.01_0a_17	
08/12/01 12:32p	1,713,220	sequences.3847.710-0004-55300-US-U-31837.01_0a_18	
08/12/01 12:32p	1,548,961	sequences.3847.710-0004-55300-US-U-31837.01_0a_19	
08/12/01 12:32p	1,548,185	sequences.3847.710-0004-55300-US-U-31837.01_0a_20	
08/12/01 12:32p	1,039,094	sequences.3847.710-0004-55300-US-U-31837.01_0a_21	
08/12/01 12:31p	839,677	sequences.3847.710-0004-55300-US-U-31837.01_0a_22	
08/12/01 12:31p	715,715	sequences.3847.710-0004-55300-US-U-31837.01_0a_23	
08/12/01 12:31p	610,467	sequences.3847.710-0004-55300-US-U-31837.01_0a_24	
08/12/01 12:31p	1,075,842	sequences.3847.710-0004-55300-US-U-31837.01_0a_25	
08/12/01 12:31p	298,443	sequences.3847.710-0004-55300-US-U-31837.01_0a_26	
08/12/01 12:33p	2,114,850	sequences.3847.710-0004-55300-US-U-31837.01_10	
08/12/01 12:33p	1,392,995	sequences.3847.710-0004-55300-US-U-31837.01_11	
08/12/01 12:33p	2,104,593	sequences.3847.710-0004-55300-US-U-31837.01_12	
08/12/01 12:32p	1,119,835	sequences.3847.710-0004-55300-US-U-31837.01_13	
08/12/01 12:32p	1,150,254	sequences.3847.710-0004-55300-US-U-31837.01_14	
08/12/01 12:32p	1,718,830	sequences.3847.710-0004-55300-US-U-31837.01_15	
08/12/01 12:32p	1,059,550	sequences.3847.710-0004-55300-US-U-31837.01_16	
08/12/01 12:32p	1,289,986	sequences.3847.710-0004-55300-US-U-31837.01_17	
08/12/01 12:32p	894,435	sequences.3847.710-0004-55300-US-U-31837.01_18	
08/12/01 12:32p	893,536	sequences.3847.710-0004-55300-US-U-31837.01_19	
08/12/01 12:32p	906,412	sequences.3847.710-0004-55300-US-U-31837.01_20	
08/12/01 12:32p	3,250,669	sequences.3847.710-0004-55300-US-U-31837.01_21	
08/12/01 12:31p	2,308,413	sequences.3847.710-0004-55300-US-U-31837.01_22	
08/12/01 12:31p	2,341,847	sequences.3847.710-0004-55300-US-U-31837.01_23	

File Create Date	File Size	File Name	CD#16
08/12/01 12:31p	2,730,277	sequences.3847.710-0004-55300-US-U-31837.01_24	
08/12/01 12:31p	4,276,026	sequences.3847.710-0004-55300-US-U-31837.01_25	
08/12/01 12:31p	906,646	sequences.3847.710-0004-55300-US-U-31837.01_26	

File Create Date	File Size	File Name	CD#17
08/17/01 04:48p	4,052,876	cdna_clusters.txt	
08/22/01 05:03p	35,153	Cluster Functions and Utilities (01).txt	
08/22/01 05:04p	40,447	Cluster Functions and Utilities (02).txt	
08/22/01 05:04p	4,473	Cluster Functions and Utilities (03).txt	
08/22/01 05:05p	7,820	Cluster Functions and Utilities (04).txt	
08/22/01 05:05p	24,047	Cluster Functions and Utilities (05).txt	
08/22/01 05:06p	18,490	Cluster Functions and Utilities (06).txt	
08/22/01 05:11p	36,273	Cluster functions and utilities (07).txt	
08/22/01 04:17p	33,962	Cluster Functions and Utilities (08).txt	
08/22/01 04:16p	23,000	Cluster functions and utilities (09).txt	
08/21/01 09:47p	2,691	Cluster functions and utilities (10).txt	
08/21/01 09:47p	2,290	Cluster functions and utilities (11).txt	
08/22/01 05:25p	23,740	Cluster Funtions and Utilities (12).txt	
08/22/01 03:14p	331,616	enhanced_amino.txt	
08/20/01 01:44p	13,132,268	gb_only_peptides.fasta	
08/21/01 03:28p	392,675	knock_in.710-0004-55300-US-U-31837.01.txt	
08/14/01 07:12p	831,736	knock_out.710-0004-55300-US-U-31837.01	
08/20/01 11:56a	16,635,460	ma_clusters.710-0004-55300-US-U-31837.01	
08/21/01 02:09p	55,307	ma_diff Aluminum.txt	
08/21/01 02:10p	27,557	ma_diff Axel.txt	
08/21/01 02:13p	41,505	ma_diff Cadium .txt	
08/21/01 02:51p	53,938	ma_diff Cauliflower .txt	
08/21/01 02:50p	98,775	ma_diff Chloroplast.txt	
08/21/01 02:50p	160,542	ma_diff Circadian 1-02.txt	
08/21/01 02:50p	127,498	ma_diff Circadian 1-03.txt	
08/21/01 02:51p	166,158	ma_diff Circadian 1-04.txt	
08/21/01 02:50p	141,971	ma_diff Circadian 1-01.txt	
08/21/01 02:52p	56,536	ma_diff Circadian 1-05.txt	
08/21/01 02:52p	121,178	ma_diff Circadian 1-06.txt	
08/21/01 02:52p	133,389	ma_diff Circadian 1-07.txt	
08/21/01 02:52p	259,096	ma_diff Circadian 1-08.txt	
08/21/01 02:52p	228,222	ma_diff Circadian 1-09.txt	
08/21/01 02:53p	54,526	ma_diff Circadian 1-10.txt	
08/21/01 02:53p	134,759	ma_diff CO2 1-1.txt	
08/21/01 02:53p	241,865	ma_diff CO2 1-2.txt	
08/21/01 02:54p	63,264	ma_diff CO2 1-3.txt	
08/21/01 02:54p	59,530	ma_diff CO2 1-4.txt	
08/21/01 02:54p	372,633	ma_diff CO2 1-5.txt	
08/21/01 02:54p	9,220	ma_diff Disease .txt	
08/21/01 02:54p	25,114	ma_diff H2O2 .txt	
08/21/01 02:55p	4,073	ma_diff Iol .txt	
08/21/01 02:55p	283,026	ma_diff Iron 1-1.txt	
08/21/01 02:55p	90,890	ma_diff Iron 1-2.txt	
08/21/01 02:55p	51,342	ma_diff Mitochondria-Electron Transp.txt	
08/21/01 02:55p	107,920	ma_diff NAA (Auxin) 1-1.txt	
08/21/01 02:55p	50,267	ma_diff NAA (Auxin) 1-2.txt	
08/21/01 02:55p	67,291	ma_diff Nitrogen.txt	
08/21/01 02:56p	6,441	ma_diff Phototropism 1-1.txt	
08/21/01 02:56p	22,229	ma_diff Phototropism 1-2.txt	
08/21/01 02:56p	28,270	ma_diff Phototropism 1-3.txt	
08/21/01 02:56p	45,620	ma_diff Shade.txt	
08/21/01 02:56p	73,438	ma_diff Sqn.txt	
08/21/01 02:56p	3,828	ma_diff Sulfur.txt	
08/21/01 02:56p	67,949	ma_diff Wounding.txt	
08/21/01 02:57p	30,836	ma_diff Zinc.txt	
08/21/01 03:54p	4,318,956	ma_diff.710-0004-55300-US-U-31837.01	
08/10/01 03:06p	2,752,459	Protein Domain Table.txt	
08/22/01 11:21a	2,310,061	protein group 710-0004-55300-US-U-31837.01 1	

File Create Date	File Size	File Name	CD#17
08/21/01 08:27p	20,964,975	protein_group_matrix.001	
08/21/01 08:31p	17,961,050	protein_group_matrix.002	
08/12/01 12:31p	1,455,871	sequences.4565.710-0004-55300-US-U-31837.01_01	
08/12/01 12:31p	1,390,325	sequences.4565.710-0004-55300-US-U-31837.01_02	
08/12/01 12:31p	1,469,239	sequences.4565.710-0004-55300-US-U-31837.01_03	
08/12/01 12:30p	1,510,762	sequences.4565.710-0004-55300-US-U-31837.01_04	
08/12/01 12:30p	1,767,251	sequences.4565.710-0004-55300-US-U-31837.01_05	
08/12/01 12:30p	1,556,895	sequences.4565.710-0004-55300-US-U-31837.01_06	
08/12/01 12:30p	1,604,610	sequences.4565.710-0004-55300-US-U-31837.01_07	
08/12/01 12:30p	1,668,865	sequences.4565.710-0004-55300-US-U-31837.01_08	
08/12/01 12:30p	1,388,145	sequences.4565.710-0004-55300-US-U-31837.01_09	
08/12/01 12:31p	1,759,069	sequences.4565.710-0004-55300-US-U-31837.01_0a_01	
08/12/01 12:31p	1,777,239	sequences.4565.710-0004-55300-US-U-31837.01_0a_02	
08/12/01 12:31p	1,791,311	sequences.4565.710-0004-55300-US-U-31837.01_0a_03	
08/12/01 12:30p	1,670,399	sequences.4565.710-0004-55300-US-U-31837.01_0a_04	
08/12/01 12:30p	1,861,173	sequences.4565.710-0004-55300-US-U-31837.01_0a_05	
08/12/01 12:30p	2,348,979	sequences.4565.710-0004-55300-US-U-31837.01_0a_06	
08/20/01 03:33p	228,792	stanford_old_new_cdna_map.txt	
08/12/01 12:30p	1,728,037	sequences.4565.710-0004-55300-US-U-31837.01_0a_07	
08/12/01 12:30p	1,907,270	sequences.4565.710-0004-55300-US-U-31837.01_0a_08	
08/12/01 12:30p	1,839,684	sequences.4565.710-0004-55300-US-U-31837.01_0a_09	
08/12/01 12:30p	2,066,667	sequences.4565.710-0004-55300-US-U-31837.01_0a_10	
08/12/01 12:30p	1,843,540	sequences.4565.710-0004-55300-US-U-31837.01_0a_11	
08/12/01 12:29p	1,760,968	sequences.4565.710-0004-55300-US-U-31837.01_0a_12	
08/12/01 12:29p	1,581,505	sequences.4565.710-0004-55300-US-U-31837.01_0a_13	
08/12/01 12:29p	1,833,741	sequences.4565.710-0004-55300-US-U-31837.01_0a_14	
08/12/01 12:29p	1,877,368	sequences.4565.710-0004-55300-US-U-31837.01_0a_15	
08/12/01 12:29p	2,304,478	sequences.4565.710-0004-55300-US-U-31837.01_0a_16	
08/12/01 12:29p	2,538,522	sequences.4565.710-0004-55300-US-U-31837.01_0a_17	
08/12/01 12:29p	2,463,631	sequences.4565.710-0004-55300-US-U-31837.01_0a_18	
08/12/01 12:29p	2,343,047	sequences.4565.710-0004-55300-US-U-31837.01_0a_19	
08/12/01 12:29p	2,356,395	sequences.4565.710-0004-55300-US-U-31837.01_0a_20	
08/12/01 12:28p	2,193,667	sequences.4565.710-0004-55300-US-U-31837.01_0a_21	
08/12/01 12:28p	1,931,561	sequences.4565.710-0004-55300-US-U-31837.01_0a_22	
08/12/01 12:28p	2,057,772	sequences.4565.710-0004-55300-US-U-31837.01_0a_23	
08/12/01 12:28p	2,023,186	sequences.4565.710-0004-55300-US-U-31837.01_0a_24	
08/12/01 12:28p	2,229,571	sequences.4565.710-0004-55300-US-U-31837.01_0a_25	
08/12/01 12:28p	2,313,213	sequences.4565.710-0004-55300-US-U-31837.01_0a_26	
08/12/01 12:28p	2,260,010	sequences.4565.710-0004-55300-US-U-31837.01_0a_27	
08/12/01 12:28p	1,767,404	sequences.4565.710-0004-55300-US-U-31837.01_0a_28	
08/12/01 12:28p	842,095	sequences.4565.710-0004-55300-US-U-31837.01_0a_29	
08/12/01 12:30p	1,612,982	sequences.4565.710-0004-55300-US-U-31837.01_10	
08/12/01 12:30p	1,484,547	sequences.4565.710-0004-55300-US-U-31837.01_11	
08/12/01 12:30p	1,609,501	sequences.4565.710-0004-55300-US-U-31837.01_12	
08/12/01 12:29p	1,787,625	sequences.4565.710-0004-55300-US-U-31837.01_13	
08/12/01 12:29p	1,516,984	sequences.4565.710-0004-55300-US-U-31837.01_14	
08/12/01 12:29p	1,772,733	sequences.4565.710-0004-55300-US-U-31837.01_15	
08/12/01 12:29p	1,407,918	sequences.4565.710-0004-55300-US-U-31837.01_16	
08/12/01 12:29p	1,115,351	sequences.4565.710-0004-55300-US-U-31837.01_17	
08/12/01 12:29p	1,139,747	sequences.4565.710-0004-55300-US-U-31837.01_18	
08/12/01 12:29p	1,295,834	sequences.4565.710-0004-55300-US-U-31837.01_19	
08/12/01 12:29p	1,225,893	sequences.4565.710-0004-55300-US-U-31837.01_20	
08/12/01 12:29p	967,637	sequences.4565.710-0004-55300-US-U-31837.01_21	
08/12/01 12:28p	1,093,025	sequences.4565.710-0004-55300-US-U-31837.01_22	
08/12/01 12:28p	891,289	sequences.4565.710-0004-55300-US-U-31837.01_23	
08/12/01 12:28p	963,017	sequences.4565.710-0004-55300-US-U-31837.01_24	
08/12/01 12:28p	574,648	sequences.4565.710-0004-55300-US-U-31837.01_25	
08/12/01 12:28p	609,860	sequences.4565.710-0004-55300-US-U-31837.01_26	
08/12/01 12:28p	640,421	sequences.4565.710-0004-55300-US-U-31837.01_27	
08/12/01 12:28p	1,321,767	sequences.4565.710-0004-55300-US-U-31837.01_28	
08/12/01 12:28p	1,301,973	sequences.4565.710-0004-55300-US-U-31837.01_29	
08/22/01 05:01p	1,476	Single gene functions and utilities (1).txt	
08/22/01 05:01p	2,223	Single gene functions and utilities (2).txt	
08/22/01 05:02p	905	Single gene functions and utilities (3).txt	
08/22/01 05:03p	1,517	Single gene functions and utilities (4).txt	
08/22/01 05:07p	4,626	Single gene functions and utilities (5).txt	
08/22/01 04:57p	4,887	Single gene functions and utilities (6).txt	

File Create Date	File Size	File Name	CD#17
08/22/01 04:57p	7,456	Single gene functions and utilities (7).txt	
08/22/01 05:06p	9,339	Single gene functions and utilities (8).txt	
08/24/01 02:54p	12,684	Cluster Functions and Utilities 01.txt	
08/24/01 02:56p	91,002	Cluster Functions and Utilities 02.txt	
08/24/01 02:57p	6,256	Cluster Functions and Utilities 03.txt	
08/24/01 02:58p	6,292	Cluster Functions and Utilities 04.txt	
08/24/01 02:58p	37,345	Cluster Functions and Utilities 05.txt	
08/24/01 03:02p	96,535	Cluster Functions and Utilities 06.txt	
08/24/01 03:44p	8,447	Cluster Functions and Utilities 07.txt	
08/24/01 04:04p	17,087	Cluster Functions and Utilities 08.txt	
08/24/01 12:59p	1,090,292	gb_only_peptides_II.fasta	
08/24/01 03:12p	1,645,031	knock_out._01	
08/24/01 05:21p	6,947	KNOCK-IN_01.txt	
08/24/01 05:22p	11,374	KNOCK-IN_02.txt	
08/10/01 03:06p	2,752,459	Protein Domain Table.txt	
08/24/01 12:46p	1,642,574	protein_group	
08/23/01 05:16p	20,971,520	protein_group_matrix.001	
08/23/01 05:16p	14,734,163	protein_group_matrix.002	
08/23/01 09:32p	307,501	reference.311987.710-0004-55300-US-U-31950.01_0a_1	
08/23/01 09:32p	701,425	reference.311987.710-0004-55300-US-U-31950.01_1	
08/23/01 09:23p	137,011	reference.3769.710-0004-55300-US-U-31950.01_0a_1	
08/23/01 09:23p	809,915	reference.3769.710-0004-55300-US-U-31950.01_1	
08/23/01 09:25p	69,159	reference.3847.710-0004-55300-US-U-31950.01_0a_1	
08/23/01 09:25p	105,695	reference.3847.710-0004-55300-US-U-31950.01_1	
08/23/01 09:32p	1,387,172	sequences.311987.710-0004-55300-US-U-31950.01_0a_1	
08/23/01 09:32p	635,667	sequences.311987.710-0004-55300-US-U-31950.01_1	
08/23/01 09:23p	762,492	sequences.3769.710-0004-55300-US-U-31950.01_0a_1	
08/23/01 09:23p	1,721,941	sequences.3769.710-0004-55300-US-U-31950.01_1	
08/23/01 09:25p	311,205	sequences.3847.710-0004-55300-US-U-31950.01_0a_1	
08/23/01 09:25p	111,913	sequences.3847.710-0004-55300-US-U-31950.01_1	
02/25/02 02:36p	10,512,576	group0.txt	
02/25/02 02:38p	10,493,605	group1.txt	
02/25/02 02:41p	10,489,244	group2.txt	
02/25/02 02:44p	10,687,170	group3.txt	
02/25/02 02:47p	10,732,414	group4.txt	
02/25/02 02:49p	10,727,807	group5.txt	
02/25/02 02:52p	10,616,591	group6.txt	
02/25/02 02:53p	6,065,227	group7.txt	
02/21/02 05:54p	10,401,255	seqs.fasta.1	
02/21/02 05:54p	3,149,009	seqs.fasta.2	
02/28/02 04:04p	3,733,718	titles	

File Create Date	File Size	File Name	CD#18
02/27/02 04:22p	290,311,988	flib2	
02/27/02 04:27p	279,711,648	flib1	

File Create Date	File Size	File Name	CD#19
02/27/02 04:17p	209,849,751	flib3	
02/27/02 04:14p	226,030,922	flib4	
02/27/02 04:40p	174,831,246	flib5	

File Create Date	File Size	File Name	CD#20
09/26/02 04:47p	4,052,876	cdna_clusters.txt	
09/26/02 04:47p	35,153	Cluster Functions and Utilities (01).txt	
09/26/02 04:47p	40,447	Cluster Functions and Utilities (02).txt	
09/26/02 04:47p	4,473	Cluster Functions and Utilities (03).txt	

File Create Date	File Size	File Name	CD#20
09/26/02 04:47p	7,820	Cluster Functions and Utilities (04).txt	
09/26/02 04:47p	24,047	Cluster Functions and Utilities (05).txt	
09/26/02 04:47p	18,490	Cluster Functions and Utilities (06).txt	
09/26/02 04:47p	36,273	Cluster functions and utilities (07).txt	
09/26/02 04:47p	33,962	Cluster Functions and Utilities (08).txt	
09/26/02 04:47p	23,000	Cluster functions and utilities (09).txt	
09/26/02 04:47p	2,691	Cluster functions and utilities (10).txt	
09/26/02 04:47p	2,290	Cluster functions and utilities (11).txt	
09/26/02 04:47p	23,740	Cluster Funtions and Utilities (12).txt	
09/26/02 04:47p	331,616	enhanced_amino.txt	
09/26/02 04:47p	13,132,268	gb_only_peptides.fasta	
09/26/02 04:47p	392,675	knock_in.710-0004-55300-US-U-31835_01.txt	
09/26/02 04:47p	831,736	knock_out.710-0004-55300-US-U-31835.01	
09/26/02 04:47p	16,635,460	ma_clusters.710-0004-55300-US-U-31835.01	
09/26/02 04:47p	55,307	ma_diff Aluminum.txt	
09/26/02 04:47p	27,557	ma_diff Axel.txt	
09/26/02 04:47p	41,505	ma_diff Cadium .txt	
09/26/02 04:47p	53,938	ma_diff Cauliflower .txt	
09/26/02 04:47p	98,775	ma_diff Chloroplast.txt	
09/26/02 04:47p	141,971	ma_diff Circadian 1-01.txt	
09/26/02 04:47p	160,542	ma_diff Circadian 1-02.txt	
09/26/02 04:47p	127,498	ma_diff Circadian 1-03.txt	
09/26/02 04:47p	166,158	ma_diff Circadian 1-04.txt	
09/26/02 04:47p	56,536	ma_diff Circadian 1-05.txt	
09/26/02 04:47p	121,178	ma_diff Circadian 1-06.txt	
09/26/02 04:47p	133,389	ma_diff Circadian 1-07.txt	
09/26/02 04:47p	259,096	ma_diff Circadian 1-08.txt	
09/26/02 04:47p	228,222	ma_diff Circadian 1-09.txt	
09/26/02 04:47p	54,526	ma_diff Circadian 1-10.txt	
09/26/02 04:47p	134,759	ma_diff CO2 1-1.txt	
09/26/02 04:47p	241,865	ma_diff CO2 1-2.txt	
09/26/02 04:47p	63,264	ma_diff CO2 1-3.txt	
09/26/02 04:47p	59,530	ma_diff CO2 1-4.txt	
09/26/02 04:47p	372,633	ma_diff CO2 1-5.txt	
09/26/02 04:47p	9,220	ma_diff Disease .txt	
09/26/02 04:47p	25,114	ma_diff H2O2 .txt	
09/26/02 04:47p	4,073	ma_diff Iol .txt	
09/26/02 04:47p	283,026	ma_diff Iron 1-1.txt	
09/26/02 04:47p	90,890	ma_diff Iron 1-2.txt	
09/26/02 04:47p	51,342	ma_diff Mitochondria-Electron Transp.txt	
09/26/02 04:47p	107,920	ma_diff NAA (Auxin) 1-1.txt	
09/26/02 04:47p	50,267	ma_diff NAA (Auxin) 1-2.txt	
09/26/02 04:47p	67,291	ma_diff Nitrogen.txt	
09/26/02 04:47p	6,441	ma_diff Phototropism 1-1.txt	
09/26/02 04:47p	22,229	ma_diff Phototropism 1-2.txt	
09/26/02 04:47p	28,270	ma_diff Phototropism 1-3.txt	
09/26/02 04:47p	45,620	ma_diff Shade.txt	
09/26/02 04:47p	73,438	ma_diff Sqn.txt	
09/26/02 04:47p	3,828	ma_diff Sulfur.txt	
09/26/02 04:47p	67,949	ma_diff Wounding.txt	
09/26/02 04:47p	30,836	ma_diff Zinc.txt	
09/26/02 04:47p	4,318,956	ma_diff.710-0004-55300-US-U-31835.01	
09/26/02 04:47p	2,752,459	Protein Domain Table.txt	
09/26/02 04:47p	14,778,004	protein_group_710-0004-55300-US-U-31835.01_01	
09/26/02 04:47p	12,953,488	protein_group_710-0004-55300-US-U-31835.01_02	
09/26/02 04:47p	12,866,803	protein_group_710-0004-55300-US-U-31835.01_03	
09/26/02 04:47p	15,451,084	protein_group_710-0004-55300-US-U-31835.01_04	
09/26/02 04:48p	20,982,878	protein_group_matrix.001	
09/26/02 04:47p	13,753,735	protein_group_710-0004-55300-US-U-31835.01_05	
09/26/02 04:47p	17,503,319	protein_group_710-0004-55300-US-U-31835.01_06	
09/26/02 04:47p	16,376,099	protein_group_710-0004-55300-US-U-31835.01_07	
09/26/02 04:47p	13,390,661	protein_group_710-0004-55300-US-U-31835.01_08	
09/26/02 04:47p	14,328,338	protein_group_710-0004-55300-US-U-31835.01_09	
09/26/02 04:47p	12,595,465	protein_group_710-0004-55300-US-U-31835.01_10	
09/26/02 04:47p	14,577,180	protein_group_710-0004-55300-US-U-31835.01_11	
09/26/02 04:47p	15,580,727	protein_group_710-0004-55300-US-U-31835.01_12	
09/26/02 04:47p	13,881,717	protein_group_710-0004-55300-US-U-31835.01_13	

File Create Date	File Size	File Name	CD#20
09/26/02 04:47p	17,139,394	protein_group_710-0004-55300-US-U-31835.01_14	
09/26/02 04:47p	14,568,663	protein_group_710-0004-55300-US-U-31835.01_15	
09/26/02 04:47p	17,242,592	protein_group_710-0004-55300-US-U-31835.01_16	
09/26/02 04:47p	16,262,656	protein_group_710-0004-55300-US-U-31835.01_17	
09/26/02 04:47p	15,432,667	protein_group_710-0004-55300-US-U-31835.01_18	
09/26/02 04:48p	17,255,427	protein_group_710-0004-55300-US-U-31835.01_19	
09/26/02 04:48p	16,933,384	protein_group_710-0004-55300-US-U-31835.01_20	
09/26/02 04:48p	17,384,042	protein_group_710-0004-55300-US-U-31835.01_21	
09/26/02 04:48p	17,437,337	protein_group_710-0004-55300-US-U-31835.01_22	
09/26/02 04:48p	15,803,056	protein_group_710-0004-55300-US-U-31835.01_23	
09/26/02 04:48p	9,103,743	protein_group_710-0004-55300-US-U-31835.01_24	
09/26/02 04:48p	20,987,975	protein_group_matrix.002	
09/26/02 04:48p	20,996,062	protein_group_matrix.003	
09/26/02 04:48p	20,991,903	protein_group_matrix.004	
09/26/02 04:48p	21,008,452	protein_group_matrix.005	
09/26/02 04:48p	20,979,474	protein_group_matrix.006.txt	
09/26/02 04:48p	20,982,002	protein_group_matrix.007.txt	
09/26/02 04:48p	20,979,286	protein_group_matrix.008	
09/26/02 04:48p	20,977,175	protein_group_matrix.009	
09/26/02 04:48p	20,996,897	protein_group_matrix.010	
09/26/02 04:48p	20,998,773	protein_group_matrix.011	
09/26/02 04:48p	20,989,913	protein_group_matrix.012	

File Create Date	File Size	File Name	CD#21
09/26/02 04:49p	20,989,913	protein_group_matrix.012	
09/26/02 04:49p	20,984,871	protein_group_matrix.013	
09/26/02 04:49p	20,995,487	protein_group_matrix.014	
09/26/02 04:49p	20,993,218	protein_group_matrix.015	
09/26/02 04:49p	20,982,759	protein_group_matrix.016	
09/26/02 04:49p	20,995,412	protein_group_matrix.017.txt	
09/26/02 04:49p	20,996,765	protein_group_matrix.018	
09/26/02 04:49p	20,998,069	protein_group_matrix.019	
09/26/02 04:49p	20,991,626	protein_group_matrix.020	
09/26/02 04:49p	21,017,411	protein_group_matrix.021	
09/26/02 04:49p	20,971,520	protein_group_matrix.022	
09/26/02 04:49p	21,002,303	protein_group_matrix.023	
09/26/02 04:49p	21,016,900	protein_group_matrix.024	
09/26/02 04:49p	20,983,971	protein_group_matrix.025	
09/26/02 04:49p	679,866	protein_group_matrix.026	
09/26/02 04:49p	20,997,864	protein_group_matrix.027.txt	
09/26/02 04:49p	21,002,425	protein_group_matrix.028.txt	
09/26/02 04:49p	20,996,492	protein_group_matrix.029.txt	
09/26/02 04:49p	21,004,685	protein_group_matrix.030	
09/26/02 04:49p	20,954,744	protein_group_matrix.031	
09/26/02 04:49p	21,002,980	protein_group_matrix.032	
09/26/02 04:49p	21,002,381	protein_group_matrix.033	
09/26/02 04:50p	21,003,176	protein_group_matrix.034	
09/26/02 04:50p	21,006,452	protein_group_matrix.035.txt	
09/26/02 04:50p	764,346	protein_group_matrix.036	
09/26/02 04:50p	20,993,554	protein_group_matrix.037	
09/26/02 04:50p	20,996,278	protein_group_matrix.038	
09/26/02 04:50p	21,000,170	protein_group_matrix.039	
09/26/02 04:50p	21,007,057	protein_group_matrix.040	
09/26/02 04:50p	20,998,118	protein_group_matrix.041	
09/26/02 04:50p	20,968,100	protein_group_matrix.042	
09/26/02 04:50p	20,967,514	protein_group_matrix.043	

File Create Date	File Size	File Name	CD#22
09/26/02 04:50p	20,994,697	protein_group_matrix.044	
09/26/02 04:50p	12,436,096	protein_group_matrix.045	
09/26/02 04:50p	20,992,494	protein_group_matrix.046	
09/26/02 04:50p	20,991,030	protein_group_matrix.047	
09/26/02 04:50p	20,994,654	protein_group_matrix.048	

File Create Date	File Size	File Name	CD#22
09/26/02 04:50p	20,994,933	protein_group_matrix.049	
09/26/02 04:50p	20,997,676	protein_group_matrix.050	
09/26/02 04:50p	21,029,042	protein_group_matrix.051	
09/26/02 04:50p	20,998,198	protein_group_matrix.052	
09/26/02 04:50p	20,994,259	protein_group_matrix.053	
09/26/02 04:51p	20,967,645	protein_group_matrix.054	
09/26/02 04:51p	21,019,749	protein_group_matrix.055	
09/26/02 04:51p	20,971,520	protein_group_matrix.056	
09/26/02 04:51p	20,997,343	protein_group_matrix.057	
09/26/02 04:51p	21,006,947	protein_group_matrix.058	
09/26/02 04:51p	21,007,310	protein_group_matrix.059	
09/26/02 04:51p	21,001,734	protein_group_matrix.060	
09/26/02 04:51p	21,002,939	protein_group_matrix.061	
09/26/02 04:51p	20,996,086	protein_group_matrix.062	
09/26/02 04:51p	21,011,491	protein_group_matrix.063	
09/26/02 04:51p	20,990,654	protein_group_matrix.064	
09/26/02 04:51p	20,995,322	protein_group_matrix.065	
09/26/02 04:51p	20,994,299	protein_group_matrix.066	
09/26/02 04:51p	21,005,223	protein_group_matrix.067	
09/26/02 04:51p	20,998,064	protein_group_matrix.068	
09/26/02 04:51p	20,995,490	protein_group_matrix.069	
09/26/02 04:51p	20,996,391	protein_group_matrix.070	
09/26/02 04:51p	21,009,903	protein_group_matrix.071	
09/26/02 04:52p	20,999,145	protein_group_matrix.072	
09/26/02 04:52p	21,002,717	protein_group_matrix.073	
09/26/02 04:52p	20,998,662	protein_group_matrix.074	

File Create Date	File Size	File Name	CD#23
09/26/02 04:52p	21,008,124	protein_group_matrix.075	
09/26/02 04:52p	20,999,010	protein_group_matrix.076	
09/26/02 04:52p	20,998,669	protein_group_matrix.077	
09/26/02 04:52p	21,003,843	protein_group_matrix.078	
09/26/02 04:52p	20,996,858	protein_group_matrix.079	
09/26/02 04:52p	21,002,445	protein_group_matrix.080	
09/26/02 04:52p	20,993,350	protein_group_matrix.081	
09/26/02 04:52p	21,003,281	protein_group_matrix.082	
09/26/02 04:52p	20,996,346	protein_group_matrix.083	
09/26/02 04:52p	15,925,561	protein_group_matrix.084	
09/26/02 04:52p	20,995,500	protein_group_matrix.085	
09/26/02 04:52p	20,996,937	protein_group_matrix.086	
09/26/02 04:52p	21,045,738	protein_group_matrix.087	
09/26/02 04:52p	21,000,815	protein_group_matrix.088	
09/26/02 04:52p	21,005,506	protein_group_matrix.089	
09/26/02 04:53p	21,002,870	protein_group_matrix.090	
09/26/02 04:53p	21,004,043	protein_group_matrix.091	
09/26/02 04:53p	20,997,289	protein_group_matrix.092	
09/26/02 04:53p	21,002,299	protein_group_matrix.093	
09/26/02 04:53p	21,005,882	protein_group_matrix.094	
09/26/02 04:53p	20,999,691	protein_group_matrix.095	
09/26/02 04:53p	21,043,968	protein_group_matrix.096	
09/26/02 04:53p	21,000,459	protein_group_matrix.097	
09/26/02 04:53p	21,000,998	protein_group_matrix.098	
09/26/02 04:53p	21,000,456	protein_group_matrix.099	
09/26/02 04:53p	21,002,623	protein_group_matrix.100	
09/26/02 04:53p	21,004,423	protein_group_matrix.101	
09/26/02 04:53p	21,001,020	protein_group_matrix.102	
09/26/02 04:53p	21,019,437	protein_group_matrix.103	
09/26/02 04:53p	20,992,527	protein_group_matrix.104	
09/26/02 04:53p	21,020,507	protein_group_matrix.105	

File Create Date	File Size	File Name	CD#24
09/26/02 04:53p	21,024,971	protein_group_matrix.106	
09/26/02 04:53p	20,971,520	protein_group_matrix.107	

File Create Date	File Size	File Name	CD#24
09/26/02 04:54p	20,971,520	protein_group_matrix.108	
09/26/02 04:54p	19,944,050	protein_group_matrix.109	
09/26/02 04:54p	4,424,295	reference.311987.710-0004-55300-US-U-31835.01_01	
09/26/02 04:54p	4,910,698	reference.311987.710-0004-55300-US-U-31835.01_02	
09/26/02 04:54p	5,572,906	reference.311987.710-0004-55300-US-U-31835.01_03	
09/26/02 04:54p	5,612,694	reference.311987.710-0004-55300-US-U-31835.01_04	
09/26/02 04:54p	5,814,130	reference.311987.710-0004-55300-US-U-31835.01_05	
09/26/02 04:54p	5,921,965	reference.311987.710-0004-55300-US-U-31835.01_06	
09/26/02 04:54p	5,206,858	reference.311987.710-0004-55300-US-U-31835.01_07	
09/26/02 04:54p	5,609,561	reference.311987.710-0004-55300-US-U-31835.01_08	
09/26/02 04:54p	5,994,678	reference.311987.710-0004-55300-US-U-31835.01_09	
09/26/02 04:54p	108,006	reference.311987.710-0004-55300-US-U-	
31835.01_0a_01			
09/26/02 04:54p	119,659	reference.311987.710-0004-55300-US-U-	
31835.01_0a_02			
09/26/02 04:54p	118,848	reference.311987.710-0004-55300-US-U-	
31835.01_0a_03			
09/26/02 04:54p	89,899	reference.311987.710-0004-55300-US-U-	
31835.01_0a_04			
09/26/02 04:54p	92,601	reference.311987.710-0004-55300-US-U-	
31835.01_0a_05			
09/26/02 04:54p	85,986	reference.311987.710-0004-55300-US-U-	
31835.01_0a_06			
09/26/02 04:54p	103,137	reference.311987.710-0004-55300-US-U-	
31835.01_0a_07			
09/26/02 04:54p	95,186	reference.311987.710-0004-55300-US-U-	
31835.01_0a_08			
09/26/02 04:54p	80,813	reference.311987.710-0004-55300-US-U-	
31835.01_0a_09			
09/26/02 04:54p	100,519	reference.311987.710-0004-55300-US-U-	
31835.01_0a_10			
09/26/02 04:54p	103,815	reference.311987.710-0004-55300-US-U-	
31835.01_0a_11			
09/26/02 04:54p	84,242	reference.311987.710-0004-55300-US-U-	
31835.01_0a_12			
09/26/02 04:54p	97,483	reference.311987.710-0004-55300-US-U-	
31835.01_0a_13			
09/26/02 04:54p	82,595	reference.311987.710-0004-55300-US-U-	
31835.01_0a_14			
09/26/02 04:54p	111,149	reference.311987.710-0004-55300-US-U-	
31835.01_0a_15			
09/26/02 04:54p	93,763	reference.311987.710-0004-55300-US-U-	
31835.01_0a_16			
09/26/02 04:54p	75,545	reference.311987.710-0004-55300-US-U-	
31835.01_0a_17			
09/26/02 04:54p	90,795	reference.311987.710-0004-55300-US-U-	
31835.01_0a_18			
09/26/02 04:54p	5,065,095	reference.311987.710-0004-55300-US-U-31835.01_10	
09/26/02 04:54p	5,333,829	reference.311987.710-0004-55300-US-U-31835.01_11	
09/26/02 04:54p	5,567,905	reference.311987.710-0004-55300-US-U-31835.01_12	
09/26/02 04:54p	5,536,744	reference.311987.710-0004-55300-US-U-31835.01_13	
09/26/02 04:54p	6,147,069	reference.311987.710-0004-55300-US-U-31835.01_14	
09/26/02 04:54p	4,939,635	reference.311987.710-0004-55300-US-U-31835.01_15	
09/26/02 04:54p	4,891,438	reference.311987.710-0004-55300-US-U-31835.01_16	
09/26/02 04:54p	5,410,676	reference.311987.710-0004-55300-US-U-31835.01_17	
09/26/02 04:54p	4,161,439	reference.311987.710-0004-55300-US-U-31835.01_18	
09/26/02 04:54p	410,644	reference.311987a.710-0004-55300-US-U-31835.01_01	
09/26/02 04:54p	31,109	reference.311987a.710-0004-55300-US-U-	
31835.01_0a_01			
09/26/02 04:54p	7,207,054	reference.311988.710-0004-55300-US-U-31835.01_01	
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09/26/02 04:56p	839,435	sequences.3769.710-0004-55300-US-U-31835.01_0a_45	

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09/26/02 04:56p	549,257	sequences.3769.710-0004-55300-US-U-31835.01_0a_46	
09/26/02 04:56p	840,353	sequences.3769.710-0004-55300-US-U-31835.01_0a_47	
09/26/02 04:56p	688,142	sequences.3769.710-0004-55300-US-U-31835.01_0a_48	
09/26/02 04:57p	665,763	sequences.3769.710-0004-55300-US-U-31835.01_0a_49	
09/26/02 04:57p	659,181	sequences.3769.710-0004-55300-US-U-31835.01_0a_50	
09/26/02 04:57p	674,477	sequences.3769.710-0004-55300-US-U-31835.01_0a_51	
09/26/02 04:57p	635,501	sequences.3769.710-0004-55300-US-U-31835.01_0a_52	
09/26/02 04:57p	1,081,543	sequences.3769.710-0004-55300-US-U-31835.01_0a_53	
09/26/02 04:57p	1,067,505	sequences.3769.710-0004-55300-US-U-31835.01_0a_54	
09/26/02 04:57p	942,170	sequences.3769.710-0004-55300-US-U-31835.01_0a_55	
09/26/02 04:57p	1,048,319	sequences.3769.710-0004-55300-US-U-31835.01_0a_56	
09/26/02 04:57p	654,320	sequences.3769.710-0004-55300-US-U-31835.01_0a_57	
09/26/02 04:57p	9,667,279	sequences.3769.710-0004-55300-US-U-31835.01_10	
09/26/02 04:57p	10,660,231	sequences.3769.710-0004-55300-US-U-31835.01_11	
09/26/02 04:57p	12,611,486	sequences.3769.710-0004-55300-US-U-31835.01_12	
09/26/02 04:57p	12,469,898	sequences.3769.710-0004-55300-US-U-31835.01_13	
09/26/02 04:57p	7,670,042	sequences.3769.710-0004-55300-US-U-31835.01_14	
09/26/02 04:57p	12,120,892	sequences.3769.710-0004-55300-US-U-31835.01_15	
09/26/02 04:57p	11,518,341	sequences.3769.710-0004-55300-US-U-31835.01_16	
09/26/02 04:57p	10,514,869	sequences.3769.710-0004-55300-US-U-31835.01_17	
09/26/02 04:57p	10,353,445	sequences.3769.710-0004-55300-US-U-31835.01_18	
09/26/02 04:57p	10,769,323	sequences.3769.710-0004-55300-US-U-31835.01_19	
09/26/02 04:57p	11,716,690	sequences.3769.710-0004-55300-US-U-31835.01_20	

File Create Date	File Size	File Name	CD#26
09/26/02 04:57p	10,911,608	sequences.3769.710-0004-55300-US-U-31835.01_21	
09/26/02 04:57p	9,146,745	sequences.3769.710-0004-55300-US-U-31835.01_22	
09/26/02 04:57p	8,350,759	sequences.3769.710-0004-55300-US-U-31835.01_23	
09/26/02 04:57p	10,309,580	sequences.3769.710-0004-55300-US-U-31835.01_24	
09/26/02 04:57p	11,047,256	sequences.3769.710-0004-55300-US-U-31835.01_25	
09/26/02 04:57p	11,293,684	sequences.3769.710-0004-55300-US-U-31835.01_26	
09/26/02 04:57p	12,147,523	sequences.3769.710-0004-55300-US-U-31835.01_27	
09/26/02 04:57p	10,755,243	sequences.3769.710-0004-55300-US-U-31835.01_28	
09/26/02 04:57p	6,097,666	sequences.3769.710-0004-55300-US-U-31835.01_29	
09/26/02 04:57p	11,075,770	sequences.3769.710-0004-55300-US-U-31835.01_30	
09/26/02 04:57p	10,207,931	sequences.3769.710-0004-55300-US-U-31835.01_31	
09/26/02 04:57p	10,174,990	sequences.3769.710-0004-55300-US-U-31835.01_32	
09/26/02 04:57p	9,373,681	sequences.3769.710-0004-55300-US-U-31835.01_33	
09/26/02 04:57p	5,953,616	sequences.3769.710-0004-55300-US-U-31835.01_34	
09/26/02 04:57p	10,973,071	sequences.3769.710-0004-55300-US-U-31835.01_35	
09/26/02 04:57p	11,253,484	sequences.3769.710-0004-55300-US-U-31835.01_36	
09/26/02 04:57p	10,596,787	sequences.3769.710-0004-55300-US-U-31835.01_37	
09/26/02 04:57p	7,015,534	sequences.3769.710-0004-55300-US-U-31835.01_38	
09/26/02 04:57p	8,168,673	sequences.3769.710-0004-55300-US-U-31835.01_39	
09/26/02 04:57p	10,432,081	sequences.3769.710-0004-55300-US-U-31835.01_40	
09/26/02 04:57p	12,363,984	sequences.3769.710-0004-55300-US-U-31835.01_41	
09/26/02 04:57p	12,861,124	sequences.3769.710-0004-55300-US-U-31835.01_42	
09/26/02 04:57p	13,086,865	sequences.3769.710-0004-55300-US-U-31835.01_43	
09/26/02 04:58p	13,047,151	sequences.3769.710-0004-55300-US-U-31835.01_44	
09/26/02 04:58p	13,150,566	sequences.3769.710-0004-55300-US-U-31835.01_45	
09/26/02 04:58p	13,114,593	sequences.3769.710-0004-55300-US-U-31835.01_46	
09/26/02 04:58p	12,718,176	sequences.3769.710-0004-55300-US-U-31835.01_47	
09/26/02 04:58p	11,518,104	sequences.3769.710-0004-55300-US-U-31835.01_48	
09/26/02 04:58p	13,023,183	sequences.3769.710-0004-55300-US-U-31835.01_49	
09/26/02 04:58p	12,817,892	sequences.3769.710-0004-55300-US-U-31835.01_50	
09/26/02 04:58p	12,049,539	sequences.3769.710-0004-55300-US-U-31835.01_51	
09/26/02 04:58p	12,732,603	sequences.3769.710-0004-55300-US-U-31835.01_52	
09/26/02 04:58p	7,988,517	sequences.3769.710-0004-55300-US-U-31835.01_53	
09/26/02 04:58p	8,501,130	sequences.3769.710-0004-55300-US-U-31835.01_54	
09/26/02 04:58p	8,393,296	sequences.3769.710-0004-55300-US-U-31835.01_55	
09/26/02 04:58p	7,796,358	sequences.3769.710-0004-55300-US-U-31835.01_56	
09/26/02 04:58p	4,622,108	sequences.3769.710-0004-55300-US-U-31835.01_57	
09/26/02 04:58p	8,714,933	sequences.3769a.710-0004-55300-US-U-31835.01_01	
09/26/02 04:58p	352,046	sequences.3769a.710-0004-55300-US-U-31835.01_02	

File Create Date	File Size	File Name	CD#26
09/26/02 04:58p	1,010,484	sequences.3769a.710-0004-55300-US-U-31835.01_0a_01	
09/26/02 04:58p	53,434	sequences.3769a.710-0004-55300-US-U-31835.01_0a_02	
09/26/02 04:58p	3,706,774	sequences.3847.710-0004-55300-US-U-31835.01_01	
09/26/02 04:58p	3,576,470	sequences.3847.710-0004-55300-US-U-31835.01_02	
09/26/02 04:58p	3,235,900	sequences.3847.710-0004-55300-US-U-31835.01_03	
09/26/02 04:58p	3,425,695	sequences.3847.710-0004-55300-US-U-31835.01_04	
09/26/02 04:58p	3,643,446	sequences.3847.710-0004-55300-US-U-31835.01_05	
09/26/02 04:58p	4,252,932	sequences.3847.710-0004-55300-US-U-31835.01_06	
09/26/02 04:58p	3,247,023	sequences.3847.710-0004-55300-US-U-31835.01_07	
09/26/02 04:58p	4,846,452	sequences.3847.710-0004-55300-US-U-31835.01_08	
09/26/02 04:58p	4,614,464	sequences.3847.710-0004-55300-US-U-31835.01_09	
09/26/02 04:58p	554,692	sequences.3847.710-0004-55300-US-U-31835.01_0a_01	
09/26/02 04:58p	696,675	sequences.3847.710-0004-55300-US-U-31835.01_0a_02	
09/26/02 04:58p	458,234	sequences.3847.710-0004-55300-US-U-31835.01_0a_03	
09/26/02 04:58p	696,796	sequences.3847.710-0004-55300-US-U-31835.01_0a_04	
09/26/02 04:59p	228,792	stanford_old_new_cdna_map.txt	
09/26/02 04:58p	596,908	sequences.3847.710-0004-55300-US-U-31835.01_0a_05	
09/26/02 04:58p	642,789	sequences.3847.710-0004-55300-US-U-31835.01_0a_06	
09/26/02 04:58p	564,751	sequences.3847.710-0004-55300-US-U-31835.01_0a_07	
09/26/02 04:58p	586,104	sequences.3847.710-0004-55300-US-U-31835.01_0a_08	
09/26/02 04:58p	628,933	sequences.3847.710-0004-55300-US-U-31835.01_0a_09	
09/26/02 04:58p	847,692	sequences.3847.710-0004-55300-US-U-31835.01_0a_10	
09/26/02 04:47p	101,007	Table A.txt	
09/26/02 04:58p	678,087	sequences.3847.710-0004-55300-US-U-31835.01_0a_11	
09/26/02 04:58p	667,633	sequences.3847.710-0004-55300-US-U-31835.01_0a_12	
09/26/02 04:58p	832,319	sequences.3847.710-0004-55300-US-U-31835.01_0a_13	
09/26/02 04:58p	794,476	sequences.3847.710-0004-55300-US-U-31835.01_0a_14	
09/26/02 04:58p	767,715	sequences.3847.710-0004-55300-US-U-31835.01_0a_15	
09/26/02 04:58p	413,077	sequences.3847.710-0004-55300-US-U-31835.01_0a_16	
09/26/02 04:58p	529,077	sequences.3847.710-0004-55300-US-U-31835.01_0a_17	
09/26/02 04:58p	477,591	sequences.3847.710-0004-55300-US-U-31835.01_0a_18	
09/26/02 04:58p	642,373	sequences.3847.710-0004-55300-US-U-31835.01_0a_19	
09/26/02 04:58p	710,210	sequences.3847.710-0004-55300-US-U-31835.01_0a_20	
09/26/02 04:58p	500,967	sequences.3847.710-0004-55300-US-U-31835.01_0a_21	
09/26/02 04:58p	266,344	sequences.3847.710-0004-55300-US-U-31835.01_0a_22	
09/26/02 04:58p	7,085,559	sequences.3847.710-0004-55300-US-U-31835.01_10	
09/26/02 04:58p	4,232,334	sequences.3847.710-0004-55300-US-U-31835.01_11	
09/26/02 04:58p	4,522,815	sequences.3847.710-0004-55300-US-U-31835.01_12	
09/26/02 04:58p	6,550,634	sequences.3847.710-0004-55300-US-U-31835.01_13	
09/26/02 04:58p	6,359,709	sequences.3847.710-0004-55300-US-U-31835.01_14	
09/26/02 04:58p	5,085,932	sequences.3847.710-0004-55300-US-U-31835.01_15	
09/26/02 04:58p	3,605,683	sequences.3847.710-0004-55300-US-U-31835.01_16	
09/26/02 04:58p	3,860,442	sequences.3847.710-0004-55300-US-U-31835.01_17	
09/26/02 04:58p	3,946,914	sequences.3847.710-0004-55300-US-U-31835.01_18	
09/26/02 04:58p	3,716,222	sequences.3847.710-0004-55300-US-U-31835.01_19	
09/26/02 04:58p	3,601,701	sequences.3847.710-0004-55300-US-U-31835.01_20	
09/26/02 04:58p	3,091,397	sequences.3847.710-0004-55300-US-U-31835.01_21	
09/26/02 04:58p	1,123,994	sequences.3847.710-0004-55300-US-U-31835.01_22	
09/26/02 04:58p	495,681	sequences.3847a.710-0004-55300-US-U-31835.01_01	
09/26/02 04:58p	258,859	sequences.3847a.710-0004-55300-US-U-31835.01_0a_01	
09/26/02 04:58p	3,626,862	sequences.4565.710-0004-55300-US-U-31835.01_01	
09/26/02 04:58p	3,662,949	sequences.4565.710-0004-55300-US-U-31835.01_02	
09/26/02 04:58p	3,743,050	sequences.4565.710-0004-55300-US-U-31835.01_03	
09/26/02 04:58p	3,983,838	sequences.4565.710-0004-55300-US-U-31835.01_04	
09/26/02 04:58p	4,326,730	sequences.4565.710-0004-55300-US-U-31835.01_05	
09/26/02 04:58p	3,784,061	sequences.4565.710-0004-55300-US-U-31835.01_06	
09/26/02 04:58p	3,748,537	sequences.4565.710-0004-55300-US-U-31835.01_07	
09/26/02 04:58p	3,625,564	sequences.4565.710-0004-55300-US-U-31835.01_08	
09/26/02 04:58p	3,830,042	sequences.4565.710-0004-55300-US-U-31835.01_09	
09/26/02 04:58p	425,232	sequences.4565.710-0004-55300-US-U-31835.01_0a_01	
09/26/02 04:58p	530,595	sequences.4565.710-0004-55300-US-U-31835.01_0a_02	
09/26/02 04:58p	471,281	sequences.4565.710-0004-55300-US-U-31835.01_0a_03	
09/26/02 04:59p	1,476	Single gene functions and utilities (1).txt	
09/26/02 04:58p	475,567	sequences.4565.710-0004-55300-US-U-31835.01_0a_04	
09/26/02 04:58p	647,920	sequences.4565.710-0004-55300-US-U-31835.01_0a_05	
09/26/02 04:58p	632,762	sequences.4565.710-0004-55300-US-U-31835.01_0a_06	
09/26/02 04:58p	594,368	sequences.4565.710-0004-55300-US-U-31835.01_0a_07	

File Create Date	File Size	File Name	CD#26
09/26/02 04:58p	504,573	sequences.4565.710-0004-55300-US-U-31835.01_0a_08	
09/26/02 04:58p	598,828	sequences.4565.710-0004-55300-US-U-31835.01_0a_09	
09/26/02 04:58p	381,699	sequences.4565.710-0004-55300-US-U-31835.01_0a_10	
09/26/02 04:58p	386,943	sequences.4565.710-0004-55300-US-U-31835.01_0a_11	
09/26/02 04:58p	393,875	sequences.4565.710-0004-55300-US-U-31835.01_0a_12	
09/26/02 04:58p	639,616	sequences.4565.710-0004-55300-US-U-31835.01_0a_13	
09/26/02 04:58p	708,494	sequences.4565.710-0004-55300-US-U-31835.01_0a_14	
09/26/02 04:58p	581,321	sequences.4565.710-0004-55300-US-U-31835.01_0a_15	
09/26/02 04:58p	574,196	sequences.4565.710-0004-55300-US-U-31835.01_0a_16	
09/26/02 04:58p	586,317	sequences.4565.710-0004-55300-US-U-31835.01_0a_17	
09/26/02 04:58p	163,869	sequences.4565.710-0004-55300-US-U-31835.01_0a_18	
09/26/02 04:58p	3,828,923	sequences.4565.710-0004-55300-US-U-31835.01_10	
09/26/02 04:58p	3,727,397	sequences.4565.710-0004-55300-US-U-31835.01_11	
09/26/02 04:58p	3,917,627	sequences.4565.710-0004-55300-US-U-31835.01_12	
09/26/02 04:59p	2,223	Single gene functions and utilities (2).txt	
09/26/02 04:58p	3,947,258	sequences.4565.710-0004-55300-US-U-31835.01_13	
09/26/02 04:59p	3,899,956	sequences.4565.710-0004-55300-US-U-31835.01_14	
09/26/02 04:59p	3,621,049	sequences.4565.710-0004-55300-US-U-31835.01_15	
09/26/02 04:59p	3,357,451	sequences.4565.710-0004-55300-US-U-31835.01_16	
09/26/02 04:59p	3,161,282	sequences.4565.710-0004-55300-US-U-31835.01_17	
09/26/02 04:59p	752,673	sequences.4565.710-0004-55300-US-U-31835.01_18	
09/26/02 04:59p	540,193	sequences.4565a.710-0004-55300-US-U-31835.01_01	
09/26/02 04:59p	169,822	sequences.4565a.710-0004-55300-US-U-31835.01_0a_01	
09/26/02 04:59p	905	Single gene functions and utilities (3).txt	
09/26/02 04:59p	1,517	Single gene functions and utilities (4).txt	
09/26/02 04:59p	4,626	Single gene functions and utilities (5).txt	
09/26/02 04:59p	4,887	Single gene functions and utilities (6).txt	
09/26/02 04:59p	7,456	Single gene functions and utilities (7).txt	
09/26/02 04:59p	9,339	Single gene functions and utilities (8).txt	

File Create Date	File Size	File Name	CD#27
08/22/01 05:03p	35,153	Cluster Functions and Utilities (01).txt	
08/22/01 05:04p	40,447	Cluster Functions and Utilities (02).txt	
08/22/01 05:04p	4,473	Cluster Functions and Utilities (03).txt	
08/22/01 05:05p	7,820	Cluster Functions and Utilities (04).txt	
08/22/01 05:05p	24,047	Cluster Functions and Utilities (05).txt	
08/22/01 05:06p	18,490	Cluster Functions and Utilities (06).txt	
08/22/01 05:11p	36,273	Cluster functions and utilities (07).txt	
08/22/01 04:17p	33,962	Cluster Functions and Utilities (08).txt	
08/22/01 04:16p	23,000	Cluster functions and utilities (09).txt	
08/21/01 09:47p	2,691	Cluster functions and utilities (10).txt	
08/21/01 09:47p	2,290	Cluster functions and utilities (11).txt	
08/22/01 05:25p	23,740	Cluster Functions and Utilities (12).txt	
08/22/01 03:14p	331,616	enhanced_amino.txt	
08/20/01 01:44p	13,132,268	gb_only_peptides.fasta	
08/21/01 03:28p	392,675	knock_in.710-0004-55300-US-U-31835.01.txt	
08/14/01 07:12p	831,736	knock_out.710-0004-55300-US-U-31835.01	
08/20/01 11:56a	16,635,460	ma_clusters.710-0004-55300-US-U-31835.01	
08/21/01 02:09p	55,307	ma_diff Aluminum.txt	
08/21/01 02:10p	27,557	ma_diff Axel.txt	
08/21/01 02:13p	41,505	ma_diff Cadmium .txt	
08/21/01 02:51p	53,938	ma_diff Cauliflower .txt	
08/21/01 02:50p	98,775	ma_diff Chloroplast.txt	
08/21/01 02:50p	160,542	ma_diff Circadian 1-02.txt	
08/21/01 02:50p	127,498	ma_diff Circadian 1-03.txt	
08/21/01 02:51p	166,158	ma_diff Circadian 1-04.txt	
08/21/01 02:50p	141,971	ma_diff Circadian 1-01.txt	
08/21/01 02:52p	56,536	ma_diff Circadian 1-05.txt	
08/21/01 02:52p	121,178	ma_diff Circadian 1-06.txt	
08/21/01 02:52p	133,389	ma_diff Circadian 1-07.txt	
08/21/01 02:52p	259,096	ma_diff Circadian 1-08.txt	
08/21/01 02:52p	228,222	ma_diff Circadian 1-09.txt	
08/21/01 02:53p	54,526	ma_diff Circadian 1-10.txt	
08/21/01 02:53p	134,759	ma_diff CO2 1-1.txt	
08/21/01 02:53p	241,865	ma_diff CO2 1-2.txt	

File Create Date	File Size	File Name	CD#27
08/21/01 02:54p	63,264	ma_diff CO2 1-3.txt	
08/21/01 02:54p	59,530	ma_diff CO2 1-4.txt	
08/21/01 02:54p	372,633	ma_diff CO2 1-5.txt	
08/21/01 02:54p	9,220	ma_diff Disease .txt	
08/21/01 02:54p	25,114	ma_diff H2O2 .txt	
08/21/01 02:55p	4,073	ma_diff Iol .txt	
08/21/01 02:55p	283,026	ma_diff Iron 1-1.txt	
08/21/01 02:55p	90,890	ma_diff Iron 1-2.txt	
08/21/01 02:55p	51,342	ma_diff Mitochondria-Electron Transp.txt	
08/21/01 02:55p	107,920	ma_diff NAA (Auxin) 1-1.txt	
08/21/01 02:55p	50,267	ma_diff NAA (Auxin) 1-2.txt	
08/21/01 02:55p	67,291	ma_diff Nitrogen.txt	
08/21/01 02:56p	6,441	ma_diff Phototropism 1-1.txt	
08/21/01 02:56p	22,229	ma_diff Phototropism 1-2.txt	
08/21/01 02:56p	28,270	ma_diff Phototropism 1-3.txt	
08/21/01 02:56p	45,620	ma_diff Shade.txt	
08/21/01 02:56p	73,438	ma_diff Sqn.txt	
08/21/01 02:56p	3,828	ma_diff Sulfur.txt	
08/21/01 02:56p	67,949	ma_diff Wounding.txt	
08/21/01 02:57p	30,836	ma_diff Zinc.txt	
08/21/01 03:54p	4,318,956	ma_diff.710-0004-55300-US-U-31835.01	
08/10/01 03:06p	2,752,459	Protein Domain Table.txt	
08/22/01 10:53a	14,778,004	protein_group_710-0004-55300-US-U-31835.01_01	
08/21/01 05:29p	12,953,488	protein_group_710-0004-55300-US-U-31835.01_02	
08/21/01 05:49p	12,866,803	protein_group_710-0004-55300-US-U-31835.01_03	
08/21/01 06:15p	15,451,084	protein_group_710-0004-55300-US-U-31835.01_04	
08/20/01 03:33p	228,792	stanford_old_new_cdna_map.txt	
08/21/01 06:40p	13,753,735	protein_group_710-0004-55300-US-U-31835.01_05	
08/21/01 07:14p	17,503,319	protein_group_710-0004-55300-US-U-31835.01_06	
08/21/01 07:53p	16,376,099	protein_group_710-0004-55300-US-U-31835.01_07	
08/21/01 08:22p	13,390,661	protein_group_710-0004-55300-US-U-31835.01_08	
08/21/01 09:05p	14,328,338	protein_group_710-0004-55300-US-U-31835.01_09	
08/21/01 09:52p	12,595,465	protein_group_710-0004-55300-US-U-31835.01_10	
08/21/01 10:51p	14,577,180	protein_group_710-0004-55300-US-U-31835.01_11	
08/21/01 11:29p	15,580,727	protein_group_710-0004-55300-US-U-31835.01_12	
08/22/01 12:01a	13,881,717	protein_group_710-0004-55300-US-U-31835.01_13	
08/22/01 12:25a	17,139,394	protein_group_710-0004-55300-US-U-31835.01_14	
08/22/01 12:47a	14,568,663	protein_group_710-0004-55300-US-U-31835.01_15	
08/22/01 01:11a	17,242,592	protein_group_710-0004-55300-US-U-31835.01_16	
08/22/01 01:34a	16,262,656	protein_group_710-0004-55300-US-U-31835.01_17	
08/22/01 01:56a	15,432,667	protein_group_710-0004-55300-US-U-31835.01_18	
08/22/01 02:21a	17,255,427	protein_group_710-0004-55300-US-U-31835.01_19	
08/22/01 02:44a	16,933,384	protein_group_710-0004-55300-US-U-31835.01_20	
08/22/01 03:07a	17,384,042	protein_group_710-0004-55300-US-U-31835.01_21	
08/22/01 03:31a	17,437,337	protein_group_710-0004-55300-US-U-31835.01_22	
08/22/01 03:53a	15,803,056	protein_group_710-0004-55300-US-U-31835.01_23	
08/22/01 04:05a	9,103,743	protein_group_710-0004-55300-US-U-31835.01_24	
08/22/01 05:01p	1,476	Single gene functions and utilities (1).txt	
08/22/01 05:01p	2,223	Single gene functions and utilities (2).txt	
08/22/01 05:02p	905	Single gene functions and utilities (3).txt	
08/22/01 05:03p	1,517	Single gene functions and utilities (4).txt	
08/22/01 05:07p	4,626	Single gene functions and utilities (5).txt	
08/22/01 04:57p	4,887	Single gene functions and utilities (6).txt	
08/22/01 04:57p	7,456	Single gene functions and utilities (7).txt	
08/22/01 05:06p	9,339	Single gene functions and utilities (8).txt	

File Create Date	File Size	File Name	CD#28
08/21/01 08:15p	20,982,878	protein_group_matrix.001	
08/21/01 08:22p	20,987,975	protein_group_matrix.002	
08/21/01 08:33p	20,996,062	protein_group_matrix.003	
08/21/01 08:32p	20,991,903	protein_group_matrix.004	
08/21/01 08:34p	21,008,452	protein_group_matrix.005	
08/21/01 08:38p	20,979,474	protein_group_matrix.006.txt	
08/21/01 08:38p	20,982,002	protein_group_matrix.007.txt	
08/21/01 08:41p	20,979,286	protein_group_matrix.008	

File Create Date	File Size	File Name	CD#28
08/21/01 08:41p	20,977,175	protein_group_matrix.009	
08/21/01 08:44p	20,996,897	protein_group_matrix.010	
08/21/01 08:44p	20,998,773	protein_group_matrix.011	
08/21/01 08:45p	20,989,913	protein_group_matrix.012	
08/21/01 08:46p	20,984,871	protein_group_matrix.013	
08/21/01 08:48p	20,995,487	protein_group_matrix.014	
08/21/01 08:49p	20,993,218	protein_group_matrix.015	
08/21/01 08:50p	20,982,759	protein_group_matrix.016	
08/21/01 08:51p	20,995,412	protein_group_matrix.017.txt	
08/21/01 08:53p	20,996,765	protein_group_matrix.018	
08/21/01 08:53p	20,998,069	protein_group_matrix.019	
08/21/01 08:54p	20,991,626	protein_group_matrix.020	
08/21/01 08:55p	21,017,411	protein_group_matrix.021	
08/21/01 08:58p	20,971,520	protein_group_matrix.022	
08/21/01 08:57p	21,002,303	protein_group_matrix.023	
08/21/01 08:58p	21,016,900	protein_group_matrix.024	
08/21/01 09:01p	20,983,971	protein_group_matrix.025	
08/21/01 08:59p	679,866	protein_group_matrix.026	
08/21/01 09:04p	20,997,864	protein_group_matrix.027.txt	
08/21/01 09:06p	21,002,425	protein_group_matrix.028.txt	
08/21/01 09:06p	20,996,492	protein_group_matrix.029.txt	
08/21/01 09:09p	21,004,685	protein_group_matrix.030	
08/21/01 09:08p	20,954,744	protein_group_matrix.031	
08/21/01 09:11p	21,002,980	protein_group_matrix.032	
08/21/01 09:11p	21,002,381	protein_group_matrix.033	
08/21/01 09:13p	21,003,176	protein_group_matrix.034	

File Create Date	File Size	File Name	CD#29
08/21/01 09:14p	21,006,452	protein_group_matrix.035.txt	
08/21/01 09:15p	764,346	protein_group_matrix.036	
08/21/01 09:16p	20,993,554	protein_group_matrix.037	
08/21/01 09:17p	20,996,278	protein_group_matrix.038	
08/21/01 09:17p	21,000,170	protein_group_matrix.039	
08/21/01 09:18p	21,007,057	protein_group_matrix.040	
08/21/01 09:21p	20,998,118	protein_group_matrix.041	
08/21/01 09:22p	20,968,100	protein_group_matrix.042	
08/21/01 09:23p	20,967,514	protein_group_matrix.043	
08/21/01 09:24p	20,994,697	protein_group_matrix.044	
08/21/01 09:25p	12,436,096	protein_group_matrix.045	
08/21/01 09:26p	20,992,494	protein_group_matrix.046	
08/21/01 09:26p	20,991,030	protein_group_matrix.047	
08/21/01 09:29p	20,994,654	protein_group_matrix.048	
08/21/01 09:28p	20,994,933	protein_group_matrix.049	
08/21/01 09:31p	20,997,676	protein_group_matrix.050	
08/21/01 09:30p	21,029,042	protein_group_matrix.051	
08/21/01 09:33p	20,998,198	protein_group_matrix.052	
08/21/01 09:34p	20,994,259	protein_group_matrix.053	
08/21/01 09:40p	20,967,645	protein_group_matrix.054	
08/21/01 09:35p	21,019,749	protein_group_matrix.055	
08/21/01 06:59p	20,971,520	protein_group_matrix.056	
08/21/01 09:37p	20,997,343	protein_group_matrix.057	
08/21/01 09:43p	21,006,947	protein_group_matrix.058	
08/21/01 09:40p	21,007,310	protein_group_matrix.059	
08/21/01 09:44p	21,001,734	protein_group_matrix.060	
08/21/01 09:43p	21,002,939	protein_group_matrix.061	
08/21/01 09:46p	20,996,086	protein_group_matrix.062	
08/21/01 09:45p	21,011,491	protein_group_matrix.063	
08/21/01 09:48p	20,990,654	protein_group_matrix.064	
08/21/01 09:47p	20,995,322	protein_group_matrix.065	
08/21/01 09:50p	20,994,299	protein_group_matrix.066	
08/21/01 09:49p	21,005,223	protein_group_matrix.067	
08/21/01 09:52p	20,998,064	protein_group_matrix.068	

File Create Date	File Size	File Name	CD#30
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File Create Date	File Size	File Name	CD#30
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08/21/01 09:54p	20,996,391	protein_group_matrix.070	
08/21/01 09:53p	21,009,903	protein_group_matrix.071	
08/21/01 09:57p	20,999,145	protein_group_matrix.072	
08/21/01 09:55p	21,002,717	protein_group_matrix.073	
08/21/01 10:00p	20,998,662	protein_group_matrix.074	
08/21/01 09:57p	21,008,124	protein_group_matrix.075	
08/21/01 10:01p	20,999,010	protein_group_matrix.076	
08/21/01 10:00p	20,998,669	protein_group_matrix.077	
08/21/01 10:06p	21,003,843	protein_group_matrix.078	
08/21/01 10:03p	20,996,858	protein_group_matrix.079	
08/21/01 10:08p	21,002,445	protein_group_matrix.080	
08/21/01 10:06p	20,993,350	protein_group_matrix.081	
08/21/01 10:10p	21,003,281	protein_group_matrix.082	
08/21/01 10:09p	20,996,346	protein_group_matrix.083	
08/21/01 10:12p	15,925,561	protein_group_matrix.084	
08/21/01 10:10p	20,995,500	protein_group_matrix.085	
08/21/01 10:16p	20,996,937	protein_group_matrix.086	
08/21/01 10:12p	21,045,738	protein_group_matrix.087	
08/21/01 10:17p	21,000,815	protein_group_matrix.088	
08/21/01 10:14p	21,005,506	protein_group_matrix.089	
08/21/01 10:19p	21,002,870	protein_group_matrix.090	
08/21/01 10:17p	21,004,043	protein_group_matrix.091	
08/21/01 10:21p	20,997,289	protein_group_matrix.092	
08/21/01 10:19p	21,002,299	protein_group_matrix.093	
08/21/01 10:23p	21,005,882	protein_group_matrix.094	
08/21/01 10:20p	20,999,691	protein_group_matrix.095	
08/21/01 10:24p	21,043,968	protein_group_matrix.096	
08/21/01 10:22p	21,000,459	protein_group_matrix.097	
08/21/01 10:26p	21,000,998	protein_group_matrix.098	
08/21/01 10:24p	21,000,456	protein_group_matrix.099	
08/21/01 10:32p	21,002,623	protein_group_matrix.100	

File Create Date	File Size	File Name	CD#31
08/21/01 10:26p	21,004,423	protein_group_matrix.101	
08/21/01 10:35p	21,001,020	protein_group_matrix.102	
08/21/01 10:28p	21,019,437	protein_group_matrix.103	
08/21/01 10:37p	20,992,527	protein_group_matrix.104	
08/21/01 10:33p	21,020,507	protein_group_matrix.105	
08/21/01 10:38p	21,024,971	protein_group_matrix.106	
08/21/01 07:25p	20,971,520	protein_group_matrix.107	
08/21/01 07:26p	20,971,520	protein_group_matrix.108	
08/21/01 07:26p	19,944,050	protein_group_matrix.109	
07/27/01 12:05p	4,424,295	reference.311987.710-0004-55300-US-U-31835.01_01	
07/27/01 04:10p	4,910,698	reference.311987.710-0004-55300-US-U-31835.01_02	
07/27/01 04:10p	5,572,906	reference.311987.710-0004-55300-US-U-31835.01_03	
07/27/01 08:08p	5,612,694	reference.311987.710-0004-55300-US-U-31835.01_04	
07/27/01 08:08p	5,814,130	reference.311987.710-0004-55300-US-U-31835.01_05	
07/27/01 08:23p	5,921,965	reference.311987.710-0004-55300-US-U-31835.01_06	
07/28/01 11:39a	5,206,858	reference.311987.710-0004-55300-US-U-31835.01_07	
07/28/01 11:39a	5,609,561	reference.311987.710-0004-55300-US-U-31835.01_08	
07/28/01 11:38a	5,994,678	reference.311987.710-0004-55300-US-U-31835.01_09	
07/27/01 12:05p	108,006	reference.311987.710-0004-55300-US-U-	
31835.01_0a_01			
07/27/01 04:10p	119,659	reference.311987.710-0004-55300-US-U-	
31835.01_0a_02			
07/27/01 04:10p	118,848	reference.311987.710-0004-55300-US-U-	
31835.01_0a_03			
07/27/01 08:08p	89,899	reference.311987.710-0004-55300-US-U-	
31835.01_0a_04			
07/27/01 08:08p	92,601	reference.311987.710-0004-55300-US-U-	
31835.01_0a_05			
07/27/01 08:23p	85,986	reference.311987.710-0004-55300-US-U-	
31835.01_0a_06			

File Create Date	File Size	File Name	CD#31
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07/28/01 11:39a	95,186	reference.311987.710-0004-55300-US-U-	
31835.01_0a_08			
07/28/01 11:38a	80,813	reference.311987.710-0004-55300-US-U-	
31835.01_0a_09			
07/28/01 11:38a	100,519	reference.311987.710-0004-55300-US-U-	
31835.01_0a_10			
07/28/01 11:37a	103,815	reference.311987.710-0004-55300-US-U-	
31835.01_0a_11			
07/28/01 11:37a	84,242	reference.311987.710-0004-55300-US-U-	
31835.01_0a_12			
07/28/01 11:36a	97,483	reference.311987.710-0004-55300-US-U-	
31835.01_0a_13			
07/28/01 11:36a	82,595	reference.311987.710-0004-55300-US-U-	
31835.01_0a_14			
07/28/01 11:36a	111,149	reference.311987.710-0004-55300-US-U-	
31835.01_0a_15			
07/28/01 11:35a	93,763	reference.311987.710-0004-55300-US-U-	
31835.01_0a_16			
07/28/01 11:35a	75,545	reference.311987.710-0004-55300-US-U-	
31835.01_0a_17			
07/28/01 11:35a	90,795	reference.311987.710-0004-55300-US-U-	
31835.01_0a_18			
07/28/01 11:38a	5,065,095	reference.311987.710-0004-55300-US-U-31835.01_10	
07/28/01 11:37a	5,333,829	reference.311987.710-0004-55300-US-U-31835.01_11	
07/28/01 11:37a	5,567,905	reference.311987.710-0004-55300-US-U-31835.01_12	
07/28/01 11:37a	5,536,744	reference.311987.710-0004-55300-US-U-31835.01_13	
07/28/01 11:36a	6,147,069	reference.311987.710-0004-55300-US-U-31835.01_14	
07/28/01 11:36a	4,939,635	reference.311987.710-0004-55300-US-U-31835.01_15	
07/28/01 11:35a	4,891,438	reference.311987.710-0004-55300-US-U-31835.01_16	
07/28/01 11:35a	5,410,676	reference.311987.710-0004-55300-US-U-31835.01_17	
07/28/01 11:35a	4,161,439	reference.311987.710-0004-55300-US-U-31835.01_18	
08/13/01 08:22p	410,644	reference.311987a.710-0004-55300-US-U-31835.01_01	
08/13/01 08:22p	31,109	reference.311987a.710-0004-55300-US-U-	
31835.01_0a_01			
07/28/01 11:34a	7,207,054	reference.311988.710-0004-55300-US-U-31835.01_01	
07/28/01 11:34a	7,110,660	reference.311988.710-0004-55300-US-U-31835.01_02	
07/28/01 11:33a	3,164,871	reference.311988.710-0004-55300-US-U-31835.01_03	
07/28/01 11:34a	69,888	reference.311988.710-0004-55300-US-U-	
31835.01_0a_01			
07/28/01 11:34a	61,254	reference.311988.710-0004-55300-US-U-	
31835.01_0a_02			
07/28/01 11:33a	31,600	reference.311988.710-0004-55300-US-U-	
31835.01_0a_03			
08/13/01 08:22p	79,225	reference.311988a.710-0004-55300-US-U-31835.01_01	
08/13/01 08:22p	839	reference.311988a.710-0004-55300-US-U-	
31835.01_0a_01			
08/01/01 06:25p	5,131,023	reference.3708.710-0004-55300-US-U-31835.01_01	
08/01/01 05:39p	4,708,075	reference.3708.710-0004-55300-US-U-31835.01_02	
08/01/01 05:17p	4,634,274	reference.3708.710-0004-55300-US-U-31835.01_03	
08/01/01 05:17p	4,657,712	reference.3708.710-0004-55300-US-U-31835.01_04	
08/01/01 05:18p	5,799,032	reference.3708.710-0004-55300-US-U-31835.01_05	
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08/01/01 05:20p	4,366,624	reference.3708.710-0004-55300-US-U-31835.01_07	
08/01/01 05:20p	3,909,036	reference.3708.710-0004-55300-US-U-31835.01_08	
08/01/01 05:21p	3,895,191	reference.3708.710-0004-55300-US-U-31835.01_09	
08/01/01 05:32p	100,392	reference.3708.710-0004-55300-US-U-31835.01_0a_01	
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08/01/01 05:33p	137,242	reference.3708.710-0004-55300-US-U-31835.01_0a_03	
08/01/01 05:34p	128,170	reference.3708.710-0004-55300-US-U-31835.01_0a_04	
08/01/01 05:35p	72,675	reference.3708.710-0004-55300-US-U-31835.01_0a_05	
07/30/01 07:14p	120,982	reference.3708.710-0004-55300-US-U-31835.01_0a_06	
07/30/01 07:26p	117,826	reference.3708.710-0004-55300-US-U-31835.01_0a_07	
07/30/01 07:37p	136,747	reference.3708.710-0004-55300-US-U-31835.01_0a_08	
07/30/01 07:49p	129,196	reference.3708.710-0004-55300-US-U-31835.01_0a_09	
07/30/01 08:00p	132,742	reference.3708.710-0004-55300-US-U-31835.01_0a_10	

File Create Date	File Size	File Name	CD#31
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07/30/01 08:47p	167,576	reference.3708.710-0004-55300-US-U-31835.01_0a_13	
07/30/01 09:03p	132,071	reference.3708.710-0004-55300-US-U-31835.01_0a_14	
07/30/01 09:18p	114,018	reference.3708.710-0004-55300-US-U-31835.01_0a_15	
07/30/01 09:20p	20,747	reference.3708.710-0004-55300-US-U-31835.01_0a_16	
08/01/01 05:22p	4,065,071	reference.3708.710-0004-55300-US-U-31835.01_0a_10	
08/01/01 05:23p	4,275,867	reference.3708.710-0004-55300-US-U-31835.01_11	
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08/01/01 05:29p	572,220	reference.3708.710-0004-55300-US-U-31835.01_16	
08/13/01 08:22p	539,475	reference.3708a.710-0004-55300-US-U-31835.01_01	
08/13/01 08:22p	28,298	reference.3708a.710-0004-55300-US-U-31835.01_0a_01	
07/25/01 07:14p	5,370,990	reference.3769.710-0004-55300-US-U-31835.01_01	
08/01/01 06:49p	5,285,989	reference.3769.710-0004-55300-US-U-31835.01_02	
08/01/01 06:52p	4,750,205	reference.3769.710-0004-55300-US-U-31835.01_03	
07/25/01 07:12p	5,606,690	reference.3769.710-0004-55300-US-U-31835.01_04	
07/25/01 07:12p	5,164,219	reference.3769.710-0004-55300-US-U-31835.01_05	
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07/25/01 07:13p	162,726	reference.3769.710-0004-55300-US-U-31835.01_0a_02	
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FIELD OF THE INVENTION

The present invention relates to over 100,000 isolated polynucleotides from plants that include a complete coding sequence, or a fragment thereof, that is expressed. In addition, the present invention relates to the polypeptide or protein corresponding to the coding sequence of these polynucleotides. The present invention also relates to isolated polynucleotides that represent regulatory regions of genes. The present invention also relates to isolated polynucleotides that represent untranslated regions of genes. The present invention further relates to the use of these isolated polynucleotides and polypeptides and proteins.

BACKGROUND OF THE INVENTION

There are more than 300,000 species of plants. They show a wide diversity of forms, ranging from delicate liverworts, adapted for life in a damp habitat, to cacti, capable of surviving in the desert. The plant kingdom includes herbaceous plants, such as corn, whose life cycle is measured in months, to the giant redwood tree, which can live for thousands of years. This diversity reflects the adaptations of plants to survive in a wide range of habitats. This is seen most clearly in the flowering plants (phylum Angiospermophyta), which are the most numerous, with over 250,000 species. They are also the most widespread, being found from the tropics to the arctic.

The process of plant breeding involving man's intervention in natural breeding and selection is some 20,000 years old. It has produced remarkable advances in adapting existing species to serve new purposes. The world's economics was largely based on the successes of agriculture for most of these 20,000 years.

Plant breeding involves choosing parents, making crosses to allow recombination of gene (alleles) and searching for and selecting improved forms. Success depends on the genes/alleles available, the combinations required and the ability to create and find the correct combinations necessary to give the desired properties to the plant. Molecular genetics technologies are now capable of providing new genes, new alleles and the means of creating and selecting plants with the new, desired characteristics.

When the molecular and genetic basis for different plant characteristics are understood, a wide variety of polynucleotides, both endogenous polynucleotides and created variants,

polypeptides, cells, and whole organisms, can be exploited to engineer old and new plant traits in a vast range of organisms including plants. These traits can range from the observable morphological characteristics, through adaptation to specific environments to biochemical composition and to molecules that the plants (organisms) exude. Such engineering can involve tailoring existing traits, such as increasing the production of taxol in yew trees, to combining traits from two different plants into a single organism, such as inserting the drought tolerance of a cactus into a corn plant. Molecular and genetic knowledge also allows the creation of new traits. For example, the production of chemicals and pharmaceuticals that are not native to particular species or the plant kingdom as a whole.

The application reports the inventions Applicants have discovered to build a foundation of scientific understanding of plant genomes to achieve these aims. These inventions include polynucleotide and polypeptide sequences, and data relating to where and when the genes are differentially expressed and phenotypic observations resulting from either aberrant gene activation or disruption. How these data are transformed into a scientific understanding of plant biology and the control of traits from a genetic perspective also is explained by the instant application. Applications of these discoveries to create new prototypes and products in the field of chemical, pharmaceutical, food, feed, and fiber production are described herein as well.

The achievements described in this application were possible because of the results from a cluster of technologies, a genomic engine, depicted below in Schematic 1, that allows information on each gene to be integrated to provide a more comprehensive understanding of gene structure and function and the deployment of genes and gene components to make new products.

I. THE DISCOVERIES OF THE INSTANT APPLICATION

Applicants have isolated and identified over one hundred thousand genes, gene components and their products and thousands of promoters. Specific genes were isolated and/or characterized from arabidopsis, soybean, maize, wheat and rice. These species were selected because of their economic value and scientific importance and were deliberately chosen to include representatives of the evolutionary divergent dicotyledonous and monocotyledonous

groups of the plant kingdom. The number of genes characterized in this application represents a large proportion of all the genes in these plant species.

The techniques used initially to isolate and characterize most of the genes, namely sequencing of full-length cDNAs, were deliberately chosen to provide information on complete coding sequences and on the complete sequences of their protein products.

Gene components and products the Applicants have identified include exons, introns, promoters, coding sequences, antisense sequences, terminators and other regulatory sequences. The exons are characterized by the proteins they encode and arabidopsis promoters are characterized by their position in the genomic DNA relative to where mRNA synthesis begins and in what cells and to what extent they promote mRNA synthesis.

Further exploitation of molecular genetics technologies has helped the Applicants to understand the functions and characteristics of each gene and their role in a plant. Three powerful molecular genetics approaches were used to this end:

- (a) Analyses of the phenotypic changes when the particular gene sequence is interrupted or activated differentially; (arabidopsis)
- (b) Analyses of in what plant organs, to what extent, and in response to what environmental signals mRNA is synthesized from the gene; (arabidopsis and maize) and
- (c) Analysis of the gene sequence and its relatives. (all species)

These were conducted using the genomics engine depicted in Figure 1 that allows information on each gene to be integrated to provide a more comprehensive understanding of gene structure and function and linkage to potential products.

The species arabidopsis was used extensively in these studies for several reasons: (1) the complete genomic sequence, though poorly annotated in terms of gene recognition, was being produced and published by others and (2) genetic experiments to determine the role of the genes in planta are much quicker to complete.

The phenotypic tables, MA tables, and reference tables and sequence tables indicate the results of these analyses and thus the specific functions and characteristics that are ascribed to the genes and gene components and products.

Schematic 1

A GENOMICS ENGINE

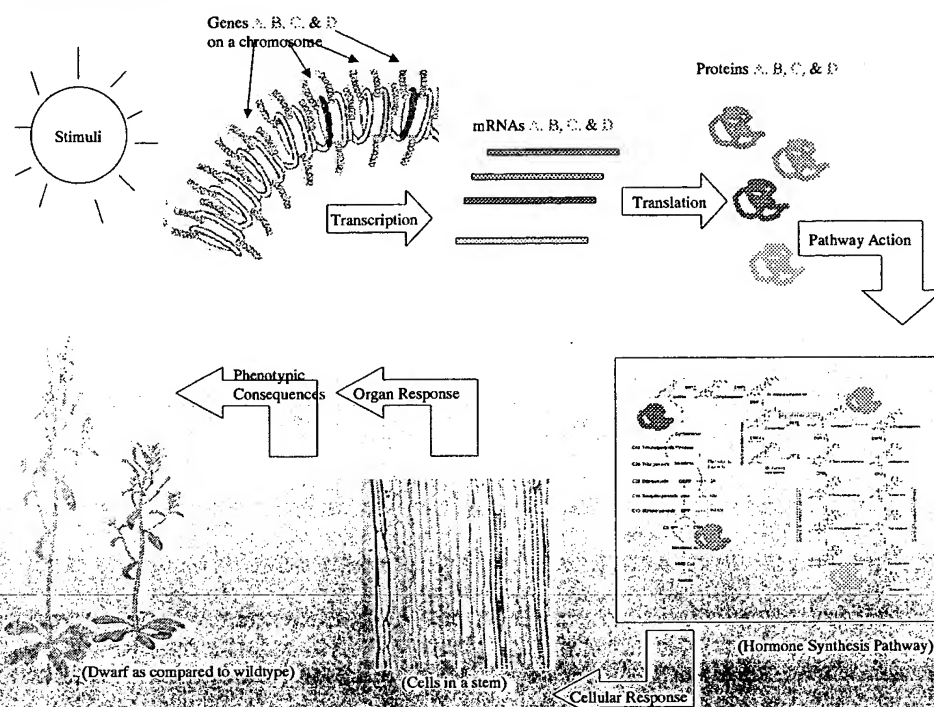
II. INTEGRATION OF DISCOVERIES TO PROVIDE SCIENTIFIC UNDERSTANDING

From the discoveries made, Applicants have deduced the biochemical activities, pathways, cellular roles, and developmental and physiological processes that can be modulated using these components. These are discussed and summarized in sections based on the gene functions characteristics from the analyses and role in determining phenotypes. These sections illustrate and emphasize that each gene, gene component or product influences biochemical activities, cells or organisms in complex ways, from which there can be many phenotypic consequences.

An illustration of how the discoveries on gene structure, function, expression and phenotypic observation can be integrated together to understand complex phenotypes is provided

in schematic 2. This sort of understanding enables conclusions to be made as to how the genes, gene components and product are useful for changing the properties of plants and other organisms. This example also illustrates how single gene changes in, for example, a metabolic pathway can cause gross phenotypic changes.

Schematic 2



Schematic 2. The figure illustrates how genes A, B, C and D are activated by internal stimuli and then their mRNA transcripts translated into proteins. These proteins are enzymes in three different but linked pathways. All three pathways are activated by the same stimuli. One of them, depicted by the green and light blue proteins determines the levels of a hormone in the shoot meristems causes cells to expand. This cell expansion leads to a longer stem and a taller plant. Genes A & C are therefore useful for controlling plant height and stem strength. The other two pathways would lead to other phenotypic characteristics.

Furthermore, the development and properties of one part of plant can be interconnected with other parts. The dependence of shoot and leaf development on root cells is a classic example. Here, shoot growth and development require nutrients supplied from roots, so the protein complement of root cells can affect plant development, including flowers and seed production. Similarly, root development is dependent on the products of photosynthesis from leaves. Therefore, proteins in leaves can influence root developmental physiology and biochemistry.

Thus, the following sections describe both the functions and characteristics of the genes, gene components and products and also the multiplicity of biochemical activities, cellular

functions, and the developmental and physiological processes influenced by them. The sections also describe examples of commercial products that can be realized from the inventions.

A. Analyses To Reveal Function And *In Vivo* Roles Of Single Genes In One Plant Species

The genomics engine has focused on individual genes to reveal the multiple functions or characteristics that are associated to each gene, gene components and products of the instant invention in the living plant. For example, the biochemical activity of a protein is deduced based on its similarity to a protein of known function. In this case, the protein may be ascribed with, for example, an oxidase activity. Where and when this same protein is active can be uncovered from differential expression experiments, which show that the mRNA encoding the protein is differentially expressed in response to drought and in seeds but not roots. The gene disruption experiments reveal that absence of the same protein causes embryo lethality.

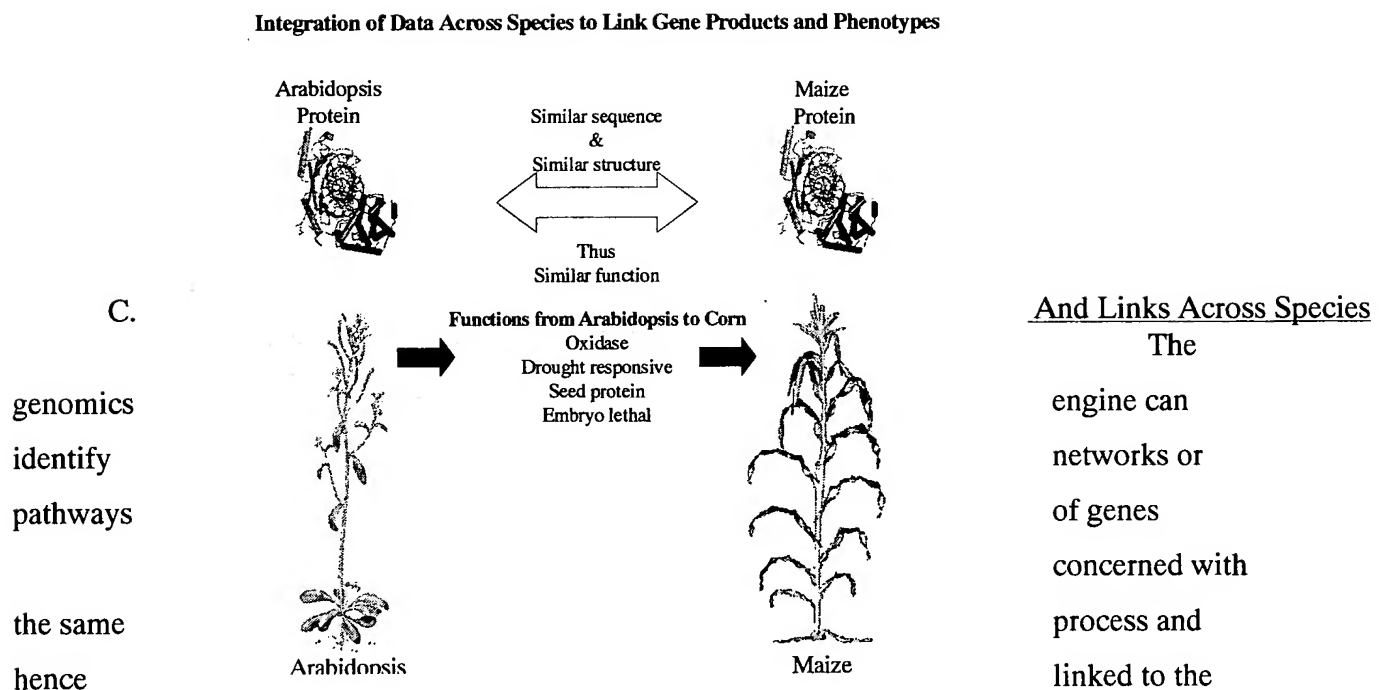
Thus, this protein is characterized as a seed protein and drought-responsive oxidase that is critical for embryo viability.

B. Analyses To Reveal Function And Roles Of Single Genes In Different Species

The genomics engine has also been used to extrapolate knowledge from one species to many plant species. For example, proteins from different species, capable of performing identical or similar functions, preserve many features of amino acid sequence and structure during evolution. Complete protein sequences have been compared and contrasted within and between species to determine the functionally vital domains and signatures characteristic of each of the proteins that is the subject of this application. Thus, functions and characteristics of arabidopsis proteins have been extrapolated to proteins containing similar domains and signatures of corn, soybean, rice and wheat and by implication to all other (plant) species.

Schematic 3 provides an example. Two proteins with related structures, one from corn, a monocot, and one from arabidopsis, a dicot, have been concluded to be orthologs. The known characteristics of the arabidopsis protein (seed protein, drought responsive oxidase) can then be attributed to the corn protein.

Schmatic 3.



same phenotype(s). Genes specifying functions of the same pathway or developmental environmental responses are frequently co-regulated i.e. they are regulated by mechanisms that result in coincident increases or decreases for all gene members in the group. The Applicants have divided the genes of arabidopsis and maize into such co-regulated groups on the basis of their expression patterns and the function of each group has been deduced. This process has

provided considerable insight into the function and role of thousands of the plant genes in diverse species included in this application.

D. Applications Of Applicant's Discoveries

It will be appreciated while reading the sections that the different experimental molecular genetic approaches focused on different aspects of the pathway from gene and gene product through to the properties of tissues, organs and whole organisms growing in specific environments. For each endogenous gene, these pathways are delineated within the existing biology of the species. However, Applicants' inventions allow gene components or products to be mixed and matched to create new genes and placed in other cellular contexts and species, to exhibit new combinations of functions and characteristics not found in nature, or to enhance and modify existing ones. For instance, gene components can be used to achieve expression of a specific protein in a new cell type to introduce new biochemical activities, cellular attributes or developmental and physiological processes. Such cell-specific targeting can be achieved by combining polynucleotides encoding proteins with any one of a large array of promoters to facilitate synthesis of proteins in a selective set of plant cells. This emphasizes that each gene, component and protein can be used to cause multiple and different phenotypic effects depending on the biological context. The utilities are therefore not limited to the existing in vivo roles of the genes, gene components, and gene products.

While the genes, gene components and products disclosed herein can act alone, combinations are useful to modify or modulate different traits. Useful combinations include different polynucleotides and/or gene components or products that have (1) an effect in the same or similar developmental or biochemical pathways; (2) similar biological activities; (3) similar transcription profiles; or (4) similar physiological consequences.

Of particular interest are the transcription factors and key factors in regulatory transduction pathways, which are able to control entire pathways, segments of pathways or large groups of functionally related genes. Therefore, manipulation of such proteins, alone or in combination is especially useful for altering phenotypes or biochemical activities in plants. Because interactions exist between hormone, nutrition, and developmental pathways, combinations of genes and/or gene products from these pathways also are useful to produce more complex changes. In addition to using polynucleotides having similar transcription profiles

and/or biological activities, useful combinations include polynucleotides that may exhibit different transcription profiles but which participate in common or overlapping pathways. Also, polynucleotides encoding selected enzymes can be combined in novel ways in a plant to create new metabolic pathways and hence new metabolic products.

The utilities of the various genes, gene components and products of the Application are described below in the sections entitled as follows:

I. Organ Affecting Genes, Gene Components, Products (Including Differentiation Function)

I.A. Root Genes, Gene Components And Products

I.A.1. Root Genes, Gene Components And Products

I.A.2. Root Hair Genes, Gene Components And Products

I.B. Leaf Genes, Gene Components And Products

I.B.1. Leaf Genes, Gene Components And Products

I.B.2. Trichome Genes And Gene Components

I.B.3. Chloroplast Genes And Gene Components

I.C. Reproduction Genes, Gene Components And Products

I.C.1. Reproduction Genes, Gene Components And Products

I.C.2. Ovule Genes, Gene Components And Products

I.C.3. Seed And Fruit Development Genes, Gene Components And Products

I.D. Development Genes, Gene Components And Products

I.D.1. Imbibition and Germination Responsive Genes, Gene Components And Products

I.D.2. Early Seedling Phase Genes, Gene Components And Products

I.D.3. Size and Stature Genes, Gene Components And Products

I.D.4. Shoot-Apical Meristem Genes, Gene Components And Products

I.D.5. Vegetative-Phase Specific Responsive Genes, Gene Components And Products

II. Hormones Responsive Genes, Gene Components And Products

II.A. Abscissic Acid Responsive Genes, Gene Components And Products

II.B. Auxin Responsive Genes, Gene Components And Products

II.C. Brassinosteroid Responsive Genes, Gene Components And Products

II.D. Cytokinin Responsive Genes, Gene Components And Products

II.E. Gibberellic Acid Responsive Genes, Gene Components And Products

III. Metabolism Affecting Genes, Gene Components And Products

III.A. Nitrogen Responsive Genes, Gene Components And Products

III.B. Circadian Rhythm Responsive Genes, Gene Components And Products

III.C. Blue Light (Phototropism) Responsive Genes, Gene Components And Products

III.D. Co2 Responsive Genes, Gene Components And Products

III.E. Mitochondria Electron Transport Genes, Gene Components And Products

III.F. Protein Degradation Genes, Gene Components And Products

III.G. Carotenogenesis Responsive Genes, Gene Components And Products

IV. Viability Genes, Gene Components And Products

IV.A. Viability Genes, Gene Components And Products

IV.B. Histone Deacetylase (Axel) Responsive Genes, Gene Components And Products

V. Stress Responsive Genes, Gene Components And Products

V.A. Cold Responsive Genes, Gene Components And Products

V.B. Heat Responsive Genes, Gene Components And Products

V.C. Drought Responsive Genes, Gene Components And Products

V.D. Wounding Responsive Genes, Gene Components And Products

V.E. Methyl Jasmonate Responsive Genes, Gene Components And Products

V.F. Reactive Oxygen Responsive Genes, Gene Components And H2O2 Products

V.G. Salicylic Acid Responsive Genes, Gene Components And Products

V.H. Nitric Oxide Responsive Genes, Gene Components And Products
V.I. Osmotic Stress Responsive Genes, Gene Components And Products
V.J. Aluminum Responsive Genes, Gene Components And Products
V.K. Cadmium Responsive Genes, Gene Components And Products
V.L. Disease Responsive Genes, Gene Components And Products
V.M. Defense Responsive Genes, Gene Components And Products
V.N. Iron Responsive Genes, Gene Components And Products
V.O. Shade Responsive Genes, Gene Components And Products
V.P. Sulfur Responsive Genes, Gene Components And Products
V.Q. Zinc Responsive Genes, Gene Components And Products

VI. Enhanced Foods

VII. Pharmaceutical Products

VIII. Precursors Of Industrial Scale Compounds

IX. Promoters As Sentinels

SUMMARY OF THE INVENTION

The present invention comprises polynucleotides, such as complete cDNA sequences and/or sequences of genomic DNA encompassing complete genes, fragments of genes, and/or regulatory elements of genes and/or regions with other functions and/or intergenic regions, hereinafter collectively referred to as Sequence-Determined DNA Fragments (SDFs) or sometimes collectively referred to as "genes or gene components", or sometimes as "genes, gene components or products", from different plant species, particularly corn, wheat, soybean, rice and *Arabidopsis thaliana*, and other plants and or mutants, variants, fragments or fusions of said SDFs and polypeptides or proteins derived therefrom. In some instances, the SDFs span the entirety of a protein-coding segment. In some instances, the entirety of an mRNA is represented. Other objects of the invention that are also represented by SDFs of the invention are control sequences, such as, but not limited to, promoters. Complements of any sequence of the invention are also considered part of the invention.

Other objects of the invention are polynucleotides comprising exon sequences, polynucleotides comprising intron sequences, polynucleotides comprising introns together with exons, intron/exon junction sequences, 5' untranslated sequences, and 3' untranslated sequences of the SDFs of the present invention. Polynucleotides representing the joinder of any exons described herein, in any arrangement, for example, to produce a sequence encoding any desirable amino acid sequence are within the scope of the invention.

The present invention also resides in probes useful for isolating and identifying nucleic acids that hybridize to an SDF of the invention. The probes can be of any length, but more typically are 12-2000 nucleotides in length; more typically, 15 to 200 nucleotides long; even more typically, 18 to 100 nucleotides long.

Yet another object of the invention is a method of isolating and/or identifying nucleic acids using the following steps:

- (a) contacting a probe of the instant invention with a polynucleotide sample under conditions that permit hybridization and formation of a polynucleotide duplex; and
- (b) detecting and/or isolating the duplex of step (a).

The conditions for hybridization can be from low to moderate to high stringency conditions. The sample can include a polynucleotide having a sequence unique in a plant genome. Probes and

methods of the invention are useful, for example, without limitation, for mapping of genetic traits and/or for positional cloning of a desired fragment of genomic DNA.

Probes and methods of the invention can also be used for detecting alternatively spliced messages within a species. Probes and methods of the invention can further be used to detect or isolate related genes in other plant species using genomic DNA (gDNA) and/or cDNA libraries. In some instances, especially when longer probes and low to moderate stringency hybridization conditions are used, the probe will hybridize to a plurality of cDNA and/or gDNA sequences of a plant. This approach is useful for isolating representatives of gene families which are identifiable by possession of a common functional domain in the gene product or which have common cis-acting regulatory sequences. This approach is also useful for identifying orthologous genes from other organisms.

The present invention also resides in constructs for modulating the expression of the genes comprised of all or a fragment of an SDF. The constructs comprise all or a fragment of the expressed SDF, or of a complementary sequence. Examples of constructs include ribozymes comprising RNA encoded by an SDF or by a sequence complementary thereto, antisense constructs, constructs comprising coding regions or parts thereof, constructs comprising promoters, introns, untranslated regions, scaffold attachment regions, methylating regions, enhancing or reducing regions, DNA and chromatin conformation modifying sequences, etc. Such constructs can be constructed using viral, plasmid, bacterial artificial chromosomes (BACs), plasmid artificial chromosomes (PACs), autonomous plant plasmids, plant artificial chromosomes or other types of vectors and exist in the plant as autonomous replicating sequences or as DNA integrated into the genome. When inserted into a host cell the construct is, preferably, functionally integrated with, or operatively linked to, a heterologous polynucleotide. For instance, a coding region from an SDF might be operably linked to a promoter that is functional in a plant.

The present invention also resides in host cells, including bacterial or yeast cells or plant cells, and plants that harbor constructs such as described above. Another aspect of the invention relates to methods for modulating expression of specific genes in plants by expression of the coding sequence of the constructs, by regulation of expression of one or more endogenous genes in a plant or by suppression of expression of the polynucleotides of the invention in a plant. Methods of

modulation of gene expression include without limitation (1) inserting into a host cell additional copies of a polynucleotide comprising a coding sequence; (2) modulating an endogenous promoter in a host cell; (3) inserting antisense or ribozyme constructs into a host cell and (4) inserting into a host cell a polynucleotide comprising a sequence encoding a variant, fragment, or fusion of the native polypeptides of the instant invention.

DETAILED DESCRIPTION OF THE INVENTION

I. DESCRIPTION OF THE TABLES

As noted above, the Applicants have obtained and analyzed an extensive amount of information on a large number of genes by use of the Ceres Genomic Engine to determine. This information can be categorized into three basic types:

- A. Sequence Information for the Inventions
- B. Transcriptional Information for the Inventions
- C. Phenotypic Information for the Inventions

I.A. SEQUENCE INFORMATION

To harness the potential of the plant genome, Applicants began by elucidating a large number gene sequences, including the sequences of gene components and products, and analyzing the data. The list of sequences and associated data are presented in the Reference and Sequence Tables of the present application (sometimes referred to as the "REF" and "SEQ" Tables). The Reference and Sequence tables include:

- cDNA sequence;
- coding sequence;
- 5' & 3' UTR;
- transcription start sites;
- exon and intron boundaries in genomic sequence; and
- protein sequence.

The Reference and Sequence Tables also include computer-based, comparative analyses between the protein sequences of the invention and sequences with known function. Proteins with similar sequences typically exhibit similar biochemical activities. The Reference table notes:

- sequences of known function that are similar to the Applicants' proteins; and
- biochemical activity that is associated with Applicants' proteins.

Also, by analyzing the protein sequences, Applicants were able to group the protein sequences into groups, wherein all the sequences in the group contain a signature sequence. The groups are presented in the Protein Group Table. The signature sequences are reported in the Protein Group Table. More detailed analyses of the signature sequences are shown in the Protein Group Matrix Table.

To identify gene components and products, Applicants took a cDNA/coding sequence approach. That is, Applicants initiated their studies either by isolating cDNAs and determining their sequences experimentally, or by identifying the coding sequence from genomic sequence with the aid of predictive algorithms. The cDNA sequences and coding sequences also are referred to as "Maximum Length Sequences" in the Reference tables. The cDNA and coding sequences were given this designation to indicate these were the maximum length of coding sequences identified by Applicants.

Due to this cDNA/coding sequence focus of the present application, the Reference and Sequence Tables were organized around cDNA and coding sequences. Each of these Maximum Length Sequences was assigned a unique identifier: Ceres Sequence ID NO, which is reported in the Tables.

All data that relate to these Maximum Length Sequences are grouped together, including 5' & 3' UTRs; transcription start sites; exon and intron boundaries in genomic sequence; protein sequence, etc.

Below, a more detailed explanation of the organization of the Reference and Sequence Tables and how the data in the tables were generated is provided.

a. cDNA

Applicants have ascertained the sequences of mRNAs from different organisms by reverse transcription of mRNA to DNA, which was cloned and then sequenced. These complementary DNA or cDNA sequences also are referred to as Maximum Length Sequences in the Reference Tables, which contain details on each of the sequences in the Sequence Tables.

Each sequence was assigned a Pat. Appln. Sequence ID NO: and an internal Ceres Sequence ID NO: as reported in the Reference Table, the section labeled "(Ac) cDNA Sequence." An example is shown below:

Max Len. Seq. :

(Ac) cDNA Sequence

- Pat. Appln. Sequence ID NO: 174538

- Ceres Sequence ID NO: 5673127

Both numbers are included in the Sequence Table to aid in tracking of information, as shown below:

<210> 174538 (Pat. Appln. Sequence ID NO:)

<211> 1846

<212> DNA (genomic)

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(1846)

<223> Ceres Seq. ID no. 5673127

<220>

<221> misc_feature

<222> ()..()

<223> n is a, c, t, g, unknown, or other

<400> 174538

acaagaacaa caaaacagag gaagaagaag aagaagatga agcttctggc tctgtttcca 60

tttctagcga tcgtgatcca actcagctgt... etc.

The Sequence and Reference Tables are divided into sections by organism: *Arabidopsis thaliana*, *Brassica napus*, *Glycine max*, *Zea mays*, *Triticum aestivum*; and *Oryza sativa*.

b. Coding Sequence

The coding sequence portion of the cDNA was identified by using computer-based algorithms and comparative biology. The sequence of each coding sequence of the cDNA is reported in the "PolyP Sequence" section of the Reference Tables, which are also divided into sections by organism. An example shown below for the peptides that relate to the cDNA sequence above

PolyP Sequence

- Pat. Appln. Sequence ID NO 174539
- Ceres Sequence ID NO 5673128
- Loc. Sequence ID NO 174538: @ 1 nt.
- Loc. Sig. P. Sequence ID NO 174539: @ 37 aa.

The polypeptide sequence can be found in the Sequence Tables by either the Pat. Appln. Sequence ID NO or by the Ceres Sequence ID NO: as shown below:

<210> 174539 (Pat. Appln. Sequence ID NO)

<211> 443

<212> PRT

<213> Arabidopsis thaliana

<220>

<221> peptide

<222> (1)..(443)

<223> Ceres Seq. ID no. 5673128

<220>

<221> misc_feature

<222> ()..()

<223> xaa is any aa, unknown or other

<400> 174539

Thr Arg Thr Thr Lys Gln Arg Lys Lys Lys Lys Met Lys Leu Leu

1 5 10 15

Ala Leu Phe Pro Phe Leu Ala Ile ... etc.

25

The PolyP section also indicates where the coding region begins in the Maximum Length Sequence. More than one coding region may be indicated for a single polypeptide due to multiple potential translation start codons. Coding sequences were identified also by analyzing genomic sequence by predictive algorithms, without the actual cloning of a cDNA molecule from a mRNA. By default, the cDNA sequence was considered the same as the coding sequence, when Maximum Length Sequence was spliced together from a genomic annotation.

c. 5' and 3' UTR

The 5' UTR can be identified as any sequence 5' of the initiating codon of the coding sequence in the cDNA sequence. Similarly, the 3' UTR is any sequence 3' of the terminating codon of the coding sequence.

d. Transcription Start Sites

Applicants cloned a number of cDNAs that encompassed the same coding sequence but comprised 5' UTRs of different lengths. These different lengths revealed the multiple transcription start sites of the gene that corresponded to the cDNA. These multiple transcription start sites are reported in the "Sequence # w. TSS" section" of the Reference Tables.

e. Exons & Introns

Alignment of the cDNA sequences and coding portions to genomic sequence permitted Applicants to pinpoint the exon/intron boundaries. These boundaries are identified in the Reference Table under the "Pub gDNA" section. That section reports the gi number of the public BAC

sequence that contains the introns and exons of interest. An example is shown below:

Max Len. Seq. :

Pub gDNA:

gi No: 1000000005

Gen. seq. in cDNA:

115777 ... 115448 by Method #1

115105 ... 114911 by Method #1

114822 ... 114700 by Method #1

114588 ... 114386 by Method #1

114295 ... 113851 by Method #1

115777 ... 115448 by Method #2

115105 ... 114911 by Method #2

114822 ... 114700 by Method #2

114588 ... 114386 by Method #2

114295 ... 113851 by Method #2

115813 ... 115448 by Method #3

115105 ... 114911 by Method #3

114822 ... 114700 by Method #3

114588 ... 114386 by Method #3

114295 ... 113337 by Method #3

(Ac) cDNA Sequence

All the gi numbers were assigned by Genbank to track the public genomic sequences except:

gi 1000000001

gi 1000000002

gi 1000000003

gi 1000000004; and

gi 1000000005.

These gi numbers were assigned by Applicants to the five *Arabidopsis* chromosome

sequences that were published by the Institute of Genome Research (TIGR). Gi 1000000001 corresponds to chromosome 1, Gi 1000000002 to chromosome 2, etc.

The method of annotation is indicated as well as any similar public annotations.

f. Promoters & Terminators

Promoter sequences are 5' of the translational start site in a gene; more typically, 5' of the transcriptional start site or sites. Terminator sequences are 3' of the translational terminator codon; more typically, 3' of the end of the 3' UTR.

For even more specifics of the Reference and Sequence Tables, see the section below titled "Brief Description of the Tables."

**I.B. TRANSCRIPTIONAL (DIFFERENTIAL EXPRESSION) INFORMATION-
INTRODUCTION TO DIFFERENTIAL EXPRESSION DATA &
ANALYSES**

A major way that a cell controls its response to internal or external stimuli is by regulating the rate of transcription of specific genes. For example, the differentiation of cells during organogenesis into forms characteristic of the organ is associated with the selective activation and repression of large numbers of genes. Thus, specific organs, tissues and cells are functionally distinct due to the different populations of mRNAs and protein products they possess. Internal signals program the selective activation and repression programs. For example, internally synthesized hormones produce such signals. The level of hormone can be raised by increasing the level of transcription of genes encoding proteins concerned with hormone synthesis.

To measure how a cell reacts to internal and/or external stimuli, individual mRNA levels can be measured and used as an indicator for the extent of transcription of the gene. Cells can be exposed to a stimulus, and mRNA can be isolated and assayed at different time points after stimulation. The mRNA from the stimulated cells can be compared to control cells that were not stimulated. The mRNA levels of particular Maximum Length Sequences that are higher in the stimulated cell versus the control indicate a stimulus-specific response of the cell. The same is true of mRNA levels that are lower in stimulated cells versus the control condition.

Similar studies can be performed with cells taken from an organism with a defined mutation in their

genome as compared with cells without the mutation. Altered mRNA levels in the mutated cells indicate how the mutation causes transcriptional changes. These transcriptional changes are associated with the phenotype that the mutated cells exhibit that is different from the phenotype exhibited by the control cells.

Applicants have utilized microarray techniques to measure the levels of mRNAs in cells from mutant plants, stimulated plants, and/or selected from specific organs. The differential expression of various genes in the samples versus controls are listed in the MA_diff Tables. Applicants have analyzed the differential data to identify genes whose mRNA transcription levels are positively correlated. From these analyses, Applicants were able to group different genes together whose transcription patterns are correlated. The results of the analyses are reported in the MA_clust Tables.

a. Experimental Detail

A microarray is a small solid support, usually the size of a microscope slide, onto which a number of polynucleotides have been spotted onto or synthesized in distinct positions on the slide (also referred to as a chip). Typically, the polynucleotides are spotted in a grid formation. The polynucleotides can either be Maximum Length Sequences or shorter synthetic oligonucleotides, whose sequence is complementary to specific Maximum Length Sequence entities. A typical chip format is as follows:

Oligo #1	Oligo #2	Oligo #3
Oligo #4	Oligo #5	Oligo #6
Oligo #7	Oligo #8	Oligo #9

For Applicants' experiments, samples were hybridized to the chips using the "two-color" microarray procedure. A fluorescent dye was used to label cDNA reverse-transcribed from mRNA isolated from cells that had been stimulated, mutated, or collected from a specific organ or developmental stage. A second fluorescent dye of another color was used to label cDNA prepared from control cells.

The two differentially-labeled cDNAs were mixed together. Microarray chips were

incubated with this mixture. For Applicants' experiments the two dyes that are used are Cy3, which fluoresces in the red color range, and Cy5, which fluoresces in the green/blue color range. Thus, if:

- cDNA#1 binds to Oligo #1;
- cDNA#1 from the sample is labeled red;
- cDNA#1 from the control is labeled green, and
- cDNA#1 is in both the sample and control,

then cDNA#1 from both the sample and control will bind to Oligo#1 on the chip. If the sample has 10 times more cDNA#1 than the control, then 10 times more of the cDNA#1 would be hybridized to Oligo#1. Thus, the spot on the chip with Oligo#1 spot would look red.

Oligo #1	Oligo #2	Oligo #3
Oligo #4	Oligo #5	Oligo #6
Oligo #7	Oligo #8	Oligo #9

If the situation were reversed, the spot would appear green. If the sample has approximately the same amount of cDNA#1 as the control, then the Oligo#1 spot on the chip would look yellow. These color differentials are measured quantitatively and used to deduce the relative concentration of mRNAs from individual genes in particular samples.

b. MA_Diff Data Table

To generate data, Applicants labeled and hybridized the sample and control mRNA in duplicate experiments. One chip was exposed to a mixture of cDNAs from both a sample and control, where the sample cDNA was labeled with Cy3, and the control was labeled with Cy5 dye. For the second labeling and chip hybridization experiments, the fluorescent labels were reversed; that is, the Cy5 dye for the sample, and the Cy3 dye for the control.

Whether Cy5 or Cy3 was used to label the sample, the fluorescence produced by the sample was divided by the fluorescence of the control. A cDNA was determined to be differentially expressed in response to the stimulus in question if a statistically-significantly ration difference in the sample versus the control was measured by both chip hybridization experiments.

The MA₋diff tables show which cDNA were significantly up-regulated as designated by a “+” and which were significantly down-regulated as designated by a “-“ for each pair of chips using the same sample and control.

I.C. PHENOTYPIC INFORMATION

One means of determining the phenotypic effect of a gene is either to insert extra active copies of the gene or coding sequence, or to disrupt an existing copy of the gene in a cell or organism and measure the effects of the genetic change on one or more phenotypic characters or traits. “Knock-in” is used herein to refer to insertion of additional active copies of a gene or coding sequence. “Knock-out” refers to a plant where an endogenous gene(s) is disrupted. Applicants have used both methods of addition or disruption to determine the phenotypic effects of gene or gene components or products, and have thereby discovered the function of the genes and their utilities.

1. Knock-in results

The coding sequence of a desired protein can be functionally linked to a heterologous promoter to facilitate expression. Here, Applicants have operably linked a number of coding sequences to either one of the promoters listed below:

<u>GFP Pattern</u>	<u>Specific Promoter activity</u>	<u>Plant Line Descriptor</u>
Root epidermis / mostly toward the lower region of root (more intense than CS9094)	Specific to the root basal region.	Root basal
Root-endodermis/cortex (initials sharp); shoot-mesophyll of one leaf, sharp guard cell marking. New leaf petioles near tip of primary inflorescence; floral stems; in flowers at base of sepal, anther stems, and pistil	Specific to the root endodermis-cortex region, leaf petiole, and flowers.	Root/Petiole/Flowers
Broad root exp. (some dermal, some cortical, some vascular); shoot apex. Faintly in petiole; stem	Specific to root and stem.	Root/Stem1
High expression in stem, excluded from 1st true leaves/High in root. Faint expression in stem	Specific to stem and root.	Root/Stem2

<u>GFP Pattern</u>	<u>Specific Promoter activity</u>	<u>Plant Line Descriptor</u>
Shoot meristem / whole root region; little bit on cotyledons. Base of leaves(axillary meristem?); base of sepals; inflorescence meristem; small amount in unfertilized pistil.	Specific to roots, shoot meristem, base of leaves and flowers.	Root/Stem/Leaves/Flowers
root tip vascular initials; vascular system throughout plant; Bud petal vasculature and pistil septum; Flower petal vasculature; Flower pistil septum; Pre fertilization ovules; Post fertilization ovule at chalazal end; Developing seed (young, maturing siliques); Seed coat and young embryos. GFP not observed in mature embryos.	Specific to vascular systems.	Vascular/Ovule/Young Seed/Embryo
Flower, sepal / vascular tissue of root, stem, and cotyledons. Stems of new flowers; vasculature or petals, anthers, sepals, and pistil/silique; Vasculature throughout seedling: root, hypocotyl, petioles, stem, cotyledons, first true leaves; Rosette vasculature; Cauline leaf vasculature; Bud pedicel vasculature; Flower vasculature: (sepals, petals, filaments, pistil); Bud vasculature (sepal, petal, filament, pistil); Funiculus in both flower and bud; Some possible seed coat expression; Silique funiculus; Very faint fluorescence in mature embryo (auto fluorescence perhaps);	Specific to flowers, seed and vasculature.	Flowers/Seed/Vasculature/Embryo
Root expression - primarily in cortex (upper region of the root). No shoot expression	Specific to root.	Roots2
Root expression - less intense in whole root of young seedling. Shoot apical meristem; organ primordia in SAM region.	Specific to root and shoot apical meristem.	Root/SAM
Root epidermis/tip; shoot epidermis/vascular; leaf epidermis; expression in developing seed/ovule - mature embryo; Primary and lateral root cortex; Very strong in root cap; Base of flower bud and epidermis of carpels; Base of flower, epidermis of filaments, epidermis of carpels; Trichomes; Weak (hardly detectable) gfp expression in vasculature throughout seedling; Strong expression in trichomes; POST- fertilization SEED only; GFP strength increases as	Specific to seed and to epidermal layers of roots, shoots and leaves.	Seed/Epidermis/Ovary/Fruit

<u>GFP Pattern</u>	<u>Specific Promoter activity</u>	<u>Plant Line Descriptor</u>
silique matures; Weak at suspensor end of the embryo; GFP observed in seed coat; Root and post fertilization seed specific gfp expression; Expression in seed coat.		
Young root dermis; dermal/cortical?/vascular in older root; general (epidermal?) shoot expression; ovules. some in sepals; vasculature of stem	Specific to roots, shoots, and ovules.	Roots/Shoots/Ovule
Vascular tissue of root; Meristem tissues: axillary meristems, floral meristems, base of flowers/sepals; Weak expression in hypocotyl, petiole and cotyledon vasculature..	Specific to root structural leaf vascular region and to floral buds and axillary meristem	Vasculature/Meristem

The chimeric constructs were transformed into *Arabidopsis thaliana*. The resulting transformed lines were screened to determine what phenotypes were changed due to introduced transgene. The phenotype changes, relative to the control, are reported in the Knock-in tables.

2. Knock-out Results

Knock-out plants in *Arabidopsis thaliana* were created by inserting a polynucleotide tag into the genome. The location of the tag was identified using primers to the tag sequence and isolation of the plant genomic sequence that flanks the tag using a variation of the polymerase chain reaction. The plants were generated using the procedure described in Feldmann et al., (1987) Molec. Gen. Genet. 208: 1-9; Feldmann (1991) Plant Journal, 1:71-83 and Forsthoefel et al., (1992) Aust. J. Plant Physiol. 19:353-366.. On average, the population of plants that was screened had ~1.5 to 2 tags. Generally, the number of tags ranged from 1 to greater than 5.

The polynucleotide tags were classified as either incorporated within a gene, or between two genes. The data in the Knock-out Table indicates which plants have a tag(s) causing a disruption in a gene, or a disruption between genes.

a. Disruption in a Gene

For the sake of this analysis, the tag was considered to be causing a disruption in a gene when the tag was located:

- 1) less than 501 upstream of the transcriptional start site;
- 2) less than 701 upstream of the translational initiation codon;
- 3) between the translational initiation and termination codons of the gene,
- 4) less than 301 downstream of the translational stop codon; or
- 5) less than 151 downstream of a transcriptional termination site.

By this definition, a tag can be inserted in two genes. For example, if two genes have only 700 nucleotides between the translational termination codon of one gene and the translational initiation codon of the other gene, the tag can be inserted into the terminator of one gene and the promoter of the other gene according to the definition above.

Genomic annotations by the method OCKHAM-OCDNA identify the transcriptional start and stop site of a gene.

b. Disruption between Genes

When a tag causes a disruption between two genes, either or both genes can be affected. Typically, a tag can affect a gene if it disrupts the genome at a location 3000 nt downstream to the start codon of a gene. More typically, insertions found 1000- 2000 nt upstream (5'), or 750-1000 nt downstream (3') could be expected to disrupt expression.

c. More Than One Insert

A plant can have multiple tags. If a mutant phenotype is observed, then it can be attributed to any one or all of the tags.

I.D. BRIEF DESCRIPTION OF THE INDIVIDUAL TABLES

1. Reference and Sequence Tables

The sequences of exemplary SDFs and polypeptides corresponding to the coding sequences of the instant invention are described in the Reference and Sequence Tables (sometimes referred to as the REF and SEQ Tables. The Reference Table refers to a number of "Maximum Length Sequences" or "MLS." Each MLS corresponds to the longest cDNA obtained, either by cloning or by the prediction from genomic sequence. The sequence of the MLS is the cDNA sequence as described in the Av subsection of the Reference Table.

The Reference Table includes the following information relating to each MLS:

- I. cDNA Sequence
 - A. 5' UTR
 - B. Coding Sequence
 - C. 3' UTR
- II. Genomic Sequence
 - A. Exons
 - B. Introns
 - C. Promoters
- III. Link of cDNA Sequences to Clone IDs
- IV. Multiple Transcription Start Sites
- V. Polypeptide Sequences
 - A. Signal Peptide
 - B. Domains
 - C. Related Polypeptides
- VI. Related Polynucleotide Sequences

I. cDNA SEQUENCE

The Reference Table indicates which sequence in the Sequence Table represents the sequence of each MLS. The MLS sequence can comprise 5' and 3' UTR as well as coding sequences. In addition, specific cDNA clone numbers also are included in the Reference Table when the MLS sequence relates to a specific cDNA clone.

A. 5' UTR

The location of the 5' UTR can be determined by comparing the most 5' MLS sequence with the corresponding genomic sequence as indicated in the Reference Table. The sequence that matches, beginning at any of the transcriptional start sites and ending at the last nucleotide before any of the translational start sites corresponds to the 5' UTR.

B. Coding Region

The coding region is the sequence in any open reading frame found in the MLS. Coding regions of interest are indicated in the PolyP SEQ subsection of the Reference Table.

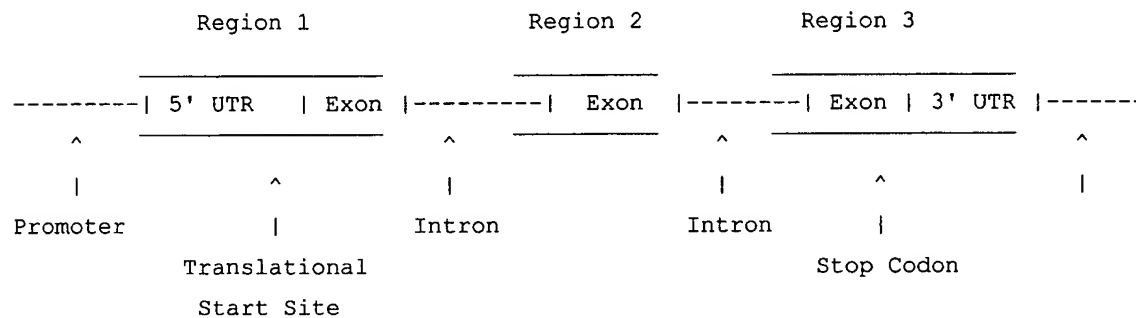
C. 3' UTR

The location of the 3' UTR can be determined by comparing the most 3' MLS sequence with the corresponding genomic sequence as indicated in the Reference Table. The sequence

that matches, beginning at the translational stop site and ending at the last nucleotide of the MLS corresponds to the 3' UTR.

II. GENOMIC SEQUENCE

Further, the Reference Table indicates the specific "gi" number of the genomic sequence if the sequence resides in a public databank. For each genomic sequence, Reference tables indicate which regions are included in the MLS. These regions can include the 5' and 3' UTRs as well as the coding sequence of the MLS. See, for example, the scheme below:



The Reference Table reports the first and last base of each region that are included in an MLS sequence. An example is shown below:

gi No. 47000:

37102 ... 37497

37593 ... 37925

The numbers indicate that the MLS contains the following sequences from two regions of gi No. 47000; a first region including bases 37102-37497, and a second region including bases 37593-37925.

A. EXON SEQUENCES

The location of the exons can be determined by comparing the sequence of the regions from the genomic sequences with the corresponding MLS sequence as indicated by the Reference Table.

i. INITIAL EXON

To determine the location of the initial exon, information from the

- (1) polypeptide sequence section;
- (2) cDNA polynucleotide section; and
- (3) the genomic sequence section

of the Reference Table is used. First, the polypeptide section will indicate where the translational start site is located in the MLS sequence. The MLS sequence can be matched to the genomic sequence that corresponds to the MLS. Based on the match between the MLS and corresponding genomic sequences, the location of the translational start site can be determined in one of the regions of the genomic sequence. The location of this translational start site is the start of the first exon.

Generally, the last base of the exon of the corresponding genomic region, in which the translational start site was located, will represent the end of the initial exon. In some cases, the initial exon will end with a stop codon, when the initial exon is the only exon.

In the case when sequences representing the MLS are in the positive strand of the corresponding genomic sequence, the last base will be a larger number than the first base. When the sequences representing the MLS are in the negative strand of the corresponding genomic sequence, then the last base will be a smaller number than the first base.

ii. INTERNAL EXONS

Except for the regions that comprise the 5' and 3' UTRs, initial exon, and terminal exon, the remaining genomic regions that match the MLS sequence are the internal exons. Specifically, the bases defining the boundaries of the remaining regions also define the intron/exon junctions of the internal exons.

iii. TERMINAL EXON

As with the initial exon, the location of the terminal exon is determined with information from the

- (1) polypeptide sequence section;
- (2) cDNA polynucleotide section; and
- (3) the genomic sequence section

of the Reference Table. The polypeptide section will indicate where the stop codon is located in the MLS sequence. The MLS sequence can be matched to the corresponding genomic sequence. Based on the match between MLS and corresponding genomic sequences, the location of the stop codon can be determined in one of the regions of the genomic sequence. The location of this stop codon is the end of the terminal exon. Generally, the first base of the exon of the corresponding genomic region that matches the cDNA sequence, in which the stop codon was located, will represent the beginning of the terminal exon. In some cases, the translational start site will represent the start of the terminal exon, which will be the only exon.

In the case when the MLS sequences are in the positive strand of the corresponding genomic sequence, the last base will be a larger number than the first base. When the MLS sequences are in the negative strand of the corresponding genomic sequence, then the last base will be a smaller number than the first base.

B. INTRON SEQUENCES

In addition, the introns corresponding to the MLS are defined by identifying the genomic sequence located between the regions where the genomic sequence comprises exons. Thus, introns are defined as starting one base downstream of a genomic region comprising an exon, and end one base upstream from a genomic region comprising an exon.

C. PROMOTER SEQUENCES

As indicated below, promoter sequences corresponding to the MLS are defined as sequences upstream of the first exon; more usually, as sequences upstream of the first of multiple transcription start sites; even more usually as sequences about 2,000 nucleotides upstream of the first of multiple transcription start sites.

III. LINK of cDNA SEQUENCES to CLONE IDs

As noted above, the Reference Table identifies the cDNA clone(s) that relate to each MLS. The MLS sequence can be longer than the sequences included in the cDNA clones. In such a case, the Reference Table indicates the region of the MLS that is included in the clone. If

either the 5' or 3' termini of the cDNA clone sequence is the same as the MLS sequence, no mention will be made.

IV. Multiple Transcription Start Sites

Initiation of transcription can occur at a number of sites of the gene. The Reference Table indicates the possible multiple transcription sites for each gene. In the Reference Table, the location of the transcription start sites can be either a positive or negative number.

The positions indicated by positive numbers refer to the transcription start sites as located in the MLS sequence. The negative numbers indicate the transcription start site within the genomic sequence that corresponds to the MLS.

To determine the location of the transcription start sites with the negative numbers, the MLS sequence is aligned with the corresponding genomic sequence. In the instances when a public genomic sequence is referenced, the relevant corresponding genomic sequence can be found by direct reference to the nucleotide sequence indicated by the "gi" number shown in the public genomic DNA section of the Reference Table. When the position is a negative number, the transcription start site is located in the corresponding genomic sequence upstream of the base that matches the beginning of the MLS sequence in the alignment. The negative number is relative to the first base of the MLS sequence which matches the genomic sequence corresponding to the relevant "gi" number.

In the instances when no public genomic DNA is referenced, the relevant nucleotide sequence for alignment is the nucleotide sequence associated with the amino acid sequence designated by "gi" number of the later PolyP SEQ subsection.

V. Polypeptide Sequences

The PolyP SEQ subsection lists SEQ ID NOs and Ceres SEQ ID NO for polypeptide sequences corresponding to the coding sequence of the MLS sequence and the location of the translational start site with the coding sequence of the MLS sequence.

The MLS sequence can have multiple translational start sites and can be capable of producing more than one polypeptide sequence.

A. Signal Peptide

The Reference tables also indicate in subsection (B) the cleavage site of the putative signal peptide of the polypeptide corresponding to the coding sequence of the MLS sequence. Typically, signal peptide coding sequences comprise a sequence encoding the first residue of the polypeptide to the cleavage site residue.

B. Domains

Subsection (C) provides information regarding identified domains (where present) within the polypeptide and (where present) a name for the polypeptide domain.

C. Related Polypeptides

Subsection (Dp) provides (where present) information concerning amino acid sequences that are found to be related and have some percentage of sequence identity to the polypeptide sequences of the Reference and Sequence Tables. These related sequences are identified by a "gi" number.

VI. Related Polynucleotide Sequences

Subsection (Dn) provides polynucleotide sequences (where present) that are related to and have some percentage of sequence identity to the MLS or corresponding genomic sequence.

Abbreviation	Description
Max Len. Seq.	Maximum Length Sequence
rel to	Related to
Clone Ids	Clone ID numbers
Pub gDNA	Public Genomic DNA
gi No.	gi number
Gen. Seq. in Cdna	Genomic Sequence in cDNA (Each region for a single gene prediction is listed on a separate line. In the case of multiple gene predictions, the

Abbreviation	Description
	group of regions relating to a single prediction are separated by a blank line)
(Ac) cDNA SEQ	cDNA sequence
- Pat. Appln. SEQ ID NO	Patent Application SEQ ID NO:
- Ceres SEQ ID NO: 1673877	Ceres SEQ ID NO:
- SEQ # w. TSS	Location within the cDNA sequence, SEQ ID NO:, of Transcription Start Sites which are listed below
- Clone ID #: # -> #	Clone ID comprises bases # to # of the cDNA Sequence
PolyP SEQ	Polypeptide Sequence
- Pat. Appln. SEQ ID NO:	Patent Application SEQ ID NO:
- Ceres SEQ ID NO	Ceres SEQ ID NO:
- Loc. SEQ ID NO: @ nt.	Location of translational start site in cDNA of SEQ ID NO: at nucleotide number
(C) Pred. PP Nom. & Annot.	Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (Title)	Name of Domain
- Loc. SEQ ID NO #: # -> # aa.	Location of the domain within the polypeptide of SEQ ID NO: from # to # amino acid residues.
(Dp) Rel. AA SEQ	Related Amino Acid Sequences
- Align. NO	Alignment number
- gi No	Gi number
- Desp.	Description
- % Idnt.	Percent identity
- Align. Len.	Alignment Length
- Loc. SEQ ID NO: # -> # aa	Location within SEQ ID NO: from # to #

Abbreviation	Description
	amino acid residue.

2. Protein Group Table

This table indicates groups of proteins that share a signature sequence (also referred to as a consensus sequence). The Protein group also referred to as the Ortholog group is named by the peptide ID with which all members were compared. Each group contains sequences that were included at the 10^{-50} , 10^{-30} , and 10^{-10} p-value cutoffs. For each group, the peptide ID and at which cutoff the peptide was included into the group. The same peptide ID may be included in the group three times as peptide ID 50, peptide ID 30 and peptide ID 10. The data indicates that peptide ID was included in the group when the threshold was either 10^{-50} , 10^{-30} , or 10^{-10} . All the peptide IDs that are followed by "50" were included in the protein group when the e-value cutoff was 10^{-50} . All the peptide IDs that are followed by either "30" or "50" were included in the protein group when the threshold e-value was 10^{-30} . All the peptide IDs that are followed by "10", "30" or "50" were included in the protein group when 10^{-10} was used as the e-value cutoff. At the end of each protein group is a list of the consensus sequence that proteins share at the 10^{-50} , 10^{-30} , or 10^{-10} . The consensus sequence contains both lower-case and upper-case letters. The upper-case letters represent the standard one-letter amino acid abbreviations. The lower case letters represent classes of amino acids:

- "t" refers to tiny amino acids, which are specifically alanine, glycine, serine and threonine.
- "p" refers to polar amino acids, which are specifically, asparagine and glutamine
- "n" refers to negatively charged amino acids, which are specifically, aspartic acid and glutamic acid
- "+" refers to positively charged residues, which are specifically, lysine, arginine, and histidine
- "r" refers to aromatic residues, which are specifically, phenylalanine, tyrosine, and tryptophan,
- "a" refers to aliphatic residues, which are specifically, isoleucine, valine, leucine, and methonine

3. Protein Group Matrix Table

In addition to each consensus sequence, Applicants have generated a scoring matrix to provide further description of the consensus sequence. The first row of each matrix indicates the

residue position in the consensus sequence. The matrix reports number of occurrences of all the amino acids that were found in the group members for every residue position of the signature sequence. The matrix also indicates for each residue position, how many different organisms were found to have a polypeptide in the group that included a residue at the relevant position. The last line of the matrix indicates all the amino acids that were found at each position of the consensus.

4. MA_DIFF TABLE

The MA_diff Table presents the results of the differential expression experiments for the mRNAs, as reported by their corresponding cDNA ID number, that were differentially transcribed under a particular set of conditions as compared to a control sample. The cDNA ID numbers correspond to those utilized in the Reference and Sequence Tables. Increases in mRNA abundance levels in experimental plants versus the controls are denoted with the plus sign (+). Likewise, reductions in mRNA abundance levels in the experimental plants are denoted with the minus (-) sign.

The Table is organized according to each set of experimental conditions, which are denoted by the term "Expt ID:" followed by a particular number. The table below links each Expt ID with a short description of the experiment and the parameters.

For each experiment ID a method of the normalization is specified. "Method: 2" represents normalization by median the goal of the method is to adjust the ratios by a factor so that the median of the ratio distribution is 1. Method 3 is the normalization procedure conducted by Agilent Technologies, Inc. Palo Alto, California, USA.

The MA_diff Table also specifies the specific parameters and the experiment number (e.g. 107871) used in compiling the data. The experiment numbers are referenced in the appropriate utility/functions sections herein. The background threshold was set to "BKG_Threshold=X" to reduce the effect of the background on the signal.

Finally, the Table includes reference to an "Organism_ID" number. This number refers to the cDNA spotted on the chip were similar to Arabidopsis thaliana (3769) sequences or whether the oligo used for the chips were similar to Zea mays (311987) sequences.

5. MA_diff (Experiment) Table

The following Table summarizes the experimental procedures utilized for the differential expression experiments, each experiment being identified by a unique "Expt ID" number.

Example No.	Experiment short name	genome	EXPT_ID	Value	PARAMETER	UNITS
3ii	3642-1	Arabidopsis	108512	3746-1	Plant Line	Hours

3n	Arab_0.001%_MeJA_1	Arabidopsis	108568	Aerial	Tissue	Tissue
				0.001%_MeJA	Treatment	Compound
				1	Timepoint	Hours
3n	Arab_0.001%_MeJA_1	Arabidopsis	108569	Aerial	Tissue	Tissue
				6	Timepoint	Hours
				0.001%_MeJA	Treatment	Compound
3j	Arab_0.1uM_Epi-Brass_1	Arabidopsis	108580	Aerial	Tissue	Tissue
				1	Timepoint	Hours
				0.1uM_Brassinosteroid	Treatment	Compound
3j	Arab_0.1uM_Epi-Brass_1	Arabidopsis	108581	Aerial	Tissue	Tissue
				6	Timepoint	Hours
				0.1uM_Brassinosteroid	Treatment	Compound
3g	Arab_100uM_ABA_1	Arabidopsis	108560	Aerial	Tissue	Tissue
				1	Timepoint	Hours
				100uM_ABA	Treatment	Compound
3g	Arab_100uM_ABA_1	Arabidopsis	108561	Aerial	Tissue	Tissue
				100uM_ABA	Treatment	Compound
				6	Timepoint	Hours
3I	Arab_100uM_BA_1	Arabidopsis	108566	Aerial	Tissue	Tissue
				1	Timepoint	Hours
				100uM_BA	Treatment	Compound
3I	Arab_100uM_BA_1	Arabidopsis	108567	Aerial	Tissue	Tissue
				100uM_BA	Treatment	Compound
				6	Timepoint	Hours
3k	Arab_100uM_GA3_1	Arabidopsis	108562	Aerial	Tissue	Tissue
				1	Timepoint	Hours
				100uM_GA3	Treatment	Compound
3k	Arab_100uM_GA3_1	Arabidopsis	108563	Aerial	Tissue	Tissue
				100uM_GA3	Treatment	Compound

				6	Timepoint	Hours
3h	Arab_100uM_NAA_1	Arabidopsis	108564	Aerial	Tissue	Tissue
				1	Timepoint	Hours
				100uM NAA	Treatment	Compound
3h	Arab_100uM_NAA_1	Arabidopsis	108565	Aerial	Tissue	Tissue
				100uM NAA	Treatment	Compound
				6	Timepoint	Hours
3r	Arab_20%_PEG_1	Arabidopsis	108570	Aerial	Tissue	Tissue
				1	Timepoint	Hours
				20%PEG	Treatment	Compound
3r	Arab_20%_PEG_1	Arabidopsis	108571	Aerial	Tissue	Tissue
				20%PEG	Treatment	Compound
				6	Timepoint	Hours
3o	Arab_2mM_SA_1	Arabidopsis	108586	Aerial	Tissue	Tissue
				2mM SA	Treatment	Compound
				1	Timepoint	Hours
3o	Arab_2mM_SA_1	Arabidopsis	108587	Aerial	Tissue	Tissue
				6	Timepoint	Hours
				2mM SA	Treatment	Compound
3u	Arab_5mM_H2O2_1	Arabidopsis	108582	Aerial	Tissue	Tissue
				1	Timepoint	Hours
				5mM H2O2	Treatment	Compound
3u	Arab_5mM_H2O2_1	Arabidopsis	108583	Aerial	Tissue	Tissue
				5mM H2O2	Treatment	Compound
				6	Timepoint	Hours
3v	Arab_5mM_NaNP_1	Arabidopsis	108584	Aerial	Tissue	Tissue
				1	Timepoint	Hours
				5mM NaNP	Treatment	Compound
3v	Arab_5mM_NaNP_1	Arabidopsis	108585	Aerial	Tissue	Tissue
				5mM NaNP	Treatment	Compound
				6	Timepoint	Hours
3t	Arab_Cold_1	Arabidopsis	108578	Aerial	Tissue	Tissue
				Cold	Treatment	Compound

				1	Timepoint	Hours
3t	Arab_Cold_1	Arabidopsis	108579	Aerial	Tissue	Tissue
				6	Timepoint	Hours
				Cold	Treatment	Compound
3g	Arab_Drought_1	Arabidopsis	108572	Aerial	Tissue	Tissue
				1	Timepoint	Hours
				Drought	Treatment	Compound
3g	Arab_Drought_1	Arabidopsis	108573	Aerial	Tissue	Tissue
				Drought	Treatment	Compound
				6	Timepoint	Hours
3s	Arab_Heat_1	Arabidopsis	108576	Aerial	Tissue	Tissue
				1	Timepoint	Hours
				Heat (42 deg C)	Treatment	Compound
3s	Arab_Heat_1	Arabidopsis	108577	Aerial	Tissue	Tissue
				Heat (42 deg C)	Treatment	Compound
				6	Timepoint	Hours
3aa (ovule)	Arab_Ler-pi ovule_1	Arabidopsis	108595	Ler_pi	Plant Line	Hours
				Ovule	Tissue	Tissue
3b	Arab_Ler-rhl root_1	Arabidopsis	108594	Ler_rhl	Plant Line	Hours
				Root	Tissue	Tissue
3l	Arab_NO3_H-to-L_1	Arabidopsis	108592	Aerial	Tissue	Tissue
				Low Nitrogen	Treatment	Compound
				12	Timepoint	Hours
3l	Arab_NO3_H-to-L_1	Arabidopsis	108593	Aerial	Tissue	Tissue
				24	Timepoint	Hours
				Low Nitrogen	Treatment	Compound
3l	Arab_NO3_L-to-H_1	Arabidopsis	108588	Aerial	Tissue	Tissue
				2	Timepoint	Hours
				Nitrogen	Treatment	Compound
3l	Arab_NO3_L-to-H_1	Arabidopsis	108589	Aerial	Tissue	Tissue
				Nitrogen	Treatment	Compound
				6	Timepoint	Hours
3l	Arab NO3 L-	Arabidopsis	108590	Aerial	Tissue	Tissue

	to-H 1					
				9	Timepoint	Hours
				Nitrogen	Treatment	Compound
3l	Arab_NO3_L- to-H 1	Arabidopsis	108591	Aerial	Tissue	Tissue
				Nitrogen	Treatment	Compound
				12	Timepoint	Hours
3p	Arab_Woundin g_1	Arabidopsis	108574	Aerial	Tissue	Tissue
				1	Timepoint	Hours
				Wounding	Treatment	Compound
3p	Arab_Woundin g_1	Arabidopsis	108575	Aerial	Tissue	Tissue
				Wounding	Treatment	Compound
				6	Timepoint	Hours
3o	Columbia/CS37 26 flower SA	Arabidopsis	108475	Columbia	species	Hours
				SA	Treatment	Compound
				5 weeks	Timepoint	Hours
3o	Columbia/CS37 26 flower SA	Arabidopsis	108476	CS3726	species	Hours
				5 weeks	Timepoint	Hours
				SA	Treatment	Compound
3p	Corn_0.001Per cent MeJA	Zea Mays	108555	Aerial	Tissue	Tissue
				24	Timepoint	Hours
				0.001%_MeJ A	Treatment	Compound
3j	Corn_0.1uM_B rassino Steroid	Zea Mays	108557	24	Timepoint	Hours
				Aerial	Tissue	Tissue
				0.1uM_Brassi no Steroid	Treatment	Compound
3g	Corn_100uM_ ABA	Zea Mays	108513	Aerial	Tissue	Tissue
				ABA	Treatment	Compound
				6	Timepoint	Hours
3g	Corn_100uM_ ABA	Zea Mays	108597	Aerial	Tissue	Tissue
				24	Timepoint	Hours
				100uM ABA	Treatment	Compound
3i	Corn_100uM_ BA	Zea Mays	108517	Aerial	Tissue	Tissue

				6	Timepoint	Hours
				BA	Treatment	Compound
3k	Corn_100uM_ GA3	Zea Mays	108519	Aerial	Tissue	Tissue
				100uM Giberillic Acid	Treatment	Compound
				1	Timepoint	Hours
3k	Corn_100uM_ GA3	Zea Mays	108520	Aerial	Tissue	Tissue
				6	Timepoint	Hours
				100uM Giberillic Acid	Treatment	Compound
3k	Corn_100uM_ GA3	Zea Mays	108521	Aerial	Tissue	Tissue
				100uM Giberillic Acid	Treatment	Compound
				12	Timepoint	Hours
3h	Corn_100uM_ NAA	Zea Mays	108516	Aerial	Tissue	Tissue
				NAA	Treatment	Compound
				6	Timepoint	Hours
3h	Corn_100uM_ NAA	Zea Mays	108554	Aerial	Tissue	Tissue
				24	Timepoint	Hours
				NAA	Treatment	Compound
3hh	Corn_1400- 6/S-17	Zea Mays	108598	Shoot apices	Tissue	Tissue
3r	Corn_150mM_ NaCl	Zea Mays	108541	Aerial	Tissue	Tissue
				1	Timepoint	Hours
				150mM NaCl	Treatment	Compound
3r	Corn_150mM_ NaCl	Zea Mays	108542	Aerial	Tissue	Tissue
				150mM NaCl	Treatment	Compound
				6	Timepoint	Hours
3r	Corn_150mM_ NaCl	Zea Mays	108553	Aerial	Tissue	Tissue
				24	Timepoint	Hours
				150mM NaCl	Treatment	Compound
3r	Corn 20% PE	Zea Mays	108539	Aerial	Tissue	Tissue

	G					
				1	Timepoint	Hours
				20%PEG	Treatment	Compound
3r	Corn_20%_PE G	Zea Mays	108540	Aerial	Tissue	Tissue
				20%PEG	Treatment	Compound
				6	Timepoint	Hours
3o	Corn_2mM_SA	Zea Mays	108515	Aerial	Tissue	Tissue
				SA	Treatment	Compound
				12	Timepoint	Hours
3o	Corn_2mM_SA	Zea Mays	108552	Aerial	Tissue	Tissue
				SA	Treatment	Compound
				24	Timepoint	Hours
3u	Corn_5mM_H2 O2	Zea Mays	108537	Aerial	Tissue	Tissue
				H2O2	Treatment	Compound
				1	Timepoint	Hours
3u	Corn_5mM_H2 O2	Zea Mays	108538	Aerial	Tissue	Tissue
				6	Timepoint	Hours
				H2O2	Treatment	Compound
3u	Corn_5mM_H2 O2	Zea Mays	108558	Aerial	Tissue	Tissue
				24	Timepoint	Hours
				H2O2	Treatment	Compound
3v	Corn_5mM_N O	Zea Mays	108526	Aerial	Tissue	Tissue
				NO	Treatment	Compound
				1	Timepoint	Hours
3v	Corn_5mM_N O	Zea Mays	108527	Aerial	Tissue	Tissue
				6	Timepoint	Hours
				NO	Treatment	Compound
3v	Corn_5mM_N O	Zea Mays	108559	Aerial	Tissue	Tissue
				12	Timepoint	Hours
				NO	Treatment	Compound
3t	Corn_Cold	Zea Mays	108533	Aerial	Tissue	Tissue
				1	Timepoint	Hours
				Cold	Treatment	Compound
3t	Corn_Cold	Zea Mays	108534	Aerial	Tissue	Tissue
				Cold	Treatment	Compound
				6	Timepoint	Hours

3q	Corn Drought	Zea Mays	108502	Drought	Treatment	Compound
				1	Timepoint	Hours
3q	Corn Drought	Zea Mays	108503	Drought	Treatment	Compound
				6	Timepoint	Hours
3q	Corn Drought	Zea Mays	108504	Drought	Treatment	Compound
				12	Timepoint	Hours
3q	Corn Drought	Zea Mays	108556	Drought	Treatment	Compound
				24	Timepoint	Hours
3s	Corn Heat	Zea Mays	108522	Aerial	Tissue	Tissue
				1	Timepoint	Hours
				Heat (42 deg C)	Treatment	Compound
3s	Corn Heat	Zea Mays	108523	Aerial	Tissue	Tissue
				6	Timepoint	Hours
				Heat (42 deg C)	Treatment	Compound
3gg	Corn_Imbibed Seeds	Zea Mays	108518	Imbibed	Treatment	Compound
				4	Age	days old
				Roots	Tissue	Tissue
3gg	Corn_Imbibed Seeds	Zea Mays	108528	Imbibed	Treatment	Compound
				Aerial	Tissue	Tissue
				5	Age	days old
3gg	Corn_Imbibed Seeds	Zea Mays	108529	Imbibed	Treatment	Compound
				5	Age	days old
				Root	Tissue	Tissue
3gg	Corn_Imbibed Seeds	Zea Mays	108530	Imbibed	Treatment	Compound
				Aerial	Tissue	Tissue
				6	Age	days old
3gg	Corn_Imbibed Seeds	Zea Mays	108531	Imbibed	Treatment	Compound
				6	Age	days old
				root	Tissue	Tissue
3gg	Corn_Imbibed Seeds	Zea Mays	108545	Imbibed	Treatment	Compound
				Aerial	Tissue	Tissue
				3	Age	days old
3gg	Corn_Imbibed Seeds	Zea Mays	108546	Imbibed	Treatment	Compound
				3	Age	days old

				Root	Tissue	Tissue
3gg	Corn_Imbibed Seeds	Zea Mays	108547	Imbibed	Treatment	Compound
				Aerial	Tissue	Tissue
				4	Age	days old
3gg	Corn_Imbibed_ Embryo_Endos perm	Zea Mays	108543	2	Age	days old
				Imbibed	Treatment	Compound
				Embryo	Tissue	Tissue
3gg	Corn_Imbibed_ Embryo_Endos perm	Zea Mays	108544	2	Age	days old
				Endosperm	Tissue	Tissue
				Imbibed	Treatment	Compound
3ee	Corn_Meristem	Zea Mays	108535	Root Meristem	Tissue	Tissue
				192	Timepoint	Hours
3ee	Corn_Meristem	Zea Mays	108536	Shoot Meristem	Tissue	Tissue
				192	Timepoint	Hours
3n	Corn_Nitrogen H to L	Zea Mays	108532	Roots	Tissue	Tissue
				Low Nitrogen	Treatment	Compound
				16	Timepoint	Hours
3n	Corn_Nitrogen H to L	Zea Mays	108548	Root	Tissue	Tissue
				Low Nitrogen	Treatment	Compound
				4	Timepoint	Hours
3m	Corn_Nitrogen L to H	Zea Mays	108549	Aerial	Tissue	Tissue
				0.166	Timepoint	Hours
				Nitrogen	Treatment	Compound
3m	Corn_Nitrogen L to H	Zea Mays	108550	Aerial	Tissue	Tissue
				Nitrogen	Treatment	Compound
				1.5	Timepoint	Hours
3m	Corn_Nitrogen L to H	Zea Mays	108551	Aerial	Tissue	Tissue
				3	Timepoint	Hours
				Nitrogen	Treatment	Compound
3ff	Corn_RT1	Zea Mays	108599	Unknown	Plant Line	Hours
				Root	Tissue	Tissue

3p	Corn_Woundin g	Zea Mays	108524	Aerial	Tissue	Tissue
				Wounding	Treatment	Compound
				1	Timepoint	Hours
3p	Corn_Woundin g	Zea Mays	108525	Aerial	Tissue	Tissue
				6	Timepoint	Hours
				Wounding	Treatment	Compound
3g	Drought_Flowe rs	Arabidopsis	108473	Flowers	Tissue	Tissue
				7 d	Timepoint	Hours
				Drought	Treatment	Compound
3g	Drought_Flowe rs	Arabidopsis	108474	Flowers	Tissue	Tissue
				Drought	Treatment	Compound
				8 d (1d- post_re- watering)	Timepoint	Hours
3k	GA Treated	Arabidopsis	108484	1	Timepoint	Hours
				1	Timepoint	Hours
3k	GA Treated	Arabidopsis	108485	6	Timepoint	Hours
				6	Timepoint	Hours
3k	GA Treated	Arabidopsis	108486	12	Timepoint	Hours
				12	Timepoint	Hours
3e	Germinating Seeds	Arabidopsis	108461	Day 1	Timepoint	Hours
3e	Germinating Seeds	Arabidopsis	108462	Day 2	Timepoint	Hours
3e	Germinating Seeds	Arabidopsis	108463	Day 3	Timepoint	Hours
3e	Germinating Seeds	Arabidopsis	108464	Day 4	Timepoint	Hours
3bb	Herbicide V3.1	Arabidopsis	108465	Round up	Treatment	Compound
				12	Timepoint	Hours
3bb	Herbicide V3.1	Arabidopsis	108466	Trimec	Treatment	Compound
				12	Timepoint	Hours
3bb	Herbicide V3.1	Arabidopsis	108467	Finale	Treatment	Compound
				12	Timepoint	Hours
3bb	Herbicide V3.1	Arabidopsis	108468	Glean	Treatment	Compound
				12	Timepoint	Hours
3bb	Herbicide v2	Arabidopsis	107871	Finale	Treatment	Compound
				4	Timepoint	Hours
3bb	Herbicide v2	Arabidopsis	107876	Finale	Treatment	Compound

				12	Timepoint	Hours
3bb	Herbicide_v2	Arabidopsis	107881	Glean	Treatment	Compound
				4	Timepoint	Hours
3bb	Herbicide_v2	Arabidopsis	107886	Trimec	Treatment	Compound
				4	Timepoint	Hours
3bb	Herbicide_v2	Arabidopsis	107891	Trimec	Treatment	Compound
				12	Timepoint	Hours
3bb	Herbicide_v2	Arabidopsis	107896	Round-up	Treatment	Compound
				4	Timepoint	Hours
3d	Trichome Inflorescences expt	Arabidopsis	108452	Hairy Influorescenc e #1	Tissue	Tissue
3o	SA treatment_1 hour	Arabidopsis	108471	Columbia	Species	Hours
				1	Timepoint	Hours
				SA	Treatment	Compound
3o	SA treatment_1 hour	Arabidopsis	108472	CS3726	Species	Hours
				1	Timepoint	Hours
				SA	Treatment	Compound
3o	SA treatment_4 hour	Arabidopsis	108469	columbia	Species	Hours
				4	Timepoint	Hours
				SA	Treatment	Compound
3o	SA treatment_4 hour	Arabidopsis	108470	CS3726	Species	Hours
				SA	Treatment	Compound
				4	Timepoint	Hours
3o	SA treatment_AJ	Arabidopsis	107953	50	Probe Amount	% of Standard Amount
				SA	Treatment	Compound
				24	Timepoint	Hours
				Clontech	Probe Type	Probe method
3o	SA treatment_AJ	Arabidopsis	107960	50	Probe Amount	% of Standard Amount
				SA	Treatment	Compound
				24	Timepoint	Hours
				Operon	Probe Type	Probe method
3o	SA treatment	Arabidopsis	108443	SA	Treatment	Compound

	24 hour					
				24	Timepoint	Hours
3o	SA_treatment 6 hour	Arabidopsis	108440	SA treatment 6 hour	Treatment	Compound
				CS3726	species	Hours
3o	SA_treatment 6 hour	Arabidopsis	108441	SA treatment 6 hour	Treatment	Compound
				Columbia	species	Hours
3l	Nitrogen High transition to Low	Arabidopsis	108454	10 min	Timepoint	Hours
3l	Nitrogen High transition to Low	Arabidopsis	108455	1 hr	Timepoint	Hours
3j	BR_Shoot Apices Expt	Arabidopsis	108478	dwf4-1	Plant Line	Hours
3j	BR_Shoot Apices Expt	Arabidopsis	108479	AOD4-4	Plant Line	Hours
3j	BR_Shoot Apices Expt	Arabidopsis	108480	Ws-2	Plant Line	Hours
				BL	Treatment	Compound
3j	BR_Shoot Apices Expt	Arabidopsis	108481	Ws-2	Plant Line	Hours
				BRZ	Treatment	Compound
3jj	Tissue Specific Expression	Arabidopsis	108429	green flower	Tissue	Tissue
				operon	Probe Type	Probe method
				50	Probe Amount	% of Standard Amount
3jj	Tissue Specific Expression	Arabidopsis	108430	white flower	Tissue	Tissue
				50	Probe Amount	% of Standard Amount
				operon	Probe Type	Probe method
3jj	Tissue Specific Expression	Arabidopsis	108431	flowers (bud)	Tissue	Tissue
				operon	Probe Type	Probe method
				50	Probe	% of

					Amount	Standard Amount
3c	Tissue Specific Expression	Arabidopsis	108436	5-10mm siliques	Tissue	Tissue
				33	Probe Amount	% of Standard Amount
				operon	Probe Type	Probe method
3c	Tissue Specific Expression	Arabidopsis	108437	<5mm siliques	Tissue	Tissue
				operon	Probe Type	Probe method
				33	Probe Amount	% of Standard Amount
3c	Tissue Specific Expression	Arabidopsis	108438	5wk siliques	Tissue	Tissue
				33	Probe Amount	% of Standard Amount
				operon	Probe Type	Probe method
3a	Tissue Specific Expression	Arabidopsis	108439	Roots (2wk)	Tissue	Tissue
				operon	Probe Type	Probe method
				33	Probe Amount	% of Standard Amount
3c	Tissue Specific Expression	Arabidopsis	108497	3 week Rossette leaves	Tissue	Tissue
				100	Probe Amount	% of Standard Amount
				operon	Probe Type	Probe method
3c	Tissue Specific Expression	Arabidopsis	108498	3-week stems	Tissue	Tissue
				operon	Probe Type	Probe method
				100	Probe Amount	% of Standard

						Amount
3dd	U.A.E. Knockout	Arabidopsis	108451	13B12	Plant Line	Hours
3q	Ws Arabidopsis Drought 2 days	Arabidopsis	108477	stems and leaves	Tissue	Tissue
				2 days	Timepoint	Hours
3q	Ws Arabidopsis Drought 4 days	Arabidopsis	108482	4 days	Timepoint	Hours
3q	Ws Arabidopsis Drought 6 days	Arabidopsis	108483	6 days	Timepoint	Hours
3cc	ap2-floral buds	Arabidopsis	108501	ap2 (Ler.)	Plant Line	Hours
				floral buds	Tissue	Tissue
3m	nitrogen-seed set	Arabidopsis	108487	0.5	Timepoint	Hours
3m	nitrogen-seed set	Arabidopsis	108488	2	Timepoint	Hours
3m	nitrogen-seed set	Arabidopsis	108489	4	Timepoint	Hours
3b	rhl mutant2	Arabidopsis	108433	mutant	Tissue	Tissue
3ee	root tips	Arabidopsis	108434	root tips	Tissue	Tissue
3f	stm mutants	Arabidopsis	108435	stem	Tissue	Tissue
	Aluminum		SMD 7304, SMD 7305			
	Axel		SMD 6654, SMD 6655			
	Cadium		SMD 7427, SMD 7428			
	Cauliflower		SMD 5329, SMD 5330			
	Chloroplast		SMD 8093, SMD 8094			
	Circadian		SMD 2344, SMD 2359, SMD 2361, SMD 2362,			

			SMD 2363, SMD 2364, SMD 2365, SMD 2366, SMD 2367, SMD 2368, SMD 3242			
	CO2		SMD7561, SMD 7562, SMD 7261, SMD 7263, SMD 3710, SMD 4649, SMD 4650			
	Disease		SMD 7342, SMD 7343			
	reactive oxygen		SMD 7523			
	Iron		SMD 7114, SMD 7115, SMD 7125			
	defense		SMD 8031, SMD 8032			
	Mitochondria- Electron Transport		SMD 8061, SMD 8063			
	NAA		SMD 3743,			

			SMD 3749, SMD 6338, SMD 6339			
	Nitrogen		SMD 3787, SMD 3789			
	Phototropism		SMD 4188, SMD 6617, SMD 6619			
	Shade		SMD 8130, SMD 7230			
	Sqn		SMD 7133, SMD 7137			
	Sulfur		SMD 8034, SMD 8035			
	Wounding		SMD 3714, SMD 3715			
	Zinc		SMD 7310, SMD 7311			

6. MA_Clusters Table

Microarray data was clustered using one of two methods: “complete linkage” or “nearest neighbor” analysis. These clustering methods are described in more detail elsewhere herein. The results of the clustering analysis are presented in the MA_clust table. The table is organized as follows:

“METHOD” refers to a method number which clustering method used.

“CL_METHOD_TYPE=TRUE” refers to complete linkage method.

“NN_METHOD_TYPE=TRUE” refers to the nearest neighbor method.

“FULL_NN_METHOD_TYPE=TRUE” refers to the nearest neighbor method, where no size limitation was placed on the cluster.

“PARAMETERS” refers to the parameters utilized for the analysis. The nature of these is also described in more detail elsewhere herein.

“ORGANISM” refers to the cDNA spotted on the chip were similar to *Arabidopsis thaliana* (3769) sequences or whether the oligo used for the chips were similar to *Zea mays* (311987) sequences.

Each cluster or group of cDNA is identified by a “Group #”, following which are the individual cDNA_Ids that are a member of that Group

7. **Knock-in Table**

The Knock-In Table presents the results of knock-in experiments wherein plants are grown from tissues transformed with a marker gene-containing insert and phenotypes are ascertained from the transformed plants. Each section of the Table relating to information on a new transformant begins with a heading “Knock-in phenotype in gene (cDNA_id):” followed by a number which represents the Ceres internal code for a proprietary cDNA sequence. The described transformant was prepared by procedures described herein, wherein the identified Ceres proprietary cDNA_id (corresponding to the cDNA_id in the Reference and Sequence Tables) was interrupted by the marker gene-containing insert. The following information is presented for each section.

- Parent plants used in cross – presents the id numbers of the parent plants which were crossed to produce the F1 generation plant for which a phenotype is described. The parent plant with the promoter is described by a plant line descriptor.
- Clone ID – presents the clone number of the Ceres proprietary clone which was the source of the cDNA_id.
- Phenotype ID – represents an internal identification code.
- Unique FI plant ID – represents the internal code for the F1 plant for which a phenotype is described.

- Assay – presents the type of growth analyzed (e.g. soil gross morphology), followed by the assay name which corresponds to the type/location of the tissue that was observed., the name of the assay conducted for which the result provided the identified phenotype.
- Phenotype – describes the phenotype noted for the F1 generation transformant.
- Notes – may provide additional information on the described phenotype for the transformant.

Each knock-in representing a transformant with an interruption in the identified cDNA_id may be correlated with more than one identified phenotype.

8. Knock-out Table

The Knock-Out Table presents the results of knock-out experiments wherein plants are grown from tissues transformed with a marker gene-containing insert wherein phenotypes are ascertained from the transformed plants. Each section of the Table relating to information on a new transformant begins with a heading “tail id:” representing an internal code. The following information is presented for each section.

br - provides another internal code for the experiment.

Phenotype_id - provides an identification number for the particular phenotype identified for the transformant.

assay - identifies the assay procedure utilized in the experiment to identify a phenotype for the transformant.

phenotype - represents an internal identification code.

ratio - represents a segregation ratio.

notes - lists any notes relevant to the identified phenotype.

Knock-out in-genes - Identifies the genes in which the tag has inserted

- 6) the less than 501 upstream of the transcriptional start site;
- 7) less than 701 upstream of the translational initiation codon;
- 8) between the translational initiation and termination codons of the gene,
- 9) less than 301 downstream of the translational stop codon; or

10) less than 151 downstream of a transcriptional termination site or a gene.
In this table the gene is identified by its cDNA ID number, the Ceres SEQ ID that is indicated in the (Ac) portion of the Reference tables. For each cDNA_id, the following information is provided:

- the cDNA_id number.
- in parenthesis, the cluster number of which the identified cDNA is a member.
- the "gDNA_Insert pos" representing the position of the insert in the corresponding gDNA sequence
- the gi number refers to the TIGR chromosome sequences for Arabidopsis.

Knock-out out of-genes: Identifies the Ceres cDNA proprietary sequences (noted by cDNA_id which are the same as those identified in the Reference and Sequence Tables) which are closest in position to the insert, both upstream and downstream from the insert. For each cDNA_id, the following information is provided:

- In the first parentheses, R indicates that the gene is to the right of the tag, L indicates that the gene is to right of the tag as the sequences is read left to right
- the cDNA_id number
- in next parentheses, the cluster number of which the identified cDNA is a member.
- the distance (in number of nucleotides) of the insert is upstream of the start of the gene annotation as described in the Reference Tables or downstream at the end the gene annotation.
- the "gDNA_Insert pos" representing the position of the insert in the corresponding gDNA sequence
- the gi number refers to the TIGR chromosome sequences for Arabidopsis.

9. Protein Domain Table

The Protein Domain table provides details concerning the protein domains noted in the Reference Table. The majority of the protein domain descriptions given in the Protein Domain Table are obtained from Prosite, (<http://www.expasy.ch/prosite/>), and Pfam, (<http://pfam.wustl.edu/browse.shtml>). Each description in The Table begins with the pfam and Prosite identifying numbers, the full name of the domain, and a detailed description, including biological and in vivo implications/functions for the domain, references which further describe such implications/functions, and references that describe tests/assays to measure the implications/functions.

10. Single Gene Functions & Utilities Table

The Single Gene Functions & Utilities Table describes particular utilities/functions of interest for individual genes. The Table identifies the cDNA_ID of interest, correlates to that cDNA the relevant phenotype, protein domain and microarray/differential expression data. The final column of the Table identifies the utilities/functions of particular interest for the identified cDNA.

11. Cluster Functions & Utilities Table

The Cluster Functions & Utilities Table describes particular utilities/functions of interest for identified clusters of genes. The Table provides the following information:

Record # - an internal identifier.

Group – identifies the group of clusters of interest, wherein each group is identified with the same utilities/functions as set forth in the right-hand most column.

CDNA – identifies the cDNA of interest with the noted utility/function.

CDNA_Cluster - identifies the cDNA Cluster ID of interest.

Gi No – refers to the public genomic sequence that matches to the cDNA

NR Hit – refers to the most relevant protein domain for the cDNA of interest.

Pfam and Pfam Desc – provide the protein domain name.

Notes/Annotations – provides some notes relevant to the data/information analysis.

Utilities/Functions – this rightmost column identifies utilities/functions of particular interest for the group of cDNAs and clusters.

12. cDNA_Clusters Table

The cDNA_Clusters Table correlates the Ceres cDNA_ID nos. (in numerical order) with the relevant cDNA cluster which contains each cDNA_ID.

13. Stanford_old_new_cDNA_map Table

During the course of the experiments reported herein, some of the cDNA sequences were assigned new Ceres internal cDNA_id numbers. The cDNA_map Table provides a list of the original "old" cDNA_ids and correlates those id numbers with any new cDNA_id which may have been assigned. Thus, any "old" and "new" cDNA ids which are on the same line in the Table are, in fact, the same sequence.

14. gb_Only_Peptides Table

In the Protein Group table, a number of proteins encoded by Genbank predictions are included. These proteins were referenced with a peptide ID number. The peptide ID number is linked to the amino acid sequence of the Genbank prediction in this table.

15. Stanford_Old_New_cDNA Table

During the course of the experiments reported herein, some of the cDNA sequences utilized in the Stanford Microarray differential expression analysis experiments were assigned new Ceres internal cDNA_id numbers. The Stanford_old_new_cDNA Table provides a list of the original "old" cDNA_ids and correlates those id numbers with any new cDNA_id which may have been assigned. Thus, any "old" and "new" cDNA ids which are on the same line in the Table are, in fact, the same sequence.

16. Enhanced_Amino Table

This table lists the peptide IDs of polypeptides with enhanced amino acid content. The table list the peptide ID following with the single letter code of the amino acid that is enhanced. The table also includes a frequency that the amino acid occurred. The frequency was calculated

by dividing the total number of the desired amino acid indicated in the column by the number of residues in the peptide. For example, if amino acid A, occurred 50 times in a polypeptide that is 100 amino acid long, the frequency would be 50 divided by 100 or 0.5.

17. Stanford_old_new_cDNA_map Table

During the course of the experiments reported herein, some of the cDNA sequences were assigned new Ceres internal cDNA_id numbers. The docket_80090_101_cDNA_map provides a list of the original "old" cDNA_ids in the Reference and Sequence tables and correlates those id numbers with any new cDNA_id which may have been assigned and utilized in the remaining tables. Thus, any "old" and "new" cDNA ids which are on the same line in the Table are, in fact, the same sequence.

II. HOW THE INVENTIONS REVEAL HOW GENES, GENE COMPONENTS AND PRODUCTS FUNCTION

The different experimental molecular genetic approaches focused on different aspects of genes, gene components, and gene products of the inventions. The variety of the data demonstrates the multiple functions and characteristics of single genes, gene components, and products. The data also explain the pathways and networks in which individual genes and products participate and interact. As a result, the circumstances or conditions are now known when these genes and networks are active. These new understandings of biology are relevant for many plant species. The following section describes the process by which Applicants analyzed the inventions generated by the Ceres Genomic Engine:

II.A. EXPERIMENTAL RESULTS REVEAL MANY FACETS OF A SINGLE GENE

The experimental results are used to dissect the function of individual components and products of the genes. For example, the biochemical activity of the encoded protein could be surmised from sequence analyses, and promoter specificity could be identified through transcriptional analyses. Generally, the data presented herein can be used to functionally annotate either the protein sequence and/or the regulatory sequence that control transcription and translation.

II.A.1. FUNCTIONS OF CODING SEQUENCES REVEALED BY THE CERES GENOMIC ENGINE

II.A.1.a. Sequence Similarity To Proteins Of Known Function Can Be Used To Associate Biochemical Activities And Molecular Interaction To The Proteins Of The Invention

The protein sequences of the invention were analyzed to determine if they shared any sequence characteristics with proteins of known activity. Proteins can be grouped together based on sequence similarity, either localized or throughout the length of the proteins. Typically, such groups of proteins exhibit common biochemical activities or interact with similar molecules.

II.A.1.a.1. Presence Of Amino Acid Motifs Indicates Biological Function

Localized protein sequence similarity, also referred to as amino acid motifs, have been attributed to enzyme or protein functions. A library of motifs, important for function, have been documented in PROSITE, a public database available at <http://www.expasy.ch/prosite/>. This library includes descriptions of the motifs and their functions. The zinc finger motif is one such entry in PROSITE, which reports that the zinc finger domain of DNA-binding proteins is typically defined by a 25-30 amino acid motif containing specific cysteine or histidine residues that are involved in the tetrahedral coordination of a zinc ion. Any protein comprising a sequence similar to the zinc finger amino acid motif will have similar functional activity (specific binding of DNA).

Protein sequences of the invention have been compared to a library of amino acid motifs in the pFAM database, which is linked to the PROSITE database. If any of Applicants' protein sequences exhibit similarity to these amino acid motifs or domains, the Reference Table notes the name and location of the motif in the "Pred. PP Nom. & Annot" section of the Reference tables. A description of any biochemical activities that are associated to these domains, and therefore associated with Applicants' proteins, is included in the Protein Domain table.

For example, polypeptide, CERES Sequence ID NO: 1545823 is associated with zinc finger motif as follows in the Reference Table:

(C) Pred. PP Nom. & Annot.

- Zinc finger, C3HC4 type (RING finger)
- Loc. Sequence ID NO 133059: 58 -> 106 aa.

II.A.1.a.2. Related Amino Acid Sequences Share Similar Biological Functions

It is apparent, when studying protein sequence families, that some regions have been better conserved than others during evolution. These regions are generally important for the function of a protein and/or for the maintenance of its three-dimensional structure.

The Reference Table reports in section "(Dp) Rel. AA Sequence" when a protein shares amino acid similarity with a protein of known activity. The section reports the gi number of the protein of known activity, a brief description of the activity, and the location where it shares sequence similarity to Applicants' polypeptide sequence.

Using this analysis, biochemical activity of the known protein is associated with Applicants' proteins. An example for the polypeptide described above is as follows:

(Dp) Rel. AA Sequence

- Align. NO 524716
- gi No 2502079
- Desp. : (AF022391) immediate early protein; ICP0 [Feline herpesvirus 1]
- % Idnt. : 33.7
- Align. Len.: 87
- Loc. Sequence ID NO 133059: 52 -> 137 aa.

II.A.1.b. Differential Expression Results Explain In Which Cellular Responses The Proteins Of The Invention Are Involved

Differential expression results show when the coding sequence is transcribed, and therefore when the activity of the protein is deployed by the cell. Similar coding sequences can have very different physiological consequences because the sequences are expressed at different times or places, rather than because of any differences in protein activity. Therefore, modified levels (increased or decreased) of expression as compared to a control provide an indication of the function of a corresponding gene, gene components, and gene products.

These experiments can determine which are genes "over-expressed" under a given stimulus. Such over-expressed genes give rise to higher transcript levels in a plant or cell that is stimulated as compared to the transcript levels of the same genes in a control organism or cell. Similarly, differential expression experiments can reveal "under-expressed" genes.

To increase the cellular response to a stimulus, additional copies of the coding sequences of a gene that is over-expressed are inserted into a cell. Increasing transcript levels of an over-expressed gene can either heighten or prolong the particular cellular response. A similar enhancement can occur when transcription of an under-expressed gene is inhibited. In contrast, the cellular response will be shortened or less severe when the over-expressed genes are inhibited or when expression of the under-expressed genes are increased.

In addition to analyzing the levels of transcription, the data were also analyzed to gain insight into the changes in transcription over time. That is, while the plants in the experiments were

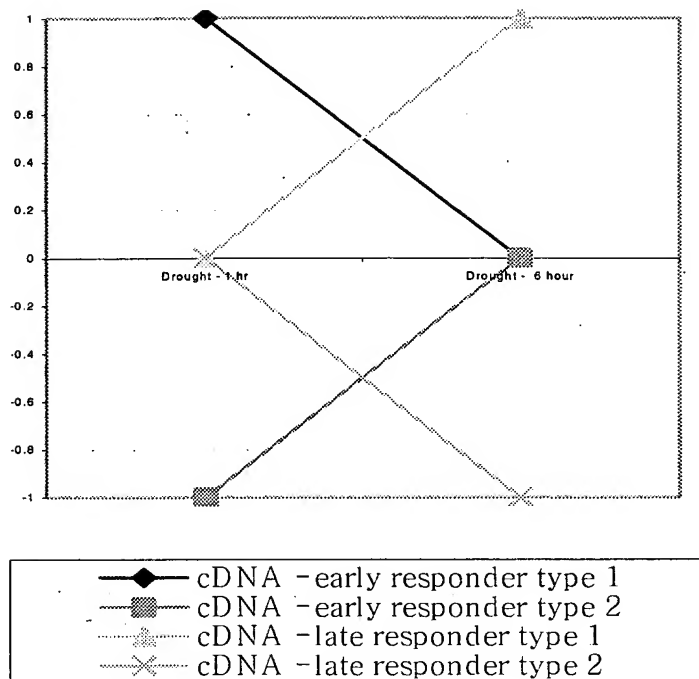
reacting to either an external or internal stimulus, a differential experiment takes a snapshot of the transcription levels in the cells at one specific time. However, a number of snap-shots can be taken at different time points during an external stimulus regime, or at different stages of development during an internal stimulus. These results show how the plant changes transcription levels over time, and therefore protein levels in response to specific stimuli to produce phenotypic changes. These results show that a protein can be implicated in a single, but more likely, in a number of cellular responses.

II.A.1.b.1. The Transcript Levels Of A Protein Over Time In Response To A Stimuli Are Revealed By Transcriptional Analyses Over Many Experiments

Applicants produced data from plants at different times after a specific stimulus. These results show whether the expression level of a gene spikes at a key moment during the cellular response, or whether the transcript level remains constant. Thus, coding sequences not only can be determined to be over- or under-expressed, but also can be classified by the initial timing and duration of differential expression. This understanding of timing can be used to increase or decrease any desired cellular response.

Generally, Applicants have assayed plants at 2 to 4 different time points after exposing the plants to the desired stimuli. From these experiments, “early” and “late” responders were identified. These labels are applied to either the regulatory sequences driving transcription of the gene as well as to the protein encoded by the gene.

The following example illustrates how the genes, gene components and products were classified as either early or late responders following a specific. The mRNAs from plants exposed to drought conditions were isolated 1 hour and 6 hours after exposure to drought conditions. These mRNAs were tested utilizing microarray techniques. The graph below illuminates possible transcription profiles over the time course, plotting all the (+) data points as +1 and all the (-) data points as -1:



(The value for each time point was determined using a pair of microarray chips as described above.)

Data acquired from this type of time course experiment are useful to understand how one may increase or decrease the speed of the cellular response. Inserting into a cell extra copies of the coding sequence of early responders in order to over-express the specific gene can trigger a faster cellular response. Alternatively, coding sequences of late responders that are over-expressed can be placed under the control of promoters of early responders as another means to increase the cellular response.

Inserting anti-sense or sense mRNA suppression constructs of the early responders that are over-expressed can retard action of the late responders, thereby delaying the desired cellular response. In another embodiment, extra copies of the promoters of both early and late responders can be added to inhibit expression of both types of over-expressed genes.

The experiments described herein can be grouped together to determine the time course of the transcript levels of different coding sequences in response to different stimuli. Examples of different groups are as follows (the examples include the IDs for both corn and Arabidopsis

experiments):

- NAA (EXPT IDs 108564, 108565, 108516, 108554)
- BA (EXPT IDs 108566, 108567, 108517)
- GA (EXPT IDs 108562, 108563, 108519, 108520, 108521, 108484, 108485, 108486)
- BR (EXPT IDs 108580, 108581, 108557, 108478, 108479, 108480, 108481)
- ABA (EXPT IDs 108560, 108561, 108513, 108597)
- Drought (EXPT IDs 108572, 108573, 108502, 108503, 108504, 108556, 108482, 108483, 108473, 108474, 108477)
- Cold (EXPT IDs 108578, 108579, 108533, 108534)
- Heat (EXPT IDs 108576, 108577, 108522, 108523)
- Osmotic stress (EXPT IDs 108570, 108571, 108541, 108542, 108553, 108539, 108540)
- Reactive Oxygen (EXPT IDs 108582, 108583, 108537, 108538, 108558)
- NO (EXPT IDs 108584, 108585, 108526, 108527, 108559)
- Wounding (EXPT IDs 108574, 108575, 108524, 108525)
- SA (EXPT IDs 108586, 108587, 108515, 108552, 108471, 108472, 108469, 108470, 107953, 107960, 108443, 108440, 108441, 108475, 108476)
- MeJA (EXPT IDs 108568, 108569)
- Finale (EXPT IDs 108467, 107871, 107876)
- Trimec (EXPT IDs 108466, 107886, 107891)
- Round-up (EXPT IDs 108465, 107896)
- Glean (EXPT IDs 108468, 107881)

II.A.1.b.2. The Transcript Levels Of A Protein Over
Different Developmental Stages Can Be Identified By
Transcriptional Analyses Over Many Experiments

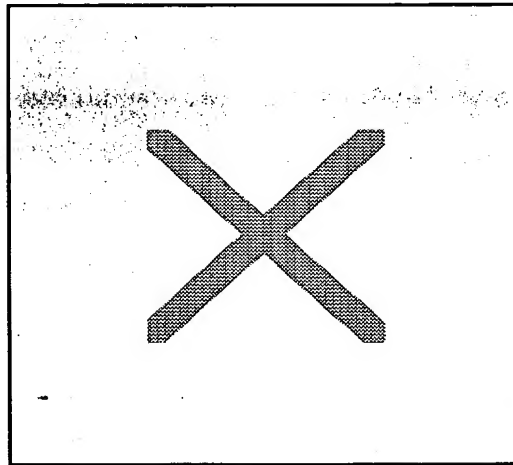
Differential expression data were produced for different development stages of various organs and tissues. Measurement of transcript levels can divulge whether specific genes give rise to spikes of transcription at specific times during development, or whether transcription levels remain constant. This understanding can be used to increase speed of development, or to arrest development at a specific stage.

Like the time-course experiments, the developmental stage data can classify genes as being transcribed at early or late stages of development. Generally, Applicants assayed different organs or tissues at 2-4 different stages.

Inhibiting under-expressed genes at either early or late stages can trigger faster development times. The overall development time also can be increased by this means to allow organs and tissue to grow to a larger size or to allow more organs or tissues to be produced. Alternatively, coding sequences of late stage genes that are under-expressed can be placed under the control of promoters of early stage genes to increase heighten development.

Inserting extra copies of the coding sequence early stage genes that are under-expressed can retard action of the late-stage genes and delay the desired development.

Fruit development of *Arabidopsis* is one example that can be studied. Siliques of varying sizes, which are representative of different stages, were assayed by microarray techniques. Specifically, mRNA was isolated from siliques between 0-5mm, between 5-10mm and > 10 mm in length. The graph below shows expression pattern of a cell wall synthesis gene, cDNAID 1595707, during fruit development:



The developmental course shows that the gene encoding a cell wall synthesis protein is up-regulated when the fruit is 0-5mm but returns to normal levels at 5-10mm and > 10mm. Increase of cell wall synthesis can lead to larger cells and/or greater number of cells. This type of increase can boost fruit yield. The coding sequence of the cell wall synthesis protein under the control of a strong early stage promoter would increase fruit size or number.

A pectinesterase gene was also differentially expressed during fruit development, cDNA ID

1396123. Pectinesterase catalyzes the hydrolysis of pectin into pectate and methanol. This biochemical activity plays an important role in cell wall metabolism during fruit ripening. To shorten the time for fruit ripening, extra copies of this gene with its endogenous promoter can be inserted into a desired plant. With its native promoter, the extra copies of the gene will be expressed at the normal time, to promote extra pectinesterase at the optimal stage of fruit development thereby shortening ripening time.

A number of Applicant's experiments can be grouped together to study changes of transcript levels over a number development stages. Below are examples of groups of experiments:

- Root, Root Tip, and rhl mutant (EXPT IDs 108594, 108433, 108599, 108434, 108439)
- Flowers Drought Exposed Flowers, SA Treated Flowers (EXPT IDs 108473, 108474, 108429, 108430, 108431, 108475, 108476, 108501)
- BR Shoot Apices, Leaves, Stm (EXPT IDs 108478, 108479, 108480, 108481, 108598, 108535, 108536, 108435)
- Leaf and Stm (EXPT IDs 108477, 108512, 108497, 108498, 108598, 108478, 108479, 108480, 108481, 108598, 108535, 108536, 108435)
- Imbibed & Germinating Seeds 1, 2, 3, And 4 Days (EXPT IDs 108461, 108462, 108463, 108464, 108528, 108529, 108530, 108531, 108545, 108546, 108547, 108518, 108529, 108543, 108544)
- Tissue Specific Expression (3 week rosette leaves, Tissue Specific Expression (3 week stems), Tissue Specific Expression (2 week roots) (EXPT IDs 108497, 108498, 108439)
- Tissue Specific Expression (3 week rosette leaves), Germinating Seeds (EXPT IDs 108497, 108461)
- Tissue Specific Expression (3 week rosette leaves, stm mutants, BR_Shoot Apices Expt, root tips, Tissue Specific Expression (2 week roots) (EXPT IDs 108497, 108435, 108480, 108434, 108439)
- BR_Shoot Apices Expt, root tips, Tissue Specific Expression (flower buds) (EXPT IDs 108480, 108434, 108431)
- Arab_Ler-pi_ovule_1, ap2-floral buds, Tissue Specific Expression (flower buds), Tissue Specific Expression (<5 mm siliques) (EXPT IDs 108595, 108501, 108431, 108437)
- Tissue Specific Expression (2 week roots), rhl mutant2, BR_Shoot Apices Expt,

Trichome Inflorescences (EXPT IDs 108439, 108433, 108480, 108452)

**II.A.1.b.3. Proteins That Are Common In A Number Of
Similar Responses Can Be Identified By Transcriptional
Analyses Over A Number Of Experiments**

The differential expression experiments also reveal the genes, and therefore the coding sequence, that are common to a number of cellular responses. By identifying the genes that are differentially expressed in a number of similar responses, the genes at the nexus of a range of responses are discovered. For example, genes that are differentially expressed in all the stress responses are at the hub of many of the stress response pathways.

These types of nexus genes, proteins, and pathways are differentially expressed in many or majority of the responses or developmental conditions of interest. Typically, a nexus gene, protein, or pathway is differentially expressed in generally the same direction in many or majority of all the desired experiments. By doing so, the nexus gene can be responsible for triggering the same or similar set of pathways or networks for various cellular responses. This type of gene is useful in modulating pleiotropic effects or triggering or inhibiting a general class of responses.

When nexus genes are differentially expressed in a set of responses, but in different directions, these data indicate that a nexus gene is responsible for creating the specificity in a response by triggering the same pathway but to a different degree. Placing such nexus genes under a constitutive promoter to express the proteins at a more constant level can remove the fluctuations. For example, a plant that is better drought adapted, but not cold adapted can be modified to be tolerant to both conditions by placing under the control of a constitutive promoter a nexus gene that is up-regulated in drought but down regulated in cold.

Applicants' experiments can be grouped together to identify such nexus genes. Examples of these groups are as follows:

- Herbicide Response
 - Trimec, Finale, Glean, Round-up (EXPT IDs 108467, 107871, 107876, 108468, 107881, 108465, 107896, 108466, 107886, 107891)
- Stress Response
 - Drought, Cold, Heat, Osmotic Stress (EXPT IDs 108578, 108579, 108533, 108534, 108572, 108573, 108502, 108503, 108504, 108556, 108482, 108483, 108473, 108474, 108477, 108576, 108577, 108522, 108523, 108570, 108571, 108541,

108542, 108553, 108539, 108540)

- Drought, Cold, Heat, PEG, Trimec, Finale, Glean, Round-up (EXPT IDs 108578, 108579, 108533, 108534, 108572, 108573, 108502, 108503, 108504, 108556, 108482, 108483, 108473, 108474, 108477, 108576, 108577, 108522, 108523, 108570, 108571, 108541, 108542, 108553, 108539, 108540)
- Wounding, SA, MeJA, Reactive Oxygen, NO (EXPT IDs 108568, 108569, 108555, 108584, 108585, 108526, 108527, 108559, 108582, 108583, 108537, 108538, 108558, 108586, 108587, 108515, 108552, 108471, 108472, 108469, 108470, 107953, 107960, 108443, 108440, 108441, 108475, 108476, 108574, 108575, 108524, 108525)
- Hormone Responses
 - NAA, BA, BR, GA, TRIMEC (EXPT IDs 108566, 108567, 108517, 108580, 108581, 108557, 108478, 108479, 108480, 108481, 108562, 108563, 108519, 108520, 108521, 108484, 108485, 108486, 108564, 108565, 108516, 108554, 108466, 107886, 107891)
 - NAA, Trimec (EXPT IDs 108566, 108567, 108517, 108580, 108581, 108557, 108478, 108479, 108480, 108481, 108562, 108563, 108519, 108520, 108521, 108484, 108485, 108486, 108564, 108565, 108516, 108554, 108466, 107886, 107891)

II.A.1.b.4. Proteins That Are Common To Disparate Responses Can Be Identified By Transcriptional Analyses Over A Number Of Experiments

Phenotypes and traits result from complex interactions between cellular pathways and networks. Which pathways are linked by expression of common genes to specify particular traits can be discerned by identifying the genes that show differential expression of seemingly disparate responses or developmental stages. For example, hormone fluxes in a plant can direct cell patterning and organ development. Genes that are differentially expressed both in the hormone experiments and organ development experiments would be of particular interest to control plant

development.

Examples Of Such Pathway Interactions Include:

- (i) The Interaction Between Stress Tolerance Pathways And Metabolism Pathways;
- (ii) Interaction Between Hormone Responses And Developmental Changes In The Plant;
- (iii) Interactions Between Nutrient Uptake And Developmental Changes;
- (iv) Mediation Of Stress Response By Hormone Responses; And
- (v) Interactions Between Stress Response And Development.

Applicant's experiments can be grouped together to identify proteins that participate in interacting pathways or networks. Specific groups of experiments include, for example:

- (i) Stress & Metabolism
 - Germinating Seeds (Day 1), Arab_0.1uM_Epi-Brass_1, Arab_NO3_H-to-L_1, Arab_100uM_GA3_1 (EXPT IDs 108461, 108580, 108592, 108562)
- (ii) Hormones & Development
 - NAA, BA & Root Tips (EXPT IDs 108566, 108567, 108517, 108564, 108565, 108516, 108554, 108434, 108466, 107886, 107891)
 - NAA, Roots & Root Tips (EXPT IDs 108564, 108565, 108516, 108554, 108599, 108434, 108439, 108466, 107886, 107891)
 - NAA, BA, Roots And/Or Root Tips (EXPT IDs 108564, 108565, 108516, 108554, 108599, 108434, 108439, 108466, 107886, 107891, 108566, 108567, 108517)
 - NAA, BA And Leaf (EXPT IDs 108566, 108567, 108517, 108518, 108529, 108512, 108497, 108498, 108598, 108564, 108565, 108516, 108554, 108466, 107886, 107891)
 - NAA, BA, Leaves, Roots And/Or Root Tips (EXPT IDs 108566, 108567, 108517, 108518, 108529, 108512, 108497, 108498, 108598, 108564, 108565, 108516, 108554, 108466, 107886, 107891, 108599, 108434, 108439)
 - ABA & Siliques (Of Any Size) (EXPT IDs 108560, 108561, 108513,

108597, 108436, 108437, 108438)

- GA, Imbibed & Germinating Seeds, ABA & Siliques (Of Any Size)
(EXPT IDs 108560, 108561, 108513, 108597, 108562, 108563, 108519,
108520, 108521, 108484, 108485, 108486, 108461, 108462, 108463,
108464, 108528, 108529, 108530, 108531, 108545, 108546, 108547,
108518, 108529, 108543, 108544, 108436, 108437, 108438)
- Tissue Specific Expression (3 week rosette leaves), Arab_0.1uM_Epi-
Brass_1, Arab_100uM_GA3_1, Germinating Seeds (Day 1), (EXPT IDs
108461, 108497, 108580, 108562, 108461)

(iii) Nutrient Uptake And Development

- Any Or All Nitrogen Experiments With Siliques (Of Any Size) (EXPT
IDs 108592, 108593, 108588, 108589, 108590, 108591, 108532,
108548, 108549, 108550, 108551, 108454, 108455, 108487, 108488,
108489, 108436, 108437, 108438)
- Any Or All Nitrogen Experiments With Roots Or Root Tips (EXPT IDs
108518, 108529, 108592, 108593, 108588, 108589, 108590, 108591,
108532, 108548, 108549, 108550, 108551, 108454, 108455, 108487,
108488, 108489, 108594, 108433, 108599, 108434, 108439)

(iv) Stress & Hormones

- ABA, Drought (EXPT IDs 108560, 108561, 108513, 108597, 108572,
108573, 108502, 108503, 108504, 108556, 108482, 108483, 108473,
108474, 108477)
- ABA, Drought, Cold, Heat, & Wounding (EXPT IDs 108560, 108561,
108513, 108597, 108578, 108579, 108533, 108534, 108572, 108573,
108502, 108503, 108504, 108556, 108482, 108483, 108473, 108474,
108477, 108576, 108577, 108522, 108523, 108574, 108575, 108524,
108525)
- Tissue Specific Expression (3 week rosette leaves),
Arab_100uM_ABA_1, Ws Arabidopsis Drought 2 days, Ws Arabidopsis

Drought 4 days (EXPT IDs 108497, 108560, 108477, 108482)

(v) Stress & Hormones Stress & Hormones

- Nitrogen High transition to Low, Arab_NO3_H-to-L_1, Tissue Specific Expression (<5mm siliques), Tissue Specific Expression (5-10mm siliques) (EXPT IDs 108455, 108592, 108437, 108436)

II.A.1.c. Observations Of Phenotypic Changes Show What
Physiological Consequences Applicants' Proteins Can
Produce

Another direct means of determining the physiological consequences of a protein is to make aberrant decreases or increases of its expression level in a cell. To this end, Applicants have produced plants where specific genes have been disrupted, or produced plants that include an extra expressed copy of the gene. The plants were then planted under various conditions to determine if any visible physiological changes are caused. These changes then are attributed to the changes in protein levels.

**II.A.2. DIFFERENTIAL EXPRESSION RESULTS EXPLAIN WHICH
EXTERNAL OR INTERNAL STIMULI TRIGGER THE
REGULATORY SEQUENCES**

Transcriptional studies can reveal the time and place that genes are expressed. Typically, regulatory sequences, such as promoters, introns, UTRs, etc., control when and in which cells transcription occurs. Differential studies can explain the temporal- and location-specific regulatory sequences that control transcription.

Using the experiments that are provided herein, one skilled in the art can choose a promoter or any other regulatory sequence that is capable of facilitating the desired pattern of transcription. For example, if a promoter is needed to give rise to increased levels of transcription in response to Auxin, but little expression in response to cytokinin, then the promoters of cDNAs that were up-regulated in the Auxin experiments, but down-regulated the cytokinin experiments would be of interest.

Time Course Experiments – Time Sensitive

Evaluation of time-course data as described above is also useful to identify time-specific promoters. Promoters or regulatory sequences, like the coding sequences, can be classified as early or late responding according to the microarray data. Promoters that facilitate expression of early or late genes are useful to direct expression of heterologous coding sequences to modulate the cellular response. In the drought data, promoters from “early” responding genes can be selected to activate expression of any desired coding sequence. Thus, a coding sequence for a salt-tolerance protein that is not typically expressed early in response to drought could be linked to an “early” responding promoter to increase salt tolerance within one hour after exposure to drought conditions.

Developmental Experiments – Time Sensitive

Another class of time-sensitive promoters and other regulatory sequence can be identified from the experiments examining different developmental stages. These regulatory sequences can drive transcription of heterologous sequence at particular times during development. For example, expression of stress-responsive genes during fruit development can protect any gain in fruit yield.

Common To Many Pathways – Cause General Effects

Promoters and other regulatory sequence associated with cDNAs that are differentially expressed in a number of similar responses can be used to cause general effects. These types of regulatory sequences can be used to inhibit or increase expression of a desired coding sequence in a number circumstances. For example, protein that is capable of acting as an insecticide can be placed under the control a general “stress” promoter to increase expression, not only when the plant is wounded, but under other stress attack.

II.B. EXPERIMENTAL RESULTS ALSO REVEAL PATHWAYS OR NETWORKS OF GENES

II.B.1. GENES WHOSE TRANSCRIPTION ARE WELL COORDINATED GENERALLY ACT TOGETHER TO PRODUCE PROTEINS THAT PARTICIPATE IN THE SAME

PATHWAY OR NETWORK

Patrick Brown, one of the pioneers of microarray chip technology, demonstrated that differential expression experiments can identify groups of genes that encode proteins that participate the same pathway or network. The work focused on phosphate accumulation and metabolism genes in yeast and was published in the paper Ogawa *et al.*, Mol Biol Cell (2000) Dec;11(12):4309-21. The authors identified by microarray analysis 22 genes whose transcription was regulated by phosphate concentration. Promoter analysis of these genes showed that 21 of them contained a sequence in their promoters that is recognized by a transcriptional activator that is regulated by phosphate. Further, phenotypic studies were completed by mutational analysis of many of these 22 genes in yeast. The mutants were shown to be either severely deficient in accumulation of inorganic polyphosphate (polyP) and P(i), or associated with normal catabolism of polyP in the yeast vacuole. This publication proves that genes with correlated transcriptional profiles do indeed participate in the same pathway or network.

II.B.1.a. Calculating The Correlation Coefficient Between Pairs Of Genes Based On The Differential Expression Data

The differential expression data obtained over many experiments reveal the global pattern of transcription of a gene. Transcription patterns, also referred to as profiles, of two different genes can be compared. From this comparison, a correlation coefficient can be calculated as a measure of the strength of the relationship between the two profiles.

Transcription profiles can be compared by plotting as a point, the differential expression of gene1 on the x-axis and gene 2 on the y-axis on one experiment. If all the pairs lie on a regression line the relationship and correlation between the two genes are strong. The correlation coefficient can be calculated using a number of methods. In the present case, the Spearman method was utilized.

The correlation coefficient can vary from -1 to 1. The coefficient indicates the strength of the relationship between two mRNA transcripts of any set of data that is examined. A zero coefficient indicates that no correlation exists between the transcription profiles of two genes in the samples examined.

Biologically, a high correlation coefficient indicates that a gene(s) triggers the activation or repression of the correlated genes, or have related functional roles. Thus, illumination of the activity of one gene can indicate the activities of the genes with highly correlated transcription profiles. This implication is true whether the activity is a biochemical activity, molecular interaction, cellular response, or physiological consequence.

II.B.1.b. The Complete Linkage Analyses Of Differential Identity Genes
With Similar Pattern Of Transcription

The complete linkage analysis can build groups (or "clusters") of genes whose transcription patterns are highly correlated or co-regulated.

Because genes with related functions are frequently expressed in similar patterns, utilities or roles can be ascribed for genes (without observation of transformed plants) based on their temporal association with other genes of known function (a "guilt-by-association" analysis). Ogawa *et al.* has used correlated mRNA transcription profiles to identify the function of proteins of unknown function.

The complete linkage analysis utilizes the correlation coefficients that are calculated for each pair of genes tested in the microarray experiments. A cluster is first seeded with any arbitrary transcript tested on the chip. The seed transcript, for this illustration, is designated mRNA#0. Next, a minimum threshold is chosen for all acceptable correlation coefficients. In this case, the threshold used was 0.75. A list of potential cluster members is compiled by choosing mRNA transcripts that have a correlation coefficient with mRNA#0 that is greater than the threshold. No limit is placed on the number of mRNAs that can be added to a cluster so long as the correlation coefficient meets the threshold limit criterion.

For this example, assume that four mRNAs were added to the cluster, mRNA_1 to mRNA_4. Once the potential cluster members are identified, the cDNA IDs of each member is added to the potential list in order its correlation coefficient to mRNA#1, the largest correlation coefficient first. For this example, let's suppose four mRNAs 1-4 are potential members, they would be ordered as follows:

MRNA#	Correlation Coefficient with mRNA#0
MRNA#1	0.9
MRNA#2	0.8
MRNA#3	0.78
MRNA#4	0.75

A potential member is accepted into the group, if its correlation coefficients with all other potential members are all greater than the threshold. Thus, for mRNA#1 to remain in the group the correlation coefficient between mRNA#1 and mRNA#2 must be greater than 0.75; and mRNA#1 and #3 > 0.75; and mRNA#1 and mRNA#4 > 0.75. Potential cluster members are removed only after reviewing the correlation coefficients in a specific order where mRNAs are reviewed in the order that they appear on the list.

Consequently, review of the correlation coefficients does not begin with any random pair, such as mRNA#3 and mRNA#4. The review begins between mRNA#1 and mRNA#2, which are the top two on the list.

If correlation coefficient between mRNA#1 and mRNA#2 is less than the threshold, then mRNA#2 is removed from the cluster. mRNA#2 is removed because its correlation coefficient with mRNA#0 is 0.8 which is less than 0.9, the correlation coefficient of mRNA#1 and mRNA#0.

This illustrates the rule that if the correlation coefficient is less than the threshold, then only one of the pair not accepted as a cluster member, specifically, the one with the lower coefficient to the seed mRNA#0.

This process of iterative reviewing of correlation coefficients between potential members continues until all pairs are reviewed. In this case, the coefficient between mRNA#1 and mRNA#3 would be reviewed because these are the two highest ones on the list besides mRNA#1 and #2. The next pair to be reviewed would be mRNA#1 and #4, etc.

Applicants have analyzed the data using several sets of parameters for the complete linkage analysis as shown in the table below:

Method	Correlation Coefficient Threshold	Max number of members in a cluster	Organism
CL_METHOD_TYPE=TRUE	0.9	MAX_SIZE=15	Arabidopsis
CL_METHOD_TYPE=TRUE	0.75	MAX_SIZE=30000	Arabidopsis
CL_METHOD_TYPE=TRUE	0.70	MAX_SIZE=30000	Arabidopsis
CL_METHOD_TYPE=	0.9	MAX_SIZE=15	Zea

TRUE			
CL_METHOD_TYPE=TRUE	0.75	MAX_SIZE=30000	Zea
CL_METHOD_TYPE=TRUE	0.70	MAX_SIZE=30000	Zea
CL_METHOD_TYPE=TRUE	0.9	MAX_SIZE=15	Arabidopsis
CL_METHOD_TYPE=TRUE	0.75	MAX_SIZE=30000	Arabidopsis
CL_METHOD_TYPE=TRUE	0.70	MAX_SIZE=30000	Arabidopsis
CL_METHOD_TYPE=TRUE	0.9	MAX_SIZE=15	Zea
CL_METHOD_TYPE=TRUE	0.75	MAX_SIZE=30000	Zea
CL_METHOD_TYPE=TRUE	0.70	MAX_SIZE=30000	Zea

The results of these cluster analyses are reported in the MA_clust table.

II.B.1.c. The Nearest Neighbor Analyses Of Differential Group Genes With Correlated But Dissimilar Transcription Profiles

The nearest neighbor analysis differs from the complete linkage algorithm by not requiring all members to meet the correlation threshold with each other. Thus, a member of a nearest neighbor cluster need only be closely correlated to one other member of the cluster. It is not even required that all members be closely correlated to the seed mRNA transcript.

In a complete linkage cluster all the transcription profile of all members are correlated to a greater or lesser extent. In contrast, a cluster deduced by the nearest neighbor analysis may include members with differing transcription profiles. However, nearest neighbor brings to light clusters of interacting genes. In the nearest neighbor analysis, the seed mRNA may not have a very high correlation coefficient with the last mRNA added to the cluster.

The nearest neighbor analysis, like the complete linkage analysis, is initiated by seeding each cluster with a mRNA_0. The cluster size is determined by setting a threshold coefficient and setting a limit on the number of members that can be added to the cluster.

The cluster is expanded in an iterative fashion determining which mRNA has the highest correlation coefficient with mRNA_0. The additional member is labeled mRNA_1. Next, a list of potential candidates is generated by finding the mRNA that has the highest correlation to mRNA_0 (besides mRNA_1) and finding the mRNA that has the highest coefficient with mRNA_1. Whichever of the candidates has the highest correlation coefficient is added to the cluster. Then, a list of three potential candidates is generated similarly.

Addition of members continues until either (1) all the correlation coefficients of potential members is lower than the threshold or (2) number of members in the cluster meets the size limitation.

Applicants have analyzed the data using several sets of parameters for the nearest neighbor analysis as shown in the table below:

Method	Correlation Coefficient Threshold	Max number of members in a cluster	Organism
NN METHOD TYPE=TRUE	0.5	MAX_HITS=15	Arabidopsis
FULL_NN_METHOD_TYPE=TRUE	0.8	NONE	Arabidopsis
FULL_NN_METHOD_TYPE=TRUE	0.6	NONE	Arabidopsis
NN METHOD TYPE=TRUE	0.5	MAX_HITS=15	Zea
FULL_NN_METHOD_TYPE=TRUE	0.8	NONE	Zea
FULL_NN_METHOD_TYPE=TRUE	0.6	NONE	Zea
NN METHOD TYPE=TRUE	0.5	MAX_HITS=15	Arabidopsis
FULL_NN_METHOD_TYPE=TRUE	0.8	NONE	Arabidopsis
FULL_NN_METHOD_TYPE=TRUE	0.6	NONE	Arabidopsis
NN METHOD TYPE=TRUE	0.5	MAX_HITS=15	Zea
FULL_NN_METHOD_TYPE=TRUE	0.8	NONE	Zea
FULL_NN_METHOD_TYPE=TRUE	0.6	NONE	Zea

The results of these cluster analyses are reported in the MA_clust table.

**II.C. EXPERIMENTAL RESULTS REVEAL THE FUNCTIONS AND
CHARACTERISTICS OF GENES, PATHWAYS AND NETWORKS**

II.C.1. LINKING BIOCHEMICAL OR METABOLIC ACTIVITIES OF ONE PROTEIN IN A CLUSTER TO THE OTHER PROTEINS IN THE SAME MICROARRAY CLUSTER

As shown in the Ogawa *et al.*, Mol Biol Cell (2000), genes whose transcription profiles cluster together as being strongly correlated typically take part in the same pathway or network. Thus, the activity of one gene in the cluster can be associated to the other genes in the cluster with highly correlated transcription profiles. This association is true whether the activity is a biochemical activity, molecular interaction, cellular response or physiological consequence.

One example of this is cluster 420 of the report (shown below). In this cluster, a protein encoded by cDNA ID 1025791 did not match to any pFAM domain. However, through the microarray data, the gene that encodes that protein had a transcription profile that was correlated with other genes that encode ribosomal proteins. Thus, the activity of the ribosomal genes can be associated with the protein with no pFAM match. All the proteins in the same cluster would be

420	<u>1025791</u>	803433	4585878	(AC005850) Unknown protein [Arabidopsis]		
420	<u>4608965</u>	671877	8567795	(AC013428) 40S ribosomal protein S17, pu	Ribosomal_S17e	Ribosomal S17
420	<u>5663116</u>	818554	7486478	hypothetical protein F6E13.17 - Arabidop	DapB	Dihydrodipicolinate reductase

associated with mRNA translation and protein synthesis.

II.C.2 USING DIFFERENTIAL EXPRESSION DATA TO DETERMINE WHEN THE GENES AND PATHWAYS ARE ACTIVE

The differential expression data can be used to associate the cellular response that results when the clusters of genes are transcribed. For the complete linkage clusters, the genes in the cluster will produce similar transcription profiles. The experiments where the genes in the cluster are differentially expressed as compared to the control define the cellular responses that all the genes of the cluster are capable of modulating.

For example, for the cluster shown above, the mRNA levels for the genes were significantly different in the nitrogen response experiments. Thus, the data shows that this cluster of genes is associated with protein synthesis in response to nutrient uptake.

II.C.3. USING PHENOTYPE DATA TO DETERMINE WHEN GENES AND PATHWAYS ARE ACTIVE

The phenotypic data can be used to demonstrate the physiological consequences of that result when a cluster of genes is active. Whether the clusters were generated by the complete linkage or the nearest neighbor analyses, if a single gene in the cluster has been implicated in phenotypic changes, then any one or combination of the other genes in the cluster can also modulate the same or similar phenotypic changes.

Utilities of Particular Interest

The following sections describe utilities/functions for the genes, gene components and products of the invention. The sequences of the invention, as discussed above, can be recognized as a particular type of gene (e.g. root gene, leaf gene, etc.) by means of particular terms utilized in the Knock-in and Knock-out Tables and by the results of the differential expression experiments. Combined analysis of those data also identify genes with utilities/functions of particular interest. The Single Gene Functions and Utilities Table correlates that data and specific genes with those utilities/functions of particular interest.

Utilities of Particular Interest for Clustered Sequences

As discussed further herein, the genes, gene components and products of the invention have been clustered together into groups. This enables one to understand the function/utility of one member of the cluster based upon knowledge about one or more other members of the cluster. In

addition, this enables an understanding of some utilities/functions of a cluster that would be of particular interest. The Cluster Functions and Utilities Table lists some of the clusters of the invention and notes the functions/utilities that are of particular interest for each of the clusters. Of course, these functions/utilities are of particular interest for each member of each particular cluster.

II.D. EXPERIMENTAL RESULTS PROVIDE AN UNDERSTANDING OF GENES, PATHWAYS AND NETWORKS IN MANY PLANT SPECIES

By analyzing the constant and variable properties of groups of similar sequences, it is possible to derive a structural and functional signature for a protein family, which distinguishes its members from all other proteins. This approach has allowed the Applicants to assign proteins into functional groups and identify orthologous proteins both within and between species. A pertinent analogy to be considered is the use of fingerprints by the police for identification purposes. A fingerprint is generally sufficient to identify a given individual. Similarly, a protein signature can be used to assign a newly sequenced protein to a specific family of proteins and thus to formulate hypotheses about its function.

Proteins can be grouped together because they share a single motif or many motifs. Typically, proteins that share a series of motifs share greater functional equivalence. Usually, signature sequences comprise more than one motif in a particular order from N-terminus to C-terminus.

A list of these groups can be found in the Protein Group Table. The sequences were grouped together using the iterative protein sequence local alignment software, PSI-BLAST. This software begins by aligning a number sequences where the probability that the alignment occurred by chance is set by a threshold e-value. In the Applicants' case, the threshold e-value was set at 10^{-50} , 10^{-30} , and 10^{-10} . The algorithm generates a consensus sequence from the sequences that were aligned together. The consensus sequence was then used to find sequences that matched to it with a probability that was less than the set threshold. The algorithm performs the iterative tasks of aligning and generating a consensus sequence any number of times. Generally, Applicants performed one iteration for the 10^{-10} e-value threshold, two iterations for the 10^{-30} threshold, and three iterations for the 10^{-50} threshold.

Each group can contain sequences from one of more organisms. The groups included both

Ceres polypeptides and public polypeptide sequences. The Ceres polypeptides are identified by their Ceres Sequence ID NO as listed in the Reference Table.

Each group contains sequences that were included at the 10^{-50} , 10^{-30} , and 10^{-10} e-value cutoffs. For each group, the peptide ID and at which cutoff the peptide was included into the group. The same peptide ID may be included in the group three times as peptide ID 50, peptide ID 30 and peptide ID 10. The data indicates that peptide ID was included in the group when the threshold was either 10^{-50} , 10^{-30} , or 10^{-10} . All the peptide IDs that are followed by "50" were included in the protein group when the e-value cutoff was 10^{-50} . All the peptide IDs that are followed by either "30" or "50" were included in the protein group when the threshold e-value was 10^{-30} . All the peptide IDs that are followed by "10", "30" or "50" were included in the protein group when 10^{-10} was used as the e-value cutoff.

II.D.1. CONSERVED SEQUENCES BETWEEN PROTEINS OF DIFFERENT SPECIES GIVE RISE TO A SIGNATURE SEQUENCE

The signature sequence for each group of proteins, also referred to as the consensus sequence. The signature sequence comprises the amino acids that are conserved throughout all the proteins in a particular protein group. The data are shown in the Protein Group table.

Not all the polypeptides in a group are the same length. Thus, some members of the group may not contain the entire signature sequence. However, throughout the length of any member protein, its sequence will match the signature sequence.

The consensus sequence contains both lower-case and upper-case letters. The upper-case letters represent the standard one-letter amino acid abbreviations. The lower case letters represent classes of amino acids:

- "t" refers to tiny amino acids, which are specifically alanine, glycine, serine and threonine.
- "p" refers to polar amino acids, which are specifically, asparagine and glutamine
- "n" refers to negatively charged amino acids, which are specifically, aspartic acid and glutamic acid

- “+” refers to positively charged residues, which are specifically, lysine, arginine, and histidine
- “r” refers to aromatic residues, which are specifically, phenylalanine, tyrosine, and tryptophan,
- “a” refers to aliphatic residues, which are specifically, isoleucine, valine, leucine, and methionine

In addition to each consensus sequence, Applicants have generated a scoring matrix to provide further description of the consensus sequence. The matrix reports the identity and number of occurrences of all the amino acids that were found in the group members for every residue position of the signature sequence. The matrix also indicates for each residue position, how many different organisms were found to have a polypeptide in the group that included a residue at the relevant position. These results are reported in the Protein Group Matrix table.

Functional equivalents share similar (1) structural characteristics; (2) biochemical activities and molecular interactions; (3) cellular responses or activities; or (4) phenotypic effects.

II.D.2. LINKING SIGNATURE SEQUENCES TO CONSERVATION OF STRUCTURAL CHARACTERISTICS

Proteins with related functions show similar three-dimensional structures but may not show extensive amino acid sequence similarity. Typically, proteins need only share a single motif or low similarity in multiple domains to exhibit similar structural features, such as alpha helix, beta sheet, charge residues, stretches of hydrophobicity, etc. Conserved structural features have been implicated in ligand binding by receptor proteins, binding to a class of substrates, polynucleotide binding, or protein-protein interactions.

Based on the signature sequences and the Matrix Tables described herein, a number of motifs can be discerned. Motifs are identified as regions in the signature sequence which are constant in a majority of the members of the group. Example motifs can be found among Applicant's data which are shared in the range of 75% to 95% of group members

Typically, a region of the consensus sequence is constant if, at each position of the region, the preferred amino acid is chosen from a single class of amino acids; even more typically, the

preferred amino acid is a single amino acid. The region can contain a number of positions where an amino acid can be chosen. However, these variable positions are usually less than 15% of the total number of residues in the region; more usually, less than 10%; even more usually, less than 5%.

Generally, a domain is considered to be well defined if the consensus sequence is constructed from sequences from at least 2 organisms; more preferably, at least 3 organisms; even more preferably four organisms or greater.

Primary domains are best identified from the data presented for the 10^{-10} probability criteria. Using this parameter, the largest number of proteins is associated into a group. Consequently, the signature sequence exhibits the greatest amount of variability. The conserved regions, the domains or motifs of the signature contrast against the variable regions. These variable regions become obvious when sequences from more proteins are compared.

Signature sequences revealed in the 10^{-30} and 10^{-50} e-value classes show more conservation in the domains, and can even display a degree of conservation in what is considered the variable regions in the 10^{-10} analyses. These more extensively-conserved domains can reflect higher similarity in function – completely orthologous functions. Proteins that share a number of conserved domains, in the same relative order from N terminus to C terminus, are even more likely to be completely orthologous. Nevertheless, because of the natural divergence that occurs in non-conserved regions during evolution and species differentiation, orthologs can be proteins with only the domains conserved and therefore be present in the 10^{-30} and 10^{-10} p value classes of the Ortholog Table.

II.D.3. LINKING SIGNATURE SEQUENCES TO CONSERVATION OF BIOCHEMICAL ACTIVITIES AND MOLECULAR INTERACTIONS

Proteins that possess the same defined domains or motifs are likely to carry out the same biochemical activity or interact with a similar class of target molecule, e.g., DNA, RNA, proteins, etc. Thus, the pFAM domains listed in the Reference Tables are routinely used as predictors of these properties. Substrates and products for the specific reactions can vary from protein to protein. Where the substrates, ligands, or other molecules bound are identical the affinities may differ between the proteins. Typically, the affinities exhibited by different functional equivalents varies no

more than 50%; more typically, no more than 25%; even more typically, no more than 10%; or even less.

Proteins with very similar biochemical activities or molecular interactions will share similar structural properties, such as substrate grooves, as well as sequence similarity in more than one motif. Usually, the proteins will share at least two motifs of the signature sequence; more usually, three motifs; even more usually four motifs or greater. Typically, the proteins exhibit 70% sequence identity in the shared motifs; more typically, 80% sequence identity; even more typically, 90% sequence identity or greater. These proteins also often share sequence similarity in the variable regions between the constant motif regions. Further, the shared motifs will be in the same order from amino- to carboxyl-termini. The length of the variable regions between the motifs in these proteins, generally, is similar. Specifically, the number of residues between the shared motifs in these proteins varies by less than 25%; more usually, does not vary by less than 20%; even more usually, less than 15%; even more usually less than 10% or even less.

II.D.4. LINKING SIGNATURE SEQUENCES TO CONSERVATION OF CELLULAR RESPONSES OR ACTIVITIES

Proteins that exhibit similar cellular response or activities will possess the structural and conserved domain/motifs as described in the Biochemical Activities and Molecular Interactions above.

Proteins can play a larger role in cellular response than just their biochemical activities or molecular interactions suggest. A protein can initiate gene transcription, which is specific to the drought response of a cell. Other cellular responses and activities include: stress responses, hormonal responses, growth and differential of a cell, cell to cell interactions, etc.

The cellular role or activities of protein can be deduced by transcriptional analyses or phenotypic analyses as well as by determining the biochemical activities and molecular interactions of the protein. For example, transcriptional analyses can indicate that transcription of gene A is greatly increased during flower development. Such data would implicate protein A encoded by gene A, in the process of flower development. Proteins that shared sequence similarity in more than one motif would also act as functional equivalents for protein A during flower development.

II.D.5. LINKING SIGNATURE SEQUENCES TO CONSERVATION OF PHENOTYPIC EFFECTS

Typically, proteins that are grouped together under the most stringent parameters, e-value $\leq 10^{-50}$, are likely orthologs and therefore, when present in the same or equivalent cells can cause similar phenotypic consequences. These proteins have very high sequence similarity. Typically, if one of the members of a group is an *Arabidopsis* protein, then the corn ortholog can rescue an *Arabidopsis* mutant plant that does not produce the *Arabidopsis* protein. The mutant plant would be rescued as the parental “wild-type” phenotype by expression of a coding sequence of the corn protein of the same orthologous group when present in the appropriate cell types of the plant.

Preferably, these functional equivalents have sequence motif identity throughout much of the length of the protein. However, proteins that share very high similarity between a number, usually more than two; even more usually, more than three motifs can act as functional equivalents to produce similar phenotypic effects.

A gene can have coding sequence similarity, i.e., is a homologous. The coding sequence can be sufficient to act as a functional equivalent, although the gene as a whole is not an ortholog. For example, two similar *dwf4* coding sequences were found in the *Arabidopsis* genome. However, this pair of coding sequences had different promoters and hence different roles in *Plantae*. But when one of the pair was placed under the control of its mates’ promoter, the phenotypic effects were similar to the effects produced by its mate coding sequence. Therefore, the coding sequence, but not the genes are orthologous.

III. DESCRIPTION OF THE GENES, GENE COMPONENTS AND PRODUCTS, TOGETHER WITH THEIR USE AND APPLICATION

As described herein, the results of Applicant's experiments provide an understanding of the function and phenotypic implications of the genes, gene components and products of the present invention. Bioinformatic analysis provides such information. The sections of the present application containing the bioinformatic analysis, together with the Sequence and Reference Tables, teach those skilled in the art how to use the genes, gene components and products of the present invention to provide plants with novel characteristics. Similarly, differential expression analysis provides additional such information and the sections of the present application on that analysis; together with the MA_Diff Tables and MA_Cluster Tables, describe the functions of the genes, gene components and products of the present invention which are understood from the results of the differential expression experiments. The same is true with respect to the phenotype data, wherein the results of the Knock-in and Knock-out experiments and the sections of the present application on those experiments provide the skilled artisan with further description of the functions of the genes, gene components and products of the present invention.

As a result, one reading each of these sections of the present application as an independent report will understand the function of the genes, gene components and products of the present invention. But those sections and descriptions can also be read in combination, in an integrated manner, to gain further insight into the functions and uses for the genes, gene components and products of the present invention. Such an integrated analysis does not require extending beyond the teachings of the present application, but rather combining and integrating the teachings depending upon the particular purpose of the reader.

Some sections of the present application describe the function of genes, gene components and products of the present invention with reference to the type of plant tissue (e.g. root genes, leaf genes, etc.), while other sections describe the function of the genes, gene components and products with respect to responses under certain conditions (e.g. Auxin-responsive genes, heat- responsive genes, etc.). Thus, if one desires to utilize a gene understood from the application to be a particular tissue-type of gene, then the condition-specific responsiveness of that gene can be understood from the differential expression tables, and very specific characteristics of actions of that gene in a transformed plant will be understood by recognizing the overlap or intersection of the gene

functions as understood from the two different types of information. Thus, for example, if one desires to transform a plant with a root gene for enhancing root growth and performance, one can know the useful root genes from the results reported in the knock-in and knock-out tables. A review of the differential expression data may then show that a specific root gene is also over-expressed in response to heat and osmotic stress. The function of that gene is then described in (1) the section of the present application that discusses root genes, (2) the section of the present application that discusses heat-responsive genes, and (3) the section of the application that discusses osmotic stress-responsive genes. The function(s) which are commonly described in those three sections will then be particularly characteristic of a plant transformed with that gene. This type of integrated analysis of data can be viewed from the following schematic that summarizes, for one particular gene, the function of that gene as understood from the phenotype and differential expression experiments.

Gene function known from phenotype experiments	Gene function known from first differential expression experiment	Gene function known from second differential expression experiment
Function A	Function A	Function A
Function B		
	Function C	Function C
	Function D	
		Function E
Function F	Function F	Function F
Function G	Function G	
		Function H
Function I		Function I
	Function J	

In the above example, one skilled in the art will understand that a plant transformed with this

particular gene will particularly exhibit functions A and F because those are the functions which are understood in common from the three different experiments.

Similar analyses can be conducted on various genes of the present invention, by which one skilled in the art can effectively modulate plant functions depending upon the particular use or conditions envisioned for the plant.

III.A. ORGAN-AFFECTING GENES, GENE COMPONENTS, PRODUCTS **(INCLUDING DIFFERENTIATION AND FUNCTION)**

III.A.1. ROOT GENES, GENE COMPONENTS AND PRODUCTS

The economic values of roots arise not only from harvested adventitious roots or tubers, but also from the ability of roots to funnel nutrients to support growth of all plants and increase their vegetative material, seeds, fruits, etc. Roots have four main functions. First, they anchor the plant in the soil. Second, they facilitate and regulate the molecular signals and molecular traffic between the plant, soil, and soil fauna. Third, the root provides a plant with nutrients gained from the soil or growth medium. Fourth, they condition local soil chemical and physical properties.

III.A.1.a. Identification Of Root Genes

Root genes identified herein are defined as genes, gene components and products capable of modulating one or more processes in or functions of the root as described below. They are active or potentially active to a greater extent in roots than in most other organs of the plant. These genes and gene products can regulate many plant traits from yield to stress tolerance. That single genes usually affect the development and function of roots and whole plants is a consequence of biological cellular complexity and the role roots play in supporting the growth of whole plants. Examples of such root genes and gene products are shown in the Reference and Sequence Reference and Sequence Tables and sequences encoding polypeptides of the Protein Group and Protein Group Matrix tables or fragments thereof, the Knock-In and Knock-Out Tables, and the MA-diff Tables. The function of many of the protein products gained from comparisons with proteins of known functions, are also given in the REF Tables.

Root Genes Identified By Phenotypic Observations

Root genes are active or potentially active to a greater extent in roots than in some other organs/tissue of the plant. Some of the root genes herein were discovered and characterized from a much larger set of genes in experiments designed to find genes that cause phenotypic changes in root morphology. Such morphological changes include primary and lateral root number, size and length, as well as phenotypic changes of other parts of that plant associated with changes in root morphology.

In these experiments, root genes were identified by either (1) ectopic expression of a cDNA in a plant or (2) mutagenesis of the plant genome. The plants were then cultivated under standardized conditions and any phenotypic differences recorded between the modified plants as compared with the parent plant. The gene(s) causing the changes were deduced from the cDNA inserted or disrupted gene. Phenotypic differences were observed in:

Primary Roots And Root System

- Size, Including Length And Girth
- Number
- Branching
- Root Waving/Curling Characteristics
- Gravitropism Changes
- Agravitropic

Lateral Roots

- Size, Including Length And Girth
- Number
- Branching

Results from screening for these phenotypic changes are reported in the Knock-in and Knock-out Tables. Therefore, any sequence reported in those Tables with one of the above-noted observations is considered a "root gene". A "root gene" is also a sequence which, in the Ortholog Tables or in the MA-clust Tables, is grouped/clustered together with at least one sequence that is identified as such by means of the Knock-in and Knock-out Tables.

Root Genes Identified By Differential Expression

Root genes were also identified by measuring the relative levels of mRNA products in the root versus the aerial portion of a plant. Specifically, mRNA was isolated from roots and root tips of Arabidopsis plants and compared to mRNA isolated from the aerial portion of the plants utilizing microarray procedures. The MA_diff Table(s) reports the transcript levels of the experiment (see EXPT ID: 108594, 108433, 108599, 108434, 108439). For transcripts that had higher levels in the samples than the control, a "+" is shown. A "-" is shown for when transcript levels were reduced in root tips as compared to the control. For more experimental detail see the Example section below.

Roots genes are those sequences that showed differential expression as compared to controls, namely those sequences identified in the MA_diff tables with a "+" or "-" indication.

Roots Genes Identified By Cluster Analyses Of Differential Expression

Roots Genes Identified By Correlation To Genes That Are Differentially Expressed

As described above, the transcription profiles of genes that act together are well correlated. Applicants not only have identified the genes that are differentially expressed in the microarray experiments, but also have identified the genes that act in concert with them. The MA_clust table indicates groups of genes that have well correlated transcription profiles and therefore participate in the same pathway or network.

A pathway or network of Roots genes is any group in the MA_clust that comprises a cDNA ID that also appears in Expt ID 108594, 108433, 108599, 108434, 108439 of the MA_diff table(s).

Roots Genes Identified By Correlation To Genes That Cause Physiological Consequences

Additionally, the differential expression data and the phenotypic observations can be merged to identify pathways or networks of Roots genes. A group in the MA_clust is considered a Roots pathway or network if the group comprises a cDNA ID that also appears in Knock-in or Knock-out tables that causes one or more of the phenotypes described in section above.

Roots Genes Identified By Amino Acid Sequence Similarity

Roots genes from other plant species typically encode polypeptides that share amino acid

similarity to the sequences encoded by corn and Arabidopsis Roots genes. Groups of Roots genes are identified in the Protein Group table. In this table, any protein group that comprises a peptide ID that corresponds to a cDNA ID member of a Roots pathway or network is a group of proteins that also exhibits Roots functions/utilities.

Examples of phenotypes, biochemical activities, and transcription profiles that can be modulated by these genes and gene products are described above and below.

III.A.1.b. Use Of Root Genes To Modulate Phenotypes

The root genes of the instant invention are capable of modulating one or more processes of root structure and/or function including (1) development; (2) interaction with the soil and soil contents; and (3) transport in the plant.

Root genes and gene products can be used to alter or modulate one or more of the following phenotypes.

1.) Development

Roots arise from meristem cells that are protected by a root cap during root elongation, but as the root grows out, the cap cells abscise and the remaining cells differentiate to the tip. Depending on the plant species, some surface cells of roots can develop into root hairs. Some roots persist for the life of the plant; others gradually shorten as the ends slowly die back; some may cease to function due to external influences. The root genes and gene products of this invention are useful to modulate any one or all of these growth and development processes generally, as in root density and root growth; including rate, timing, direction and size.

Root genes and gene products are useful to modulate either the growth and development or other processes in one or more of the following types of roots, including primary, lateral, and adventitious.

Root genes and gene products are useful to modulate cellular changes in cell size, cell division, rate direction and/or number, cell elongation, cell differentiation, lignified cell walls, epidermal cells, such as trichoblasts, and root apical meristem cells (growth and initiation).

Parts of roots (i.e. root architecture) can be modulated by these genes root and gene products to affect root architecture in, for example, the epidermis cortex (including the epidermis,

hypodermis, endodermis, casparian strips, suberized secondary walls, parenchyma, and aerenchyma), stele (including vacuature, xylem, phloem, and pericycle), vasculature, xylem, phloem, root cap, root apical meristem, elongating region, and symmetry.

The polynucleotides and polypeptides of this invention can be used to control the responses to internal plant and root programs as well as to environmental stimuli in the seminal system, nodal system, hormone systems (including Auxin and cytokinin), root cap abscission, root senescence, gravitropism, coordination of root growth and development with that of other organs (including leaves, flowers, seeds, fruits, stems, and changes in soil environment (including water, minerals, ph, and microfauna and flora).

2.) Interaction With Soil And Soil Contents

Roots are sites of intense chemical and biological activities and as a result can strongly modify the soil they contact. Roots coat themselves with surfactants and mucilage to facilitate these activities. Specifically, roots are responsible for nutrient uptake by mobilizing and assimilating water, organic and inorganic compounds, ions and attracting and interacting with beneficial microfauna and flora. Roots also help to mitigate the effects of toxic chemicals, pathogens and stress. Examples of root properties and activities that the genes and gene products of this invention are useful to modulate are root surfactants and mucilage (including mucilage composition, secretion rate and time, surfactant); nutrient uptake of water, nitrate and other sources of nitrogen, phosphate, potassium, and micronutrients (e.g. iron, copper, etc.); microbes and nematodes associations (such as bacteria including nitrogen-fixing bacteria, mycorrhizae, and nodule-forming and other nematodes); oxygen (including transpiration); detoxification of iron, aluminum, cadmium, mercury, salt, and other heavy metals and toxins); pathogen interactions/control (including chemical repellents (includes glucosinolates (GSL), which release pathogen-controlling isothiocyanates); and changes in soil properties, (such as Ph, mineral depletion, and rhizosheath).

3) Transport Of Materials In Plants

Uptake of nutrients by roots produces a "source-sink" effect in a plant. The greater the source of nutrients, the larger "sinks," such as stems, leaves, flowers, seeds, fruits, etc. can grow.

Thus, root genes and gene products are useful to modulate the vigor and yield of the plant overall as well as distinct cells, organs, or tissues. The root genes and gene products are, therefore, useful to modulate vigor (including plant nutrition, growth rate (such as whole plant, including height, flowering time, etc.), seedling, coleoptile elongation, young leaves, stems, flowers, seeds, fruit, and yield (including biomass (such as fresh and dry weight during any time in plant life, including maturation and senescence), root/tuber yield (such as number, size, weight, harvest index, content and composition, (i.e. amino acid, jasmonate, oil, protein and starch), number of flowers, seed yield, number, size, weight, harvest index, content and composition (e.g. amino acid, jasmonate, oil, protein and starch), and fruit yield (such as number, size, weight, harvest index, post harvest quality, content and composition, (e.g. amino acid, jasmonate, oil, protein and starch)).

Additional Uses Of Plants With Modified Roots

Plants with roots modified in one or more of the properties described above are used to provide:

- A. Higher vigor and yield of plants and harvested products due to pathogen resistance from conditioning the soil with plant-derived chemicals and/or more tolerance to stresses such as drought, flooding and anoxia.
- B. Better Animal (Including Human) Nutrition
- C. Improved Dietary Mineral Nutrition
- D. Better Plant Survival
 - (a) Decreased Lodging
 - (b) More Efficient Transport
 - (c) More Efficient Physiology
 - (d) More Efficient Metabolism
- E. Better Resistance To Plant Density Effects
- F. Increased Yield Of Valuable Molecules
- G. More Efficient Root Nodulation
- H. Better Access To Rhizobia Spray Application, For Anaerobic Soils
- I. Easier Crop Harvesting And Ground Tillage

J. Decreased Soil Erosion

To regulate any of the phenotype(s) above, activities of one or more of the root genes or gene products is modulated and tested by screening for the desired trait. Specifically, the gene, mRNA levels, or protein levels can be altered in a plant utilizing the procedures described herein and the phenotypes can be assayed. As an example, a plant can be transformed according to Bechtold and Pelletier (1998, Methods. Mol. Biol. 82:259-266) and/or screened for variants as in Winkler et al. (1998) Plant Physiol 118: 743-50 and visually inspected for the desired phenotype or metabolically and/or functionally assayed according to Dolan et al. (1993, Development 119: 71-84), Dolan et al. (1997, Development 124: 1789-98), Crawford and Glass (1998, Trends Plant Science 3: 389-95), Wang et al. (1998, PNAS USA 95: 15134-39), Gaxiola et al. (1998, PNAS USA 95: 4046-50), Apse et al. (1999, Science 285: 1256-58), Fisher and Long (1992, Nature 357: 655-60), Schneider et al. (1998, Genes Devel 12: 2013-21) and Hirsch (1999, Curr Opin Plant Biol. 2: 320-326).

III.A.1.c. Use Of Root Genes To Modulate Biochemical Activities

The activities of one or more of the root genes can be modulated to change biochemical or metabolic activities and/or pathways such as those noted below. Such biological activities can be measured according to the citations included in the Table below:

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
Association Of Root Morphology With Nitrogen Fixing Bacteria	<ul style="list-style-type: none"> • Cell-Cell Recognition • Cell Wall Degradation 	Gage et al. (1996) J Bacteriol 178: 7159-66
Primary Root, Lateral Root, And Root Hair <ul style="list-style-type: none"> • Initiation • Spacing 	<ul style="list-style-type: none"> • Cell Division/Elongation • Cell Differentiation • Cell Expansion • Auxin Mediated Response 	Schneider et al. (1998) Genes Devel 12: 2013-21 Casimiro et al. (2001). Plant Cell 13:843-852.

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
<ul style="list-style-type: none"> Elongation Branching 	Pathways	<p>Rogg et al. (2001). Plant Cell 13:465-480.</p> <p>Gaedeke et al. (2001). EMBO J. 20:1875-1887.</p> <p>Neuteboom et al. (1999). Plant Mol. Biol. 39:273-287.</p> <p>Schindelman et al. (2001). Genes and Dev. 15:1115-1127.</p> <p>Rashotte et al. (2001) Plant Cell 13:1683-1697.</p> <p>Zhang et al. (2000). J Exp Bot 51:51-59.</p> <p>Zhang et al. (1998) Science 279: 407-409.</p>
Metabolism	<ul style="list-style-type: none"> Organic Molecule Export 	<p>Moody et al. (1988) Phytochemistry 27: 2857-61.</p>
	<ul style="list-style-type: none"> Ion Export 	<p>Uozumi et al. (2000) Plant Physiol 122: 1249-59</p> <p>Frachisse et al. (2000) Plant J 21: 361-71</p>
	<ul style="list-style-type: none"> Nutrient Uptake 	<p>Frachisse et al. (2000) Plant J. 21: 361-71</p> <p>Uozumio et al. (2000) Plant Physiol 122: 1249-59</p> <p>Williamson et al. (2001).</p>

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
		Plant Physiol. 126:875-882. Zhang et al. (2000). J Exp Bot 51:51-59. Zhang et al. (1998). Science 279:4 07-409. Coruzzi et al. (2001). Plant Physiol. 125: 61-64.
Root Gravitropism And Waving	<ul style="list-style-type: none"> Reactive Oxygen Species (ROS) Such As Superoxide Anions And H₂O₂ Production Auxin Transport Pathways Flavonoid Inhibition Of Auxin Transport Function Changes In Root Cap Ph Starch Synthesis And Storage Cell Differentiation Cell Elongation 	Joo et al. (2001) Plant Physiol. 126:1055-60. Vitha et al. (2000). Plant Physiol. 122: 453-461. Tasaka et al. (2001) Int Rev Cytol 206:135-54. Brown et al. (2001) Plant Physiol 126:524-35. Fasano et al. (2001) Plant Cell 13:907-22. MacCleery et al. (1999). Plant Physiol 120:183-92 Blancaflor et al. (1998). Plant Physiol 116:213-22 Schneider et al. (1998) Genes Devel 12: 2013-21

Other biological activities that can be modulated by the root genes and gene products are listed in the Reference tables. Assays for detecting such biological activities are described in the Protein Domain table.

III.A.1.d. Use Of Root Genes To Modulate Transcription Levels Of
Plant Genes

Many genes are “up regulated “ or “down regulated” because they belong to networks or cascades of genes. Thus some root genes are capable of regulating many other gene activities via these networks and hence complex phenotypes. Examples of transcription profiles of root genes are described in the Table below with associated biological activities. “Up-regulated” profiles are those where the concentrations of the mRNA in total mRNA are higher in roots as compared to aerial parts of a plant; and vice-versa for “down-regulated” profiles.

TRANSCRIPT LEVELS	TYPE OF GENES	PHYSIOLOGICAL CONSEQUENCES	EXAMPLES OF BIOCHEMICAL ACTIVITY
Up Regulated Transcripts	<p>Genes Expressed In Root Development</p> <p>Responders To Micro-Organismal Symbionts And Parasites</p> <p>Genes involved in polar Auxin transport</p>	<ul style="list-style-type: none"> • Primary Root, Lateral Root, and/or Root Hair Growth and Differentiation • Microorganism Perception • Entrapment Of Microorganismal Symbionts • Nutrient Uptake • Synthesis Of Metabolites And/Or Proteins • Modulation Of Transduction Pathways 	<ul style="list-style-type: none"> • Transporters • Metabolic Enzymes • Change In Cell Membrane Structure And Potential • Kinases, Phosphatases, G-Proteins • Transcription Activators • Change In Chromatin Structure And/Or Localized DNA Topology • Cell Wall Proteins • Ca⁺⁺ Fluctuation

TRANSCRIPT LEVELS	TYPE OF GENES	PHYSIOLOGICAL CONSEQUENCES	EXAMPLES OF BIOCHEMICAL ACTIVITY
	<p>Genes involved in starch deposition in the roots</p> <p>Genes involved in production of reactive oxygen species</p> <p>Genes involved in flavonoid synthesis</p>	<ul style="list-style-type: none"> • Specific Gene Transcription Initiation • Nutrient Uptake Enhancement • Gravitropic growth of roots • Associations with rhizobia are stimulated 	<ul style="list-style-type: none"> • Reactive Oxygen Species (ROS) production
Down-Regulated Transcripts	<p>Genes Repressed In Root Development</p> <p>Responders To Micro-Organismal Symbionts And Parasites</p> <p>Genes With Discontinued Expression Or</p>	<ul style="list-style-type: none"> • Negative Regulation Of Primary Root, Lateral Root, and/or Root Hair Production Released • Changes In Pathways And Processes Operating In Cells • Changes In Metabolism 	<ul style="list-style-type: none"> • Transcription Factors • Kinases, Phosphatases, G-Proteins • Change In Chromatin Structure And/Or DNA Topology • Stability Of Factors For Protein Synthesis And Degradation

TRANSCRIPT LEVELS	TYPE OF GENES	PHYSIOLOGICAL CONSEQUENCES	EXAMPLES OF BIOCHEMICAL ACTIVITY
	UnsTable mRNA In Presence Of Root And/Or Micro- Organismal Symbionts	<ul style="list-style-type: none">• Inhibition of root gravitropism	<ul style="list-style-type: none">• Metabolic Enzymes

Changes in the function or development of roots are the result of modulation of the activities of one or more of these many root genes and gene products. These genes and/or products are responsible for effects on traits such as plant vigor and seed yield, especially when plants are growing in the presence of soil borne biotic or abiotic stresses or when they are growing in barren conditions or in soils depleted of certain minerals.

Root genes, gene components and gene products can act alone or in combination as described in the introduction. Of particular interest are combinations of these genes and gene products with those that modulate stress tolerance and/or metabolism. Stress tolerance and metabolism genes and gene products are described in more detail in the sections below.

USE OF PROMOTERS OF ROOT GENES

Promoters of root genes, as described in the Reference tables, for example, can be used to modulate transcription that is induced by root development or any of the root biological processes or activities above. For example, when a selected polynucleotide sequence is operably linked to a promoter of a root gene, then the selected sequence is transcribed in the same or similar temporal, development or environmentally-specific patterns as the root gene from which the promoter was taken. The root promoters can also be used to activate antisense copies of any coding sequence to achieve down regulation of its protein product in roots. They can also be used to activate sense copies of mRNAs by RNA interference or sense suppression in roots.

III.A.2. ROOT HAIR GENES, GENE COMPONENTS AND PRODUCTS

Root hairs are specialized outgrowths of single epidermal cells termed trichoblasts. In many and perhaps all species of plants, the trichoblasts are regularly arranged around the perimeter of the root. In Arabidopsis, for example, trichoblasts tend to alternate with non-hair cells or atrichoblasts. This spatial patterning of the root epidermis is under genetic control, and a variety of mutants have been isolated in which this spacing is altered or in which root hairs are completely absent.

III.A.2.a. Identification Of Root Hair Genes

Root hair genes identified herein are defined as genes, gene components and products capable of modulating one or more processes in or the function of root hairs as described below. Root hairs are capable of controlling or influencing many plant traits, also as shown below. Examples of such root hair development genes and gene products are shown in the Reference and Sequence Tables. The protein products of many of these genes are also identified in these Tables.

Root Hair Genes Identified by Differential Expression

These genes were discovered and characterized from a much larger set of genes by experiments designed to find genes whose mRNA products are associated specifically with root hairs. These experiments made use of the arabidopsis mutant "root hairless" (rhl), which does not develop root hairs. By comparing gene expression profiles of rhl roots with those of wild type roots grown in identical conditions, genes specifically expressed in root hairs were revealed. The MA_diff Table(s) reports the transcript levels of the experiment (see EXPT ID: 108594, 108433). For transcripts that had higher levels in the samples than the control, a "+" is shown. A "-" is shown for when transcript levels were reduced in root tips as compared to the control. For more experimental detail see the Example section below.

Root Hairs genes are those sequences that showed differential expression as compared to controls, namely those sequences identified in the MA_diff tables with a "+" or "-" indication.

Root Hairs Genes Identified By Cluster Analyses Of Differential Expression

Root Hairs Genes Identified By Correlation To Genes That Are Differentially Expressed

As described above, the transcription profiles of genes that act together are well correlated. Applicants not only have identified the genes that are differentially expressed in the microarray experiments, but also have identified the genes that act in concert with them. The MA_clust table indicates groups of genes that have well correlated transcription profiles and therefore participate in the same pathway or network.

A pathway or network of Root Hairs genes is any group in the MA_clust that comprises a cDNA ID that also appears in Expt ID 108594, 108433 the MA_diff table(s).

Root Hairs Genes Identified By Correlation To Genes That Cause Physiological Consequences

Additionally, the differential expression data and the phenotypic observations can be merged to identify pathways or networks of Root Hairs genes. A group in the MA_clust is considered a Root Hairs pathway or network if the group comprises a cDNA ID that also appears in Knock-in or Knock-out tables that causes one or more of the phenotypes described in section above.

Root Hairs Genes Identified By Amino Acid Sequence Similarity

Root Hairs genes from other plant species typically encode polypeptides that share amino acid similarity to the sequences encoded by corn and Arabidopsis Root Hairs genes. Groups of Root Hairs genes are identified in the Protein Group table. In this table, any protein group that comprises a peptide ID that corresponds to a cDNA ID member of a Root Hairs pathway or network is a group of proteins that also exhibits Root Hairs functions/utilities.

Examples of phenotypes, biochemical activities, and transcript profiles that can be modulated by these genes and gene products are described above and below.

III.A.2.b. Use Of Root Hair Development Genes To Modulate Phenotypes

The root hair development genes of the instant invention are useful to modulate one or more processes of root hair structure and/or function including (1) development; (2) interaction with the soil and soil contents; (3) uptake and transport in the plant; and (4) interaction with microorganisms.

1.) Development

The surface cells of roots can develop into single epidermal cells termed trichoblasts or root hairs. Some of the root hairs will persist for the life of the plant; others will gradually die back; some may cease to function due to external influences. The genes and gene products of this invention are useful to modulate any one or all of these growth and development process generally, as in root hair density or root hair growth; including rate, timing, direction, and size, for example. Processes that are regulated by these genes and gene products include cell properties such as cell size, cell division, rate and direction and number, cell elongation, cell differentiation, lignified cell walls, epidermal cells (including trichoblasts) and root apical meristem cells (growth and initiation); and root hair architecture such as leaf cells under the trichome, cells forming the base of the trichome, trichome cells, and root hair responses.

The genes and gene products of this invention are useful to modulate one or more of the growth and development processes in response to internal plant programs or environmental stimuli in, for example, the seminal system, nodal system, hormone responses, Auxin, root cap abscission, root senescence, gravitropism, coordination of root growth and development with that of other organs (including leaves, flowers, seeds, fruits, and stems), and changes in soil environment (including water, minerals, Ph, and microfauna and flora).

2.) Interaction With Soil And Soil Contents

Root hairs are sites of intense chemical and biological activity and as a result can strongly modify the soil they contact. Roots hairs can be coated with surfactants and mucilage to facilitate these activities. Specifically, roots hairs are responsible for nutrient uptake by

mobilizing and assimilating water, reluctant ions, organic and inorganic compounds and chemicals. In addition, they attract and interact with beneficial microfauna and flora. Root hairs also help to mitigate the effects of toxic ions, pathogens and stress. Examples of root hair properties and activities that the genes and gene products of the invention are useful to modulate include root hair surfactant and mucilage (including composition and secretion rate and time); nutrient uptake (including water, nitrate and other sources of nitrogen, phosphate, potassium, and micronutrients (e.g. iron, copper, etc.); microbe and nematode associations (such as bacteria including nitrogen-fixing bacteria, mycorrhizae, nodule-forming and other nematodes, and nitrogen fixation); oxygen transpiration; detoxification effects of iron, aluminum, cadmium, mercury, salt, and other soil constituents; pathogens (including chemical repellents) glucosinolates (GSLI), which release pathogen-controlling isothiocyanates; and changes in soil (such as Ph, mineral excess and depletion), and rhizosheath.

3.) Transport Of Materials In Plants

Uptake of the nutrients by the root and root hairs contributes a source-sink effect in a plant. The greater source of nutrients, the more sinks, such as stems, leaves, flowers, seeds, fruits, etc. can draw sustenance to grow. Thus, root hair development genes and gene products are useful to modulate the vigor and yield of the plant overall as well as of distinct cells, organs, or tissues of a plant. The genes and gene products, therefore, can modulate Vigor, including plant nutrition, growth rate (such as whole plant, including height, flowering time, etc., seedling, coleoptile elongation, young leaves, stems, flowers, seeds and fruit) and yield, including biomass (fresh and dry weight during any time in plant life, including maturation and senescence), number of flowers, number of seeds, seed yield, number, size, weight and harvest index (content and composition, e.g. amino acid, jasmonate, oil, protein and starch) and fruit yield (number, size, weight, harvest index, and post harvest quality).

Additional Uses of Plants with Modified Root Hairs

Plants with root hairs modified in one or more of the properties described above are used to provide:

- A. Higher vigor and yield of plant and harvested products due to pathogen resistance from conditioning the soil with plant-derived chemicals and/or more tolerance to stresses such as drought, flooding and anoxia
- B. Better Animal (Including Human) Nutrition
- C. Improved Dietary Mineral Nutrition
- D. Increased Plant Survival By Decreasing Lodging
- E. Better Plant Survival By:
 - (a) Decreased Lodging
 - (b) More Efficient Transport
 - (c) More Efficient Physiology
 - (d) More Efficient Metabolism
- F. Increased Yield Of Valuable Molecules

Root Hair Modulation

To regulate any of the phenotype(s) above, activities of one or more of the root hair genes or gene products is modulated and tested by screening for the desired trait. Specifically, the gene, mRNA levels, or protein levels are altered in a plant utilizing the procedures described herein and the phenotypes can be assayed. As an example, a plant can be transformed according to Bechtold and Pelletier (1998, Methods. Mol. Biol. 82:259-266) and/or screened for variants as in Winkler et al. (1998) Plant Physiol 118: 743-50 and visually inspected for the desired phenotype or metabolically and/or functionally assayed according to Dolan et al. (1993, Development 119: 71-84), Dolan et al. (1997, Development 124: 1789-98), Crawford and Glass (1998, Trends Plant Science 3: 389-95), Wang et al. (1998, PNAS USA 95: 15134-39), Gaxiola et al. (1998, PNAS USA 95: 4046-50), Apse et al. (1999, Science 285: 1256-58), Fisher and Long (1992, Nature 357: 655-60), Schneider et al. (1998, Genes Devel 12: 2013-21) and Hirsch (1999, Curr Opin Plant Biol. 2: 320-326).

III.A.2.c. Use Of Root Hair Development Genes To Modulate Biochemical Activities

The activities of one or more of the root hair development genes can be modulated to change biochemical or metabolic activities and/or pathways such as those noted below. Such biological activities can be measured according to the citations included in the table below:

Process	Biochemical Or-Metabolic Activities And/Or Pathways	Citations Including Assays
Association Of Root Hair With Nitrogen Fixing Bacteria	<ul style="list-style-type: none"> Functions Associated With Root Hair Curling And Signal Transduction 	Gage et al. (1996) J Bacteriol 178: 7159-66
Root Hair <ul style="list-style-type: none"> Spacing Initiation Elongation 		Schneider et al. (1998) Genes Devel 12: 2013-21
Metabolism	<ul style="list-style-type: none"> Organic Molecule Export 	Moody et al. (1988) Phytochemistry 27: 2857-61
	<ul style="list-style-type: none"> Ion Export 	Uozumi et al. (2000) Plant Physiol 122: 1249-59 Frachisse et al. (2000) Plant J 21: 361-71
Nutrient Uptake	<ul style="list-style-type: none"> Nutrient Uptake 	Frachisse et al. (2000) Plant J 21: 361-71 Uozumio et al. (2000) Plant Physiol 122: 1249-59

Other biological activities that can be modulated by the root hair genes and gene products are listed in the Reference tables. Assays for detecting such biological activities are described in the Protein Domain table.

III.A.2.d. Use Of Root Hair Genes, Gene Components And Product
To Modulate Transcription Levels

Many genes are “up regulated” or “down regulated” in root hairs or associated with root hair formation because genes are regulated in networks. Thus some root hairs genes are useful to regulate the activities of many other genes, directly or indirectly to influence complex phenotypes. Examples of transcription profiles of root genes are described in the Table below with associated biological activities. “Up regulated” profiles are those where the mRNA levels are higher when the rhl gene is inhibited as compared to when rhl gene is not inhibited; and vice-versa for “down-regulated” profiles.

Transcript Levels	Type Of Genes	Physiological Consequences	Examples Of Biochemical Activity
Down Regulated Transcripts	<ul style="list-style-type: none"> Genes Expressed In Root Hair Development Responders To Micro-Organismal Symbionts And Parasites 	<ul style="list-style-type: none"> Root Hair Formation Microorganism Perception Entrapment Of Microorganismal Symbionts Nutrient Uptake Synthesis Of Metabolites And/Or Proteins Modulation Of Transduction Pathways Specific Gene Transcription Initiation 	<ul style="list-style-type: none"> Transporters Metabolic Enzymes Change In Cell Membrane Structure And Potential Kinases, Phosphatases, G-Proteins Transcription Activators Change In Chromatin Structure And/Or Localized DNA Topology Cell Wall Proteins

Transcript Levels	Type Of Genes	Physiological Consequences	Examples Of Biochemical Activity
		<ul style="list-style-type: none"> Nutrient Uptake Enhancement 	
Up-Regulated Transcripts	<ul style="list-style-type: none"> Genes Repressed In Roots Making Hairs Responders To Micro-Organismal Symbionts And Parasites Genes With Discontinued Expression Or Unstable mRNA In Presence Of Root Hairs And/Or Micro-Organismal Symbionts 	<ul style="list-style-type: none"> Negative Regulation Of Hair Production Released Changes In Pathways And Processes Operating In Cells Changes In Metabolism 	<ul style="list-style-type: none"> Transcription Factors Kinases, Phosphatases, G-Proteins Change In Chromatin Structure And/Or DNA Topology Stability Of Factors For Protein Synthesis And Degradation Metabolic Enzymes Cell Wall Proteins

Changes in the patterning or development of root hairs are the result of modulation of the activities of one or more of these many root hair genes and gene products. These genes and/or products are responsible for effects on traits such as plant vigor and seed yield, especially when

plants are growing in the presence of biotic or abiotic stresses or when they are growing in barren conditions or in soils depleted of certain minerals.

Root hair genes and gene products can act alone or in combination as described in the introduction. Of particular interest are combination of these genes and gene products with those that modulate stress tolerance and/or metabolism. Stress tolerance and metabolism genes and gene products are described in more detail in the sections below.

USE OF PROMOTERS OF ROOT HAIR GENES

Promoters of root hair development genes, as described in the Reference tables, for example, are useful to modulate transcription that is induced by root hair development or any of the following phenotypes or biological activities above. For example, any desired sequence can be transcribed in similar temporal, tissue, or environmentally-specific patterns as the root hair genes when the desired sequence is operably linked to a promoter of a root hair responsive gene.

III.A.3. LEAF GENES, GENE COMPONENTS AND PRODUCTS

Leaves are responsible for producing most of the fixed carbon in a plant and are critical to plant productivity and survival. Great variability in leaf shapes and sizes is observed in nature. Leaves also exhibit varying degrees of complexity, ranging from simple to multi-compound. Leaf genes as defined here, not only modulate morphology, but also influence the shoot apical meristem, thereby affecting leaf arrangement on the shoot, internodes, nodes, axillary buds, photosynthetic capacity, carbon fixation, photorespiration and starch synthesis. Leaf genes elucidated here can be used to modify a number of traits of economic interest from leaf shape to plant yield, including stress tolerance, and to modify the efficiency of synthesis and accumulation of specific metabolites and macromolecules.

III.A.3.a. Identification Of Leaf Gene, Gene Components And Products

Leaf genes identified herein are defined as genes, active or potentially active to greater extent in leaves than in some other organs of the plant or as genes that affect leaf properties. These genes and gene components are useful for modulating one or more processes in or functions of leaves, as described below, to improve plant traits ranging from yield to stress

tolerance. Examples of such leaf genes and gene products are shown in the Reference and Sequence Tables and sequences encoding polypeptides of the Protein Group and Protein Group Matrix tables or fragments thereof, Knock-In, Knock-Out and MA_diff Tables. The biochemical functions of the protein products of many of these genes determined from comparisons with known proteins are also given in the Reference tables.

Leaf Genes Identified by Phenotypic Observations

Some leaf genes were discovered and characterized from a much larger set of genes by experiments designed to find genes that cause phenotypic changes in leaf, petiole, internode, and cotyledon morphology.

In these experiments, leaf genes were identified by either (1) ectopic expression of a cDNA in a plant or (2) mutagenesis of the plant genome. The plants were then cultivated and one or more of the following leaf phenotypes, which varied from the parental "wild-type", were observed:

- A. Changes In Seedling Stage Cotyledons
 - Cup Shaped
 - Curled
 - Horizontally Oblong
 - Long Petioles
 - Short Petioles
 - Silver
 - Tricot
 - Wilted
- B. Changes In Rosette And Flowering Stage Leaf Shapes
 - Cordate
 - Cup-Shaped
 - Curled
 - Fused
 - Lanceolate
 - Lobed

- Long Petioles
 - Short Petioles
 - Oval
 - Ovate
 - Serrate
 - Trident
 - Undulate
 - Vertically Oblong
- C. Changes In Cauline, Flowering Leaf Shape
- Misshapen
 - Other
- D. Changes In Leaf Pigment
- Albino
 - Dark Green Pigment
 - High Anthocyanin
 - Interveinal Chlorosis
 - Yellow Pigment
- E. Changes In Leaf Size
- F. Changes In Seedling Stage Hypocotyl
- Long
 - Short
- G. Changes In Leaf Number
- H. Changes In Wax Deposition
- Glossy Rosette And Flowering Stage Leaves
 - Altered Wax Deposition On The Bolt

Leaf Genes Identified by Differential Expression

Also, leaf genes were identified in experiments in which the concentration of mRNA products in the leaf, or stem, or Knock-out mutant 3642-1 were compared with to a control. The MA_diff Table(s) reports the transcript levels of the experiment (see EXPT ID: 108477, 108512,

108497, 108498, 108598). For transcripts that had higher levels in the samples than the control, a "+" is shown. A "-" is shown for when transcript levels were reduced in root tips as compared to the control. For more experimental detail see the Example section below.

Leaf genes are those sequences that showed differential expression as compared to controls, namely those sequences identified in the MA_diff tables with a "+" or "-" indication.

Leaf Genes Identified By Cluster Analyses Of Differential Expression

Leaf Genes Identified By Correlation To Genes That Are Differentially Expressed

As described above, the transcription profiles of genes that act together are well correlated. Applicants not only have identified the genes that are differentially expressed in the microarray experiments, but also have identified the genes that act in concert with them. The MA_clust table indicates groups of genes that have well correlated transcription profiles and therefore participate in the same pathway or network.

A pathway or network of Leaf genes is any group in the MA_clust that comprises a cDNA ID that also appears in Expt ID 108477, 108512, 108497, 108498, 108598 of the MA_diff table(s).

Leaf Genes Identified By Correlation To Genes That Cause Physiological Consequences

Additionally, the differential expression data and the phenotypic observations can be merged to identify pathways or networks of Leaf genes. A group in the MA_clust is considered a Leaf pathway or network if the group comprises a cDNA ID that also appears in Knock-in or Knock-out tables that causes one or more of the phenotypes described in section above.

Leaf Genes Identified By Amino Acid Sequence Similarity

Leaf genes from other plant species typically encode polypeptides that share amino acid similarity to the sequences encoded by corn and Arabidopsis Leaf genes. Groups of Leaf genes are identified in the Protein Group table. In this table, any protein group that comprises a peptide ID that corresponds to a cDNA ID member of a Leaf pathway or network is a group of proteins that also exhibits Leaf functions/utilities.

It is assumed that (i) the genes preferentially expressed in leaves are concerned with

specifying leaf structures and the synthesis of all the constituent molecules and (ii) that the genes repressed in leaves specify products that are not required in leaves or that could inhibit normal leaf development and function.

Examples of phenotypes, biochemical activities, and transcription profiles that are modulated by using selected members of these genes and gene products, singly or in combination, are described below.

III.A.3.b. Use Of Leaf Genes, Genes Components And Products To Modulate Phenotypes

Leaves are critical for the performance and industrial utility of plants. There is extensive evidence that the number, size, shape, position, timing of synthesis, timing of senescence and chemical constitution are very important for agriculture, horticulture and uses of plants as chemical factories for making valuable molecules. Many improvements already demonstrated over past decades have involved genetic modifications to leaves. Therefore, the leaf genes and gene components of this invention offer considerable opportunities for further improving plants for industrial purposes. When the leaf genes and/or gene components are mutated or regulated differently, they are capable of modulating one or more of the processes determining leaf structure and/or function including (1) development; (2) interaction with the environment and (3) photosynthesis and metabolism.

1.) Development

The leaf genes, gene components and products of the instant invention are useful to modulate one or more processes of the stages of leaf morphogenesis including: stage 1- organogenesis that gives rise to the leaf primordium; stage 2- delimiting basic morphological domains; and stage 3- a coordinated processes of cell division, expansion, and differentiation. Leaf genes include those genes that terminate as well as initiate leaf development. Modulating any or all of the processes leads to beneficial effects either at specific locations or throughout the plant, such as in the cotyledons, major leaves, cauline leaves, or petioles.

Leaf genes, gene components and gene products are useful to modulate changes in leaf cell size, cell division (rate and direction), cell elongation, cell differentiation, stomata size,

number, spacing and activity, trichome size and number, xylem and phloem cell numbers, cell wall composition, and all cell types. The leaf genes are also useful to modulate to change overall leaf architecture, including venation (such as improvements in photosynthetic efficiency, stress tolerance efficiency of solute and nutrient movement to and from the leaf are accomplished by increases or decreases in vein placement and number of cells in the vein); shape, either elongated versus rounded or symmetry, around either (e.g. abaxial-adaxial (dorsiventral) axis, apical-basal (proximodistal) axis, and margin-blade-midrib (lateral) axis; and branching (improved plant performance to biotic and abiotic stress in heavy density planting is achieved by increases or decreases in leaf branch position or leaf branch length).

Shoot apical meristem cells differentiate to become leaf primordia that eventually develop into leaves. The genes, gene components and gene products of this invention are useful to modulate any one or all of these growth and development processes, by affecting timing and rate or planes of cell divisions for example, in response to the internal plant stimuli and/or programs such as embryogenesis; germination; hormones like Auxin leaf senescence; phototropism; coordination of leaf growth and development with that of other organs (such as roots, flowers, seeds, fruits, and stems; and stress-related programs.

2.) Interaction With The Environment

Leaves are the main sites of photosynthesis and have various adaptations for that purpose. Flat laminae provide a large surface for absorbing sunlight; leaves are rich in chloroplasts and mitochondria; stomata in the lower surface of the laminae allow gases to pass into and out of the leaves including water; and an extensive network of veins brings water and minerals into the leaves and transports the sugar products produced by photosynthesis to the rest of the plant. examples of leaf properties or activities that are modulated by leaf genes, gene components and their products to facilitate interactions between a plant and the environment including pigment accumulation; wax accumulation on the surface of leaves (e.g. improved protection of young leaves from water borne pathogen attack such as downey mildew with increased wax production); oxygen gain/loss control; carbon dioxide gain/loss control; water gain/loss control; nutrient transport; light harvesting; chloroplast biogenesis; circadian rhythm control; light/dark adaptation; defense systems against biotic and abiotic stresses; metabolite accumulation; and

secondary metabolite production in leaf mesophyl, epidermis and trichomes (such as increases in antifeeding secondary metabolites such as strictosiden reduce herbivory and decreases in secondary metabolites improve plants as forage by reducing allergens or undigestible compounds).

3.) Photosynthesis And Metabolism

Many of the uses for plants depend on the success of leaves as the powerhouses for plant growth, their ability to withstand stresses and their chemical composition. Leaves are organs with many different cell types and structures. Most genes of a plant are active in leaves and therefore leaves have very diverse of pathways and physiological processes. Pathways and processes that are modulated by leaf genes, gene components and products include photosynthesis, sugar metabolism, starch synthesis, starch degradation, nitrate and ammonia metabolism, amino acid biosynthesis, transport, protein biosynthesis, dna replication, repair, lipid biosynthesis and breakdown, protein biosynthesis, storage and breakdown, nucleotide transport and metabolism, cell envelope biogenesis, membrane formation, mitochondrial and chloroplast biogenesis, transcription and RNA metabolism, vitamin biosynthesis, steroid and terpenoid biosynthesis, devise secondary metabolite synthesis, co-enzyme metabolism, flavonoid biosynthesis and degradation , synthesis of waxes, glyoxylate metabolism, and hormone perception and response pathways.

Uses of Plants that Are Modified as Described Above

Altering leaf genes or gene products in a plant modifies one or more plant traits, to make the plants more useful for specific purposes in agriculture, horticulture and for the production of valuable molecules. The modified plant traits include A higher yield of leaves and their molecular constituents (due to different number, size, weight, harvest index, composition including and amounts and types of carbohydrates, proteins, oils, waxes, etc.; photosynthetic efficiency (e.g. reduced photorespiration), absorption of water and nutrients to enhance yields, including under stresses such as high light, herbicides, and heat, pathways to accumulate new valuable molecules); more optimal leaf shape and architecture – enhancing photosynthesis and enhancing appeal in ornamental species (including size, number, pigment, and aroma; a better

overall plant architecture – enhancing photosynthesis and enhancing appeal in ornamental species petals, sepals, stamens, and carpels; better shade avoidance for maximizing photosynthesis by, for example, altering leaf placement, to improve light capture and photosynthetic efficiency, thereby increasing yields; Reduced negative effects of high planting density, by altering leaf placement to be more vertical instead of parallel to the ground, for instance; More resistance to the deleterious effects of wind and mechanical damage; Better stress tolerance (including without limitation drought resistance, by decreasing water loss, and pathogen resistance, including, for instance, insect resistance through internal insecticide levels and optimizing the leaf shape to prevent runoff of insecticides); and better overall yield and vigor.

Plant yield of biomass and of constituent molecules and plant vigor are modulated to create benefits by genetically changing the growth rate of the whole plant, (including height, flowering time, etc.), seedling, coleoptile elongation, young leaves flowers, seeds, and/or fruit, or by changing the biomass, including fresh and dry weight during any time in plant life, (including maturation and senescence), number of flowers, seed yield including for example, number, size, weight, harvest index, content and composition (e.g. amino acid, jasmonate, oil, protein and starch), and fruit yield (such as number, size, weight, harvest index, content and composition, e.g. amino acid, jasmonate, oil, protein and starch).

To change any of the phenotype(s) in I, II, or III above, activities of one or more of the leaf genes or gene products are modulated in an organism and the consequence evaluated by screening for the desired trait. Specifically, the gene, mRNA levels, or protein levels are altered in a plant utilizing the procedures described herein and the phenotypes can be assayed. As an example, a plant can be transformed according to Bechtold and Pelletier (Methods. Mol. Biol. 82:259-266 (1998)) with leaf gene constructs and/or screened for variants as in Winkler et al., Plant Physiol. 118: 743-50 (1998) and visually inspected for the desired phenotype and metabolically and/or functionally assayed for altered levels of relevant molecules.

III.A.3.c. Use Of Leaf Genes, Gene Components And Products To
Modulate Biochemical Activities

Leaves are complex organs and their structure, function and properties result from the integration of many processes and biochemical activities. Some of these are known from the published literature and some can be deduced from the genes and their products described in this application. Leaf genes, and gene components are used singly or in combination to modify these processes and biochemical activities and hence modify the phenotypic and trait characteristics described above. Examples of the processes and metabolic activities are given in the Table below. The resulting changes are measured according to the citations included in the Table.

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
Metabolism – anabolic and catabolic	<ul style="list-style-type: none"> • Farnesylation • Cell Wall Biosynthesis • Nitrogen Metabolism • Secondary Metabolite Biosynthesis and Degradation 	Pei et al., <u>Science</u> 282 : 287-290 (1998); Cutler et al., <u>Science</u> 273 : 1239 (1996) Goupil et al., <u>J Exptl. Botany</u> 49 :1855-62 (1998) Walch-Liu et al., <u>J Exptl. Botany</u> 51 , 227-237 (2000)
Water Conservation And Resistance To Drought And Other Related Stresses	<ul style="list-style-type: none"> • Stomatal Development And Physiology • Production of polyols • Regulation of salt concentration • ABA response(s) 	Allen et al., <u>Plant Cell</u> 11 : 1785-1798 (1999) Li et al., <u>Science</u> 287 : 300-303 (2000) Burnett et al., <u>J Exptl. Botany</u> 51 : 197-205 (2000) Raschke, In: <u>Stomatal Function</u> , Zeiger et al. Eds., 253-279 (1987)
Transport Anion and Cation Fluxes	<ul style="list-style-type: none"> • Ca²⁺ Accumulation • K⁺ Fluxes • Na⁺ Fluxes • Receptor – ligand binding • Anion and Cation fluxes 	Lacombe et al., <u>Plant Cell</u> 12 : 837-51 (2000); Wang et al., <u>Plant Physiol.</u>

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
		<p><u>118</u>:1421-1429 (1998); Shi et al., <u>Plant Cell</u> <u>11</u>: 2393-2406 (1999) Gaymard et al., <u>Cell</u> <u>94</u>:647-655 (1998) Jonak et al., <u>Proc. Natl. Acad. Sci.</u> <u>93</u>: 11274-79 (1996); Sheen, <u>Proc. Natl. Acad. Sci.</u> <u>95</u>: 975-80 (1998); Allen et al., <u>Plant Cell</u> <u>11</u>: 1785-98 (1999)</p>
Carbon Fixation	<ul style="list-style-type: none"> • Calvin Cycle <ul style="list-style-type: none"> - Photorespiration - Oxygen evolution - RuBisCO • Chlorophyll metabolism • Chloroplast Biogenesis and Metabolism • Fatty Acid and Lipid Biosynthesis • Glyoxylate metabolism • Sugar Transport • Starch Biosynthesis and Degradation 	<p>Wingler et al., <u>Philo Trans R Soe Lond B Biol Sci</u> <u>355</u>, 1517-1529 (2000);</p> <p>Palecanda et al., <u>Plant Mol Biol</u> <u>46</u>, 89-97 (2001); Baker et al., <u>J Exp Bot</u> <u>52</u>, 615-621 (2001)</p> <p>Chen et al., <u>Acta Biochim Pol</u> <u>41</u>, 447-457 (1999) Imlau et al., <u>PlantCell</u> <u>II</u>, 309-322 (1999)</p>

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
Hormone Perception and Growth	<ul style="list-style-type: none"> • Hormone Receptors and Downstream Pathways for <ul style="list-style-type: none"> - ethylene - jasmonic acid - brassinosteroid - gibberellin - Auxin - cytokinin • Activation Of Specific Kinases And Phosphatases 	<p>Tieman et al., <u>Plant J</u> 26, 47-58 (2001)</p> <p>Hilpert et al., <u>Plant J</u> 26, 435-446 (2001)</p> <p>Wenzel et al., <u>Plant Phys</u> 124, 813-822 (2000)</p> <p>Dengler and Kang, <u>Curr Opin Plant Biol</u> 4, 50-56 (2001)</p> <p>Tantikanjana et al., <u>Genes Dev</u> 15, 1577-1580 (2001)</p>

Other biological activities that are modulated by the leaf genes and gene products are listed in the Reference tables. Assays for detecting such biological activities are described in the Protein Domain table, for example.

III.A.3.d. Use Of Leaf Genes, Gene Components And Products To Modulate Transcription Levels

The expression of many genes is “upregulated” or downregulated” in leaves because some leaf genes and their products are integrated into complex networks that regulate transcription of many other genes. Some leaf genes, gene components and products are therefore useful for modifying the transcription of other genes and hence complex phenotypes, as described above. Profiles of leaf gene activities are described in the Table below with associated biological activities. “Up-regulated” profiles are those where the mRNA transcript levels are

higher in leaves as compared to the plant as a whole. "Down-regulated" profiles represent higher transcript levels in the whole plant as compared to leaf tissue only.

TRANSCRIPT LEVELS	TYPE OF GENES WHOSE TRANSCRIPTS ARE CHANGED	PHYSIOLOGICAL CONSEQUENCES OF MODIFYING GENE PRODUCT LEVELS	EXAMPLES OF BIOCHEMICAL ACTIVITIES OF GENE PRODUCTS WITH MODIFIED LEVELS
Up Regulated Transcripts	Genes Involved In Leaf Cell Differentiation, Cell Division, Cell Expansion	<ul style="list-style-type: none"> • Leaf Cells Proliferate And Differentiate; 	<ul style="list-style-type: none"> • Transcription Factors, Signal Transduction Proteins, Kinase And Phosphatases
	Genes Involved In Positive Regulation Of Leaf Genes	<ul style="list-style-type: none"> • Leaf Structures Form And Expand 	<ul style="list-style-type: none"> • Chromatin Remodeling • Hormone Biosynthesis Enzymes • Receptors
	Repressors Of Root And Other Non Leaf Cell Types	<ul style="list-style-type: none"> • Photosynthesis And Plastid Differentiation 	<ul style="list-style-type: none"> • Light Harvesting Coupled To ATP Production • Chlorophyll Biosynthesis

TRANSCRIPT LEVELS	TYPE OF GENES WHOSE TRANSCRIPTS ARE CHANGED	PHYSIOLOGICAL CONSEQUENCES OF MODIFYING GENE PRODUCT LEVELS	EXAMPLES OF BIOCHEMICAL ACTIVITIES OF GENE PRODUCTS WITH MODIFIED LEVELS
	Genes Involved In Photosynthesis	<ul style="list-style-type: none"> • Calvin Cycle Activated • Chloroplast Biogenesis And Plastid Differentiation Activated 	<ul style="list-style-type: none"> • Ribulose Biphosphate Carboxylase • Chloroplast Membranes Synthesis • Chloroplast Ribosome Biogenesis
	Other Genes Involved In Metabolism	<ul style="list-style-type: none"> • Starch Biosynthesis • Lipid Biosynthesis • Nitrogen Metabolism – NO₃ Reduced And Amino Acids Made • Secondary Metabolites Produced 	<ul style="list-style-type: none"> • Starch Synthase • Nitrate Reductase • Terpenoid Biosynthesis • Transcription Factors • Transporters • Kinases • Phosphatases And Signal Transduction Protein • Chromatin Structure Modulators

TRANSCRIPT LEVELS	TYPE OF GENES WHOSE TRANSCRIPTS ARE CHANGED	PHYSIOLOGICAL CONSEQUENCES OF MODIFYING GENE PRODUCT LEVELS	EXAMPLES OF BIOCHEMICAL ACTIVITIES OF GENE PRODUCTS WITH MODIFIED LEVELS
Down Regulated Genes	Genes Involved In Negative Regulation Of Leaf Genes	<ul style="list-style-type: none"> • Leaf Genes Activated And Leaf Functions Induced; • Dark-Adapted Metabolism Suppressed • Meristematic Genes Suppressed • Leaf Metabolic Pathways Induced 	<ul style="list-style-type: none"> • Transcription Factors • Signal Transduction Proteins – Kinases And Phosphatases • Metabolic Enzymes • Chromatin Remodeling Proteins

While leaf polynucleotides and gene products are used singly, combinations of these polynucleotides are often better to optimize new growth and development patterns. Useful combinations include different leaf polynucleotides and/or gene products with a hormone responsive polynucleotide. These combinations are useful because of the interactions that exist between hormone-regulated pathways, nutritional pathways and development.

USE OF LEAF GENE PROMOTERS

Promoters of leaf genes are useful for transcription of desired polynucleotides, both plant and non-plant. If the leaf gene is expressed only in leaves, or specifically in certain kinds of leaf cells, the promoter is used to drive the synthesis of proteins specifically in those cells. For example, extra copies of carbohydrate transporter cDNAs operably linked to a leaf gene

promoter and inserted into a plant increase the “sink” strength of leaves. Similarly, leaf promoters are used to drive transcription of metabolic enzymes that alter the oil, starch, protein, or fiber contents of a leaf. Alternatively, leaf promoters direct expression of non-plant genes that can, for instance, confer insect resistance specifically to a leaf. Additionally the promoters are used to synthesize an antisense mRNA copy of a gene to inactivate the normal gene expression into protein. The promoters are used to drive synthesis of sense RNAs to inactivate protein production via RNA interference.

III.A.4. TRICHOME GENES AND GENE COMPONENTS

Trichomes, defined as hair-like structures that extend from the epidermis of aerial tissues, are present on the surface of most terrestrial plants. Plant trichomes display a diverse set of structures, and many plants contain several types of trichomes on a single leaf. The presence of trichomes can increase the boundary layer thickness between the epidermal tissue and the environment, and can reduce heat and water loss. In many species, trichomes are thought to protect the plant against insect or pathogen attack, either by secreting chemical components or by physically limiting insect access to or mobility on vegetative tissues. The stellate trichomes of *Arabidopsis* do not have a secretory anatomy, but at a functional level, they might limit herbivore access to the leaf in the field. In addition, trichomes are known to secrete economically valuable substances, such as menthol in mint plants.

III.A.4.a. Identification Of Trichome Genes, Gene Components And Products

Trichome genes identified herein are defined as genes or gene components capable of modulating one or more processes in or functions of a trichome, as described below. These genes, their components and products are useful for modulating diverse plant traits from production of secondary metabolites to pathogen resistance. Examples of such trichome genes and gene products are shown in the Reference and Sequence Tables and sequences encoding polypeptides of the Protein Group and Protein Group Matrix tables or fragments thereof, Knock-in, Knock-out, MA-diff and MA-clust. The biochemical functions of the protein products of

many of these genes determined from comparisons with known proteins are also given in the Reference tables.

Trichome Genes Identified by Phenotypic Observation

Trichome genes were discovered and characterized from a much larger set of genes by experiments designed to find genes that cause phenotypic changes in trichome number and morphology on leaf, internode, cotyledon, petiole, and inflorescence. In these experiments, trichome genes were identified by either (1) ectopic expression of a cDNA in a plant or (2) mutagenesis of the plant genome. The plants were then cultivated and one or more of the following phenotypes, which varied from parental "wild-type", were observed: (1) trichome number; (2) trichome spacing (clustering); or (3) trichome branching. The genes regulating trichome phenotypes are identified in the Knock-In and Kncok-Out Tables.

Trichome Genes Identified by Differential Expression

Trichome genes were also discovered and characterized from a much larger set of genes by experiments designed to find genes whose mRNA products are associated specifically or preferentially with trichomes. These experiments made use of an Arabidopsis glabrous mutant and a hairy mutant. By comparing gene expression profiles of the glabrous mutant with those of the hairy mutant grown under identical conditions, genes specifically or preferentially expressed in trichomes were revealed. The MA_diff Table(s) reports the transcript levels of the experiment (see EXPT ID: 108452). For transcripts that had higher levels in the samples than the control, a "+" is shown. A "-" is shown for when transcript levels were reduced in root tips as compared to the control. For more experimental detail see the Example section below.

Trichome genes are those sequences that showed differential expression as compared to controls, namely those sequences identified in the MA_diff tables with a "+" or "-" indication.

Trichome Genes Identified By Cluster Analyses Of Differential Expression

Trichome Genes Identified By Correlation To Genes That Are Differentially Expressed

As described above, the transcription profiles of genes that act together are well correlated. Applicants not only have identified the genes that are differentially expressed in the microarray experiments, but also have identified the genes that act in concert with them. The MA_clust table indicates groups of genes that have well correlated transcription profiles and therefore participate in the same pathway or network.

A pathway or network of Trichome genes is any group in the MA_clust that comprises a cDNA ID that also appears in Expt ID 108452 of the MA_diff table(s).

Trichome Genes Identified By Correlation To Genes That Cause Physiological Consequences

Additionally, the differential expression data and the phenotypic observations can be merged to identify pathways or networks of Trichome genes. A group in the MA_clust is considered a Trichome pathway or network if the group comprises a cDNA ID that also appears in Knock-in or Knock-out tables that causes one or more of the phenotypes described in section above.

Trichome Genes Identified By Amino Acid Sequence Similarity

Trichome genes from other plant species typically encode polypeptides that share amino acid similarity to the sequences encoded by corn and Arabidopsis Trichome genes. Groups of Trichome genes are identified in the Protein Group table. In this table, any protein group that comprises a peptide ID that corresponds to a cDNA ID member of a Trichome pathway or network is a group of proteins that also exhibits Trichome functions/utilities.

It is assumed that the genes differentially expressed in trichomes or leaves producing trichomes are concerned with specifying trichomes and their functions and therefore modulations of such genes and their products modify trichomes and their products.

Examples of phenotypes, biochemical activities, and transcription profiles that can be modulated by selected numbers of these genes and gene products singly or in combinations are described above and below.

III.A.4.b. Use Of Trichome Genes, Gene Components And Products
To Modulate Phenotypes

Trichome genes of the instant invention, when mutated or activated differently, are useful for modulating one or more processes of trichome structure and/or function including: (1) development; (2) plant stress tolerance; and (3) biosynthesis or secretion of trichome-specific molecules. Trichome genes, components and gene products are useful to alter or modulate one or more of the following phenotypes:

1.) Development

Trichome differentiation is integrated with leaf development, hormone levels and the vegetative development phase. The first trichome at the leaf tip appears only after the leaf grows to ~100 μ m in length. Subsequent events proceed basipetally as the leaf grows. As leaf development progresses, cell division patterns become less regular and islands of dividing cells can be observed among differentiated pavement cells with their characteristic lobed morphology. Trichome initiation in the expanding leaf occurs within these islands of cells and often defines points along the perimeter of a circle, with an existing trichome defining the center.

Once a cell enters the trichome pathway it undergoes an elaborate morphogenesis program that has been divided into different stages based on specific morphological hallmarks. The trichome genes, gene components and gene products of this invention are useful to modulate any one or all of these growth and development processes by affecting rate, timing, direction and size, for example. Trichome genes can also affect trichome number and the organs on which they occur, type of trichomes such as glandular trichomes and stellate trichomes; cell properties such as cell size, cell division rate and direction, cell elongation, cell differentiation, secretory cells, trichome number (average trichome number per leaf for mint:13,500,000), cell walls, cell death, and response to reactive oxygen species; trichome architecture such as trichome cell structure, placement on leaf, and secretory systems; and trichome responses. Trichome genes, gene components and gene products of this invention are useful to modulate one or more of the growth and development processes above; as in timing and rate, for example. In addition, the polynucleotides and polypeptides of the invention can control the response of these processes to internal plant programs and signaling molecules such as leaf development, hormones (including

abscisic acid, Auxin, cytokinin, gibberellins, and brassinosteroids, apoptosis; and coordinated trichome growth and development in flowers, stems, petioles, cotyledons, and hypocotyls.

2.) Plant Stress Tolerance

The physical characteristics of trichomes as well as the substances secreted by trichomes are useful in protecting the plant from both biotic and abiotic attacks. Thus, selected trichome genes and gene products can be used to help protect distinct cells, organs, or tissues as well as overall plant yield and vigor. Examples of stresses, tolerances to which are modulated by trichome genes and gene products are drought (e.g., trichome number variation can decrease the surface area that allows evaporation), heat (e.g., trichomes can produce shade and provide protection for meristems), salt, insects (e.g., trichomes can prevent insects from settling on plant surfaces), herbivory (e.g., trichomes can produce harmful chemicals), and ultraviolet light.

3.) Biosynthesis, Accumulation Or Secretion Of Metabolites

The glandular trichomes from various species are shown to secrete and, sometimes, locally synthesize a number of substances including salt, monoterpenes and sesquiterpenes, terpenoids, exudate, insect entrapping substances, antifeedants, pheromones, and others. Therefore, trichome genes can be used to modulate the synthesis, accumulation and secretion of a large number of metabolites especially related to trichome biology. Some are synthesized in response to biotic and abiotic stresses. For a more detailed description of these metabolites see the section "Use of Trichome Genes to Modulate Biochemical Activities" below.

Uses of Plants that Are Modified as Described Above

Altering trichome properties is useful for modifying one or more plant traits making the plants more useful in agriculture, horticulture and for the production of valuable molecules. These plant traits include Production of specific carbohydrates, proteins, oils, aromas, flavors, pigments, secondary metabolites such as menthol (and other monoterpenes), etc., that can be used in situ or purified and used in a wide variety of industries; Increased production of molecules synthesized in trichomes by increasing the trichome number on different plant organs, such as cotyledons, leaves, hypocotyls, stems, petioles, etc.; Increased cotton fibers per boll due

to decreased numbers of trichomes that reduces insect hiding and contamination; More optimal growth rate of a whole plant or specific parts of a plant due to more optimal trichome cellular development and the better resistance to biotic/abiotic stresses (including plant parts such as whole plant seedling, coleoptile elongation, young leaves, flowers, seeds, and fruit); increased harvested yield of plants, organs and their constituent molecules including biomass (such as fresh and dry weight during any time in plant life, including maturation and senescence, number of flowers, seed yield in terms of number, size, weight, harvest index, content and composition, e.g. amino acid, jasmonate, oil, protein and starch, and fruit yield in terms of number, size, weight, harvest index, post harvest quality, content and composition, e.g. amino acid, jasmonate, oil, protein and starch).

To regulate any of the phenotype(s) above, activities of one or more of the trichome genes or gene products can be modulated in an organism and tested by screening for the desired trait. Specifically, the gene, mRNA levels, or protein levels can be altered in a plant utilizing the procedures described herein and the phenotypes can be assayed. As an example, a plant can be transformed according to Bechtold and Pelletier (Methods. Mol. Biol. 82:259-266 (1998)) and/or screened for variants as in Winkler et al., Plant Physiol. 118: 743-50 (1998) and visually inspected for the desired phenotype or metabolically and/or functionally assayed.

III.A.4.c. Use Of Trichome Genes, Gene Components And Products To Modulate Biochemical Activities

The phenotype traits outlined above result from the integration of many cellular trichome associated processes and biochemical activities. Some of these are known from published literature and some can be deduced from the genes discovered in the MA Tables, etc. One or more of these trichome genes, gene components and products are useful to modulate these cellular processes, biochemical or metabolic activities and/or pathways such as those noted below. Such biological activities can be measured according to the citations included in the table below:

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
Growth , Differentiation And Development	<ul style="list-style-type: none"> Cell wall biosynthetic enzymes Cell fate determination proteins Major pathways of carbon and nitrogen metabolism 	<p>Molhoj et. al. (2001). Plant Mol.Biol. 46, 263-275</p> <p>Krishnakumar and Oppenheimer (1999). Development 1221, 3079-3088.</p> <p>Kroumova et al. (1994). PNAS 91, 11437-11441</p>
Water Conservation And Resistance To Drought And Other Related Stresses	<ul style="list-style-type: none"> Cytoskeleton and Trichome morphology and spacing controls 	<p>Schnittger et al. (1999). Plant Cell 11, 1105-1116</p> <p>Hulskamp et al (1994). Cell 76, 555-566</p>
Trichome exudate	<ul style="list-style-type: none"> Insect repellant 	<p>Insects and The Plant Surface, pp 151-172, Edward Arnold, London (1986)</p>
Terpenoid biosynthesis including monoterpenes and sesquiterpenes	<ul style="list-style-type: none"> Terpenoid biosynthesis enzymes including: <ul style="list-style-type: none"> Farnesyltranstransferase Geranylgeranyl-diphosphate synthase Geranyltranstransferase Farnesyl-diphosphate synthase 	<p>Alonso et al. (1992). J. Biol. Chem. 267, 7582-7587</p> <p>Rajonarivony et al (1992). Arch. Biochem. Biophys. 299, 77-82</p>

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
	<ul style="list-style-type: none"> • Dimethylallyltranstransferase • Geranyl-diphosphate synthase 	
H ₂ O ₂ accumulation and activation of SAR	<ul style="list-style-type: none"> • NADPH oxidase (subunit) synthesis and function 	Alvarez et al (1998) Cell 92, 773-784 Grant Orozco-Cardenas and Ryan (1999) PNAS 96, 6553-6557
Antifeedants biosynthesis and secretion	<ul style="list-style-type: none"> • Lactone biosynthesis enzymes 	Paruch et al. (2000). J. Agric. Food Chem. 48, 4973-4977
Pheromone biosynthesis and secretion	<ul style="list-style-type: none"> • Farnesine biosynthesis enzymes 	Teal et al. (1999) Arch. Insect Biochem Physiol. 42, 225-232
Endoreplication	<ul style="list-style-type: none"> • Cyclin and cyclin dependant kinases 	De Veylder et al. (2001) Plant Cell 13, 1653-1668 De Veylder et al. (2001) Plant J. 25, 617-626

Specific enzyme and other activities associated with the functions of individual trichome genes that can be modulated by the trichome genes and gene products are listed in the Reference tables where the functions of individual genes and their products are listed. Assays for detecting such biological activities are described in the Protein Domain table, for example.

III.A.4.d. Use Of Trichome Genes, Gene Components And Products
To Modulate Phenotypes By Modulating Transcription
Levels Of Other Genes

Many of the genes are “up regulated” or “down regulated” in trichomes because they are regulated as members of networks or cascade of genes under the control of regulatory genes. Thus some trichome genes are useful to influence levels of other genes and so orchestrate the complex phenotypes. Examples of the types of genes with altered transcript levels in trichomes are described in the Table below, together with associated biological activities. “Up-regulated” profiles are those where the mRNA levels are higher in the glabrous plants as compared to the “hairy” plant. “Down-regulated” profiles represent higher transcript levels in the “hairy” plant as compared to the glabrous plant.

TRANSCRIPT LEVELS	TYPE OF GENES WHOSE TRANSCRIPTS ARE CHANGED	PHYSIOLOGICAL CONSEQUENCES OF MODIFYING GENE PRODUCT LEVELS	EXAMPLES OF BIOCHEMICAL ACTIVITIES WHOSE TRANSCRIPTS ARE CHANGED
Up Regulated Transcripts	Genes active in suppressing trichome formation	<ul style="list-style-type: none"> • Changes in Hormone Perception • Changes in Hormone Biosynthesis • Changes in Specific Gene Transcription Initiation • Changes in 	<ul style="list-style-type: none"> • Transcription Factors • Transporters • Change In Cell G-proteins • Kinases And Phosphatases • Transcription factors • Ca-binding proteins • Transcription

TRANSCRIPT LEVELS	TYPE OF GENES WHOSE TRANSCRIPTS ARE CHANGED	PHYSIOLOGICAL CONSEQUENCES OF MODIFYING GENE PRODUCT LEVELS	EXAMPLES OF BIOCHEMICAL ACTIVITIES WHOSE TRANSCRIPTS ARE CHANGED
		cytoskeleton and cell wall assembly and structure	<p>Activators</p> <ul style="list-style-type: none"> • Change In Chromatin Structure And/OR Localized DNA Topology • Specific Factors (Initiation And Elongation) For Protein Synthesis • Maintenance Of mRNA Stability • Maintenance Of Protein Stability • Maintenance Of Protein-Protein Interaction
Down-Regulated Transcripts	Genes active in inducing formation of trichomes	<ul style="list-style-type: none"> • Changes in Hormone Perception • Changes in Hormone Biosynthesis • Changes in 	<ul style="list-style-type: none"> • Transcription Factors • Change In Protein Structure By Phosphorylation (Kinases) Or Dephosphorylation

TRANSCRIPT LEVELS	TYPE OF GENES WHOSE TRANSCRIPTS ARE CHANGED	PHYSIOLOGICAL CONSEQUENCES OF MODIFYING GENE PRODUCT LEVELS	EXAMPLES OF BIOCHEMICAL ACTIVITIES WHOSE TRANSCRIPTS ARE CHANGED
	Genes associated with Trichome differentiation and structure	<p>Specific Gene Transcription Initiation</p> <ul style="list-style-type: none"> • Changes in cytoskeleton and cell wall assembly and structure • Changes in cell size, cell shape 	<p>(Phosphatases)</p> <ul style="list-style-type: none"> • Change In Chromatin Structure And/Or DNA Topology • G-proteins, Ca²⁺-binding proteins
	Genes associated with trichome-specific metabolic pathways	<ul style="list-style-type: none"> • Changes in terpenoid biosynthesis • Changes in antifeedant and pheromone biosynthesis 	

While trichome polynucleotides and gene products can act alone, combinations of these polynucleotides also affect growth, development and leaf biochemistry. Combinations of trichome polynucleotide(s) and/or gene product(s) with genes or gene products involved in leaf development, hormone responses, or vegetative development are useful because trichome development is integrated with these processes.

USE OF PROMOTERS OF TRICHOME GENES

Promoters of trichome genes are useful for facilitating transcription of desired polynucleotides, both plant and non-plant in trichomes. For example, extra copies of existing terpenoid synthesis coding sequences can be operably linked to a trichome gene promoter and inserted into a plant to increase the terpenoids in the trichome. Alternatively, trichome promoters can direct expression of non-plant genes or genes from another plant species that can, for instance, lead to new terpenoids being made. The promoters can also be operably linked to antisense copies of coding sequences to achieve down regulation of these gene products in cells.

III.A5. CHLOROPLAST GENES, GENE COMPONENTS AND PRODUCTS

The chloroplast is a complex and specialized organelle in plant cells. Its complexity comes from the fact that it has at least six suborganellar compartments subdivided by double-membrane envelope and internal thylakoid membranes. It is specialized to carry out different biologically important processes including photosynthesis and amino acid and fatty acid biosynthesis. The biogenesis and development of chloroplast from its progenitor (the proplastid) and the conversion of one form of plastid to another (e.g., from chloroplast to amyloplast) depends on several factors that include the developmental and physiological states of the cells.

One of the contributing problems that complicate the biogenesis of chloroplast is the fact that some, if not most, of its components must come from the outside of the organelle itself. The import mechanisms must take into account to what part within the different sub-compartments

the proteins are being targeted; hence the proteins being imported from the cytoplasm must be able to cross the different internal membrane barriers before they can reach their destinations. The import mechanism must also take into account how to tightly coordinate the interaction between the plastid and the nucleus such that both nuclear and plastidic components are expressed in a synchronous and orchestrated manner. Changes in the developmental and physiological conditions within or surrounding plant cells can consequently change this tight coordination and therefore change how import mechanisms are regulated as well. Manipulation of these conditions and modulation of expression of the import components and their function can have critical and global consequences to the development of the plant and to several biochemical pathways occurring outside the chloroplast. Expression patterns of such genes have been determined using microarray technology.

Microarray technology allows monitoring of gene expression levels for thousands of genes in a single experiment. This is achieved by hybridizing labeled fluorescent cDNA pools to glass slides that contain spots of DNA (Schena et al. (1995) Science 270: 467-70). The US Arabidopsis Functional Genomics Consortium (AFGC) has recently made public the results from such microarray experiments conducted with AFGC chips containing about 10,000 non-redundant ESTs, selected from about 37,000 randomly sequenced ESTs generated from mRNA of different tissues and developmental stages.

The sequences of the ESTs showing at least two-fold increases or decreases in a mutant in a mutant (CiA2) of *Arabidopsis thaliana*, that is distributed in chloroplast biogenesis relative to wild type grown in the same conditions were identified, compared to the Ceres full length cDNA and genomic sequence databanks, and equivalent Ceres clones identified. The MA_diff table reports the results of this analysis, indicating those Ceres clones which are up or down regulated over controls, thereby indicating the Ceres clones that are involved in the import of proteins to chloroplast and chloroplast biogenesis.

Examples of genes and gene products that are involved in the import of proteins to chloroplast are shown in the Reference, Sequence, Protein Group, and Protein Group Matrix tables. While chloroplast protein import polynucleotides and gene products can act alone, combinations of these polynucleotides also affect growth and development. Useful combinations include different chloroplast protein import responsive polynucleotides and/or gene products that have

similar transcription profiles or similar biological activities, and members of the same or functionally related biochemical pathways. Whole pathways or segments of pathways are controlled by transcription factor proteins and proteins controlling the activity of signal transduction pathways. Manipulation of one or more chloroplast protein import gene activities are useful to modulate the biological processes and/or phenotypes listed below. Chloroplast protein import responsive genes and gene products can act alone or in combination. Useful combinations include chloroplast protein import responsive genes and/or gene products with similar transcription profiles, similar biological activities, or members of the same or functionally related biochemical pathways. Here, in addition to polynucleotides having similar transcription profiles and/or biological activities, useful combinations include polynucleotides that may have different transcription profiles but which participate in common or overlapping pathways. Whole pathways or segments of pathways are controlled by transcription factor proteins and proteins controlling the activity of signal transduction pathways. Therefore, manipulation of such protein levels is especially useful for altering phenotypes and biochemical activities of plants. Manipulation of one or more chloroplast protein import gene activities are useful to modulate the biological processes and/or phenotypes listed below.

Such chloroplast protein import responsive genes and gene products can function to either increase or dampen the above phenotypes or activities in response to changes in the regulation of import mechanisms. Further, promoters of chloroplast protein transport responsive genes, as described in the Reference tables, for example, are useful to modulate transcription that is induced by chloroplast protein transport or any of the following phenotypes or biological activities below. Further, any desired sequence can be transcribed in similar temporal, tissue, or environmentally specific patterns as the chloroplast protein transport responsive genes when the desired sequence is operably linked to a promoter of a chloroplast protein transport responsive gene. The MA_diff Table(s) reports the transcript levels of the experiment (see EXPT ID: Chloroplast (relating to SMD 8093, SMD 8094)). For transcripts that had higher levels in the samples than the control, a "+" is shown. A "-" is shown for when transcript levels were reduced in root tips as compared to the control. For more experimental detail see the Example section below.

Chloroplast genes are those sequences that showed differential expression as compared to controls, namely those sequences identified in the MA_diff tables with a "+" or "-" indication.

Chloroplast Genes Identified By Cluster Analyses Of Differential Expression Chloroplast

Genes Identified By Correlation To Genes That Are Differentially Expressed

As described above, the transcription profiles of genes that act together are well correlated. Applicants not only have identified the genes that are differentially expressed in the microarray experiments, but also have identified the genes that act in concert with them. The MA_clust table indicates groups of genes that have well correlated transcription profiles and therefore participate in the same pathway or network.

A pathway or network of Chloroplast genes is any group in the MA_clust that comprises a cDNA ID that also appears in Expt ID Chloroplast (relating to SMD 8093, SMD 8094) of the MA_diff table(s).

Chloroplast Genes Identified By Correlation To Genes That Cause Physiological Consequences

Additionally, the differential expression data and the phenotypic observations can be merged to identify pathways or networks of Chloroplast genes. A group in the MA_clust is considered a Chloroplast pathway or network if the group comprises a cDNA ID that also appears in Knock-in or Knock-out tables that causes one or more of the phenotypes described in section above.

Chloroplast Genes Identified By Amino Acid Sequence Similarity

Chloroplast genes from other plant species typically encode polypeptides that share amino acid similarity to the sequences encoded by corn and Arabidopsis Chloroplast genes. Groups of Chloroplast genes are identified in the Protein Group table. In this table, any protein group that comprises a peptide ID that corresponds to a cDNA ID member of a Chloroplast pathway or network is a group of proteins that also exhibits Chloroplast functions/utilities.

III.A.5.a. Use Of Chloroplast Protein Import Responsive Genes To
Modulate Phenotypes

Chloroplast protein import responsive genes and gene products are useful to or modulate one or more phenotypes, including growth, roots, stems, and leaves; development, including plastid biogenesis, plastid division, plastid development and thylakoid membrane structures differentiation including plastid/chloroplast differentiation; photosynthesis including carbon dioxide fixation; transport including transcription/translation regulation within transport complex, phosphate translocation, and targeted starch deposition and accumulation; and biosynthesis of essential compounds such as lipid biosynthesis, riboflavin biosynthesis, carotenoid biosynthesis, and aminoacid biosynthesis.

To improve any of the phenotype(s) above, activities of one or more of the chloroplast protein import responsive genes or gene products can be modulated and the plants tested by screening for the desired trait. Specifically, the gene, mRNA levels, or protein levels can be altered in a plant utilizing the procedures described herein and the phenotypes can be assayed. As an example, a plant can be transformed according to Bechtold and Pelletier (1998, Methods. Mol. Biol. 82:259-266) and/or screened for variants as in Winkler et al. (1998) Plant Physiol 118: 743-50 and visually inspected for the desired phenotype or metabolically and/or functionally assayed according to Saito et al. (1994, Plant Physiol. 106: 887-95), Takahashi et al (1997, Proc. Natl. Acad. Sci. USA 94: 11102-07) and Koprivova et al. (2000, Plant Physiol. 122: 737-46).

III.A.5.b. Use Of Chloroplast Protein Import-Responsive Genes To
Modulate Biochemical Activities

The activities of one or more of the chloroplast protein import responsive genes can be modulated to change biochemical or metabolic activities and/or pathways such as those noted below. Such biological activities can be measured according to the citations included in the table below:

GENERAL CATEGORY	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS

GENERAL CATEGORY	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
Cell Growth and Differentiation	<ul style="list-style-type: none"> Regulation of Leaf Development Including Photosynthetic Apparatus 	Reinbothe et al. (1997) Proc. Natl. Acad. Sci. USA. 94:8890-8894 Eggink and Hooper (2000) J. Biol. Chem. 275:9087-9090 Jagtap et al. (1998) J Exptl Botany 49:1715-1721
	<ul style="list-style-type: none"> Regulation of Plastid Biogenesis and Plastid Division 	Lawrence and Kindle (1997) J. Biol. Chem. 272:20357-20363 Lahiri and Allison (2000) Plant Physiol. 123:883-894
	<ul style="list-style-type: none"> Development of Plastid Inner/Outer and thylakoid Membrane Structures 	Kouranov et al. (1999) J. Biol. Chem. 274:25181-25186 Jackson et al. (1998) J. Biol. Chem. 273:16583-16588 Li and Chen (1997) J. Biol. Chem. 272:10968-10974 Lawrence and Kindle (1997) J. Biol. Chem. 272:20357-20363 Silva-Filho et al. (1997) J. Biol. Chem. 272:15264-15269
	<ul style="list-style-type: none"> Regulation of 	May and Soll (2000) Plant

GENERAL CATEGORY	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
	transcription and/or translation related to maintenance of stability of protein-protein interaction within transport complex	Cell 12:53-63 Caliebe et al. (1997) EMBO J. 16:7342-7350
Physiology	<ul style="list-style-type: none"> • Modulation of Photosynthesis 	Sung and Krieg (1979) Plant Physiol 64: 852-56
	<ul style="list-style-type: none"> • Regulation of Lipid Biosynthesis 	Bourgis et al. (1999) Plant Physiol. 120:913-922 Reverdatto et al. (1999) Plant Physiol. 119:961-978 Roesler et al. (1997) Plant Physiol. 113:75-81
	<ul style="list-style-type: none"> • Regulation of Riboflavin (Vitamin B) biosynthesis 	Jordan et al. (1999) J. Biol. Chem. 274:22114-22121
	<ul style="list-style-type: none"> • Regulation of phosphate translocation across chloroplast membrane 	Flugge (1999) Annu. Rev. Plant Physiol. Plant Mol. Biol. 50:27-45 Silva-Filho et al. (1997) J. Biol. Chem. 272:15264-15269
	<ul style="list-style-type: none"> • Regulation of targeted starch depostion and accumulation 	Yu et al. (1998) Plant Physiol. 116:1451-1460
	<ul style="list-style-type: none"> • Modulation of protein 	Summer and Cline (1999)

GENERAL CATEGORY	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
	targeting and translocation across chloroplast membrane	Plant Physiol. 119:575-584 Dabney-Smith et al. (1999) J. Biol. Chem. 274:32351- 32359 Hinnah et al. (1997) EMBO J. 16:7351-7360
	<ul style="list-style-type: none"> Regulation of carotenoid biosynthesis 	Bonk et al. (1996) Plant Physiol. 111:931-939
	<ul style="list-style-type: none"> Regulation of amino acid biosynthesis 	Flugge (1999) Annu. Rev. Plant Physiol. Plant Mol. Biol. 50:27-45
	<ul style="list-style-type: none"> Regulation of secondary metabolism 	Flugge (1999) Annu. Rev. Plant Physiol. Plant Mol. Biol. 50:27-45
Signal Transduction	<ul style="list-style-type: none"> Regulation of gene transcriptional activity specific to chloroplast protein import 	Chen et al. (2000) Plant Physiol. 122:813-822. Macasev et al. (2000) Plant Physiol. 123:811-816
	<ul style="list-style-type: none"> Regulation of protein target signal cleavage and protein degradation 	Lang et al. (1998) J. Biol. Chem. 273:30973-30978 Jackson et al. (1998) J. Biol. Chem. 273:16583-16588 Richter and Lamppa (1998)

GENERAL CATEGORY	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
		Proc. Natl. Acad. Sci. USA. 95:7463-7468
	<ul style="list-style-type: none"> Regulation of ion channel conformation and activity 	Van der Wijngaard and Vredenberg (1999) J. Biol. Chem. 274:25201-25204
	<ul style="list-style-type: none"> Regulation of kinase and phosphatases synthesis and activity 	Waegemann and Soll (1996) J. Biol. Chem. 271:6545-6554 Li et al. (2000) Science 287-300-303 Muller et al. (2000) J. Biol. Chem. 275:19475-19481
	<ul style="list-style-type: none"> Modulation of Molecular Chaperone and Other Protein Folding Activity 	Bonk et al. (1996) Plant Physiol. 111:931-939 Walker et al. (1996) J. Biol. Chem. 271:4082-4085 Kessler and Blobel (1996). Proc. Natl. Acad. Sci. USA 93:7684-7689 Jackson et al. (1998) J. Biol. Chem. 273:16583-16588

Other biological activities that can be modulated by the chloroplast protein import responsive genes and gene products are listed in the Reference tables. Assays for detecting such biological activities are described in the Protein Domain table.

Chloroplast protein import responsive genes are characteristically differentially transcribed in response to fluctuating chloroplast protein import levels or concentrations, whether internal or external to an organism or cell. The MA_diff reports the changes in transcript levels of various chloroplast protein import responsive genes that are differentially expressed among the mutants and the wild type.

Profiles of some of these chloroplast protein import responsive genes are shown in the Table below together with examples of the kinds of associated biological activities.

TRANSCRIPT LEVELS	TYPE OF GENES	PHYSIOLOGICAL CONSEQUENCES	EXAMPLES OF BIOCHEMICAL ACTIVITY
Up regulated transcripts	<p>Responders to defective chloroplast protein import</p> <p>Genes induced by defective import</p>	<ul style="list-style-type: none"> Chloroplast protein import regulation Chloroplast protein import and transport Chloroplast import metabolism Synthesis of secondary metabolites and/or proteins Modulation of chloroplast import response transduction pathways Changes in 	<ul style="list-style-type: none"> Transporters Metabolic enzymes Change in cell membrane structure and potential Kinases and phosphatases Transcription activators Change in chromatin structure and/or localized DNA topology Redox control Metabolic enzymes concerned with chloroplast biochemistry Organelle gene

TRANSCRIPT LEVELS	TYPE OF GENES	PHYSIOLOGICAL CONSEQUENCES	EXAMPLES OF BIOCHEMICAL ACTIVITY
		chloroplast membranes • Specific gene transcription initiation • Chloroplast and non-chloroplast metabolic pathways	expression and translation
Down-regulated transcripts	Responders to defective chloroplast protein import. Genes repressed by defective chloroplast protein import Genes with unstable mRNAs when chloroplast import is defective Genes with discontinued expression or unstable mRNA in	• Regulation of chloroplast protein import pathways released • Chloroplast protein import and transport • Chloroplast import metabolism • Changes in pathways and processes operating in chloroplasts • Changes in organelle	• Transcription factors • Change in protein structure by phosphorylation (kinases) or dephosphorylation (phosphatases) • Change in chromatin structure and/or DNA topology • Stability factors for protein mRNA synthesis and degradation • Organelle

TRANSCRIPT LEVELS	TYPE OF GENES	PHYSIOLOGICAL CONSEQUENCES	EXAMPLES OF BIOCHEMICAL ACTIVITY
	presence of chloroplast protein import	membranes <ul style="list-style-type: none"> • Loss of organelle gene expression, RNA and protein synthesis • Changes in metabolism other than chloroplast protein import pathways • Chloroplast import metabolism 	transcription and translation proteins <ul style="list-style-type: none"> • Metabolic enzymes

USE OF PROMOTERS OF CHLOROPLAST GENES

Promoters of Chloroplast genes are useful for transcription of any desired polynucleotide or plant or non-plant origin. Further, any desired sequence can be transcribed in a similar temporal, tissue, or environmentally specific patterns as the Chloroplast genes where the desired sequence is operably linked to a promoter of a Chloroplast gene. The protein product of such a polynucleotide is usually synthesized in the same cells, in response to the same stimuli as the protein product of the gene from which the promoter was derived. Such promoter are also useful to produce antisense mRNAs to down-regulate the product of proteins, or to produce sense mRNAs to down-regulate mRNAs via sense suppression

III.A.6. REPRODUCTION GENES, GENE COMPONENTS AND PRODUCTS

Reproduction genes are defined as genes or components of genes capable of modulating any aspect of sexual reproduction from flowering time and inflorescence development to fertilization and finally seed and fruit development. These genes are of great economic interest as well as biological importance. The fruit and vegetable industry grosses over \$1 billion USD a year. The seed market, valued at approximately \$15 billion USD annually, is even more lucrative.

Expression of many reproduction genes and gene products is orchestrated by internal programs or the surrounding environment of a plant, as described below. These genes and/or products have great importance in determining traits such as fruit and seed yield. Examples of such reproduction genes and gene products are shown in the Reference, Sequence, Protein Group, Protein Group Matrix tables, Knock-in, Knock-out, MA-diff and MA-clust. The biochemical functions of the protein products of many of these genes determined from comparisons with known proteins are also given in the Reference tables.

Reproduction Genes Identified by Phenotypic Observation

Reproduction genes were discovered and characterized from a much larger set of genes by experiments designed to find genes that cause phenotypic changes in flower, silique, and seed morphology. In these experiments, reproduction genes were identified by either (1) ectopic expression of a cDNA in a plant or (2) mutagenesis of the plant genome. The plants were then cultivated and phenotypes, which varied from the parental "wild-type", were observed.

One particular example of reproductive genes are those that are regulated by AP2. AP2 is a transcription factor that regulates many genes, both as a repressor of some genes and as an activator of others. Some of these genes are those which establish the floral meristem or those which regulate floral organ identity and development. As such, AP2 has an effect on reproduction. This is, loss of AP2 activity is correlated with decreased male and female reproduction. AP2 is also known to have an effect on seed mass, and therefore on yield. That is, overexpression of AP2 is correlated with smaller seeds or seedless fruit while repression of AP2 correlates with larger seeds (see, e.g. US Patent No.: 5,994,622).

Another example of reproduction genes are those that are regulated by PISTILLATA (PI). PI is a transcription factor that regulates many genes both as a repressor and activator. Some of these genes are those which regulate floral organ identity and development, in conjunction

with other transcription factors such as AP2 and AGAMOUS. As such, PI has an effect on reproduction in that loss of PI activity is correlated with decreased male reproduction. PI is also known to have an effect on carpel number, and therefore potentially on ovule/seed number and yield. Specifically, repression of PI results in increased carpel number and therefore ovule number.

Yet another example of reproductive genes are those that are regulated by MEDEA (MEA). MEA is a SET-domain containing protein that associates with other proteins to form complexes that affect chromatin structure and therefore gene expression. As such, loss of MEA function is correlated with global gene activation and repression leading to many phenotypes including decreased female reproduction and therefore reduced seed set and yield.

In the characterization of these and other reproduction genes, the following phenotypes were scored:

I. Flower

- Size
 - Large
 - Small
- Shape
 - Abnormal organ numbers
 - Agamous
 - AP-2 like
- Color
- Number
- Fused Sepals

II. Silique

- Size
- Seed number
 - Reduced
 - Absent
- Seed color

The identified genes regulating reproduction are identified in the Knock-in and Knock-out Tables.

Reproduction Genes Identified by Differential Expression

Reproduction genes were also identified in experiments designed to discover genes whose mRNA products were in different concentrations in whole flowers, flower parts, and siliques relative to the plant as a whole. The MA_diff Table(s) reports the transcript levels of the experiment (see EXPT ID: 108473, 108474, 108429, 108430, 108431, 108475, 108476, 108501). For transcripts that had higher levels in the samples than the control, a "+" is shown. A "-" is shown for when transcript levels were reduced in root tips as compared to the control. For more experimental detail see the Example section below.

Reproduction genes are those sequences that showed differential expression as compared to controls, namely those sequences identified in the MA_diff tables with a "+" or "-" indication.

Reproduction Genes Identified By Cluster Analyses Of Differential Expression

Reproduction Genes Identified By Correlation To Genes That Are Differentially Expressed

As described above, the transcription profiles of genes that act together are well correlated. Applicants not only have identified the genes that are differentially expressed in the microarray experiments, but also have identified the genes that act in concert with them. The MA_clust table indicates groups of genes that have well correlated transcription profiles and therefore participate in the same pathway or network.

A pathway or network of Reproduction genes is any group in the MA_clust that comprises a cDNA ID that also appears in Expt ID 108473, 108474, 108429, 108430, 108431, 108475, 108476, 108501 of the MA_diff table(s).

Reproduction Genes Identified By Correlation To Genes That Cause Physiological Consequences

Additionally, the differential expression data and the phenotypic observations can be merged to identify pathways or networks of Reproduction genes. A group in the MA_clust is considered a Reproduction pathway or network if the group comprises a cDNA ID that also appears in Knock-in or Knock-out tables that causes one or more of the phenotypes described in section above.

Reproduction Genes Identified By Amino Acid Sequence Similarity

Reproduction genes from other plant species typically encode polypeptides that share amino acid similarity to the sequences encoded by corn and Arabidopsis Reproduction genes. Groups of Reproduction genes are identified in the Protein Group table. In this table, any protein group that comprises a peptide ID that corresponds to a cDNA ID member of a Reproduction pathway or network is a group of proteins that also exhibits Reproduction functions/utilities.

It is assumed that the reproduction genes differentially expressed in floral parts and seeds are concerned with specifying flowers and seeds and their functions, and therefore modulations of such genes produce variant flowers and seeds.

Reproductive genes and gene products can function to either increase or dampen the phenotypes, biochemical activities and transcription profiles, either in response to changes of internal plant programs or to external environmental fluctuations.

III.A.5.a. Use Of Reproduction Genes, Gene Components And Products To Modulate Phenotypes

The reproduction genes of the instant invention, when mutated or activated differently, are capable of modulating one or more processes of flower, seed and fruit development. They are thus useful for improving plants for agriculture and horticulture and for providing seeds with a better chemical composition for diverse industries including the food, feed and chemical industries. Reproduction genes, gene components and products are useful to alter the following traits and properties of plants, including development, such as flowering time and number of inflorescences, flower development (including anther, stamen, pollen, style, stigma, ovary, ovule, and gametes), pollination and fertilization (including sporogenesis gametogenesis, zygote formation, embryo development, endosperm development, and male sterility, hybrid breeding

systems and heterosis); cellular properties, such as cell size, cell shape, cell death, cell division, cell elongation, cell differentiation, and meiosis; organ characteristics, such as flowers, receptacle, sepals, petals, and tepals color, shape, and size, number, and petal drop); androecium, such as stamen (including anther size, pollen sterile, size, shape, weight and color, number, and filament size), gynoecium, such as carpel, ovary. number. and length) and style (stigma, ovule, size, shape, and number); pedicel and peduncle (size and shape), seeds, such as placenta, embryo. cotyledon, endosperm, suspensor, seed coat (testa), aleurone, development, including apomixis (gametophytic, apospory, diplospory), dormancy and germination; fruits, such as pericarp – thickness, texture (exocarp, mesocarp, endocarp); development (seed set, fruit set, false fruit, fruit elongation and maturation, and dehiscence), and fruit drop; plant seed yield, such as increased biomass, better harvest index, attraction of favorable insects, better seed quality, and better yield of constituent chemicals; and plant population features, such as architecture (shade avoidance and planting density).

To regulate any of the phenotype(s) above, activities of one or more of the reproduction genes or gene products can be modulated in an organism and tested by screening for the desired trait. Specifically, the gene, mRNA levels or protein levels can be altered in a plant using the procedures described herein and the phenotypes can be assayed. As an example, a plant can be transformed according to Bechtold and Pelletier (Methods Mol. Biol. 82:259-266 (1998)) and/or screened for variants as in Winkler et al. (Plant Physiol 118:743-50 (1998)) and visually inspected for the desired phenotype or metabolically and/or functionally assayed.

III.A.5.b. Use Of Reproduction Genes To Modulate Biochemical Activities

The activities of one or more of the reproduction genes can be modulated to change biochemical or metabolic activities and/or pathways such as those examples noted below. Such biological activities can be measured according to the citations included in the Table below:

FUNCTION/PROCESS	EXAMPLES OF BIOCHEMICAL/MOLECU	Reference AND ASSAY

	LAR ACTIVITIES	
Metabolism	<p>Energy production and conversion</p> <ul style="list-style-type: none"> - Glucosyl-transferase (CLONE_ID 1040) - Heme-binding protein (putative cytochrom B5) (CLONE_ID 3743) <p>Storage protein synthesis</p> <p>Inorganic ion transport and metabolism</p> <ul style="list-style-type: none"> - Peroxidase (CLONE_ID 100990) - Cystathione beta synthase (CLONE_ID 21847) <p>Amino acid transport and metabolism</p> <ul style="list-style-type: none"> - l-asparaginase (CLONE_ID 92780) - Putative peptide/amino acid transporter (CLONE_ID 113723) <p>Carbohydrate transport and</p>	<p>Ap Rees, T. (1974). In "Plant Biochemistry. Biochemistry, Series One", Vol. 11. (H.L. Kornberg and D.C.Phillips, eds.), Butterworths, London.</p> <p>Juliano, B.O. and Varner, J.E. (1969). Plant Physiol. 44, 886-892.</p> <p>Bewley et al. (1993). Plant Physiol. Biochem. 31, 483-490.</p> <p>Hills, M. J. and Beevers, H. (1987). Plant Physiol. 84, 272-276.</p> <p>Olsen, L. J. and Harada, J. J. (1991). In "Molecular Approaches to Compartmentalization and Metabolic Regulation (A. H. C. Huang and L. Taiz, eds.), ASPP, Rockville, Md.</p> <p>Mitsuhashi, W. and Oaks, A. (1994). Plant Physiol. 104, 401-407.</p> <p>Walker-Smith, D. J., and Payne, J. W. (1985). Planta 164, 550-556.</p> <p>Salmenkallio, M. and</p>

	<p>metabolism</p> <ul style="list-style-type: none"> - Glucose transport protein (CLONE_ID 33727) - Putative sugar transporter (CLONE_ID 3250) - Starch biosynthesis <p>Coenzyme metabolism</p> <ul style="list-style-type: none"> - Tyrosine aminotransferase (ROOTY/SUPERROOT1) (CLONE_ID 14570) - Formate dehydrogenase (CLONE_ID 7530) <p>Lipid metabolism</p> <ul style="list-style-type: none"> - Branched chain α-ketoacid dehydrogenase E2 subunit (CLONE_ID 25116) - Acyl carrier protein-1 (CLONE_ID 14291) - Lipid metabolic enzymes <p>Secretion</p> <ul style="list-style-type: none"> - Sensor protein RcsC-like 	<p>Sopanen, T. (1989). Plant Physiol. 89, 1285-1291.</p> <p>Baumgartner, B. and Chrispeels, M. J. (1976). Plant Physiol. 58, 1-6.</p> <p>Elpidina, E. N. et al. (1991). Planta 185, 46-52.</p> <p>Ericson, M. C. and Chrispeels, M. J. (1973). Plant Physiol. 52, 98-104.</p> <p>Kern, R. and Chrispeels, M. J. 1978) Plant Physiol. 62, 815-819.</p> <p>Dilworth, M. F. and Dure, L. III. (1978). Plant Physiol. 61, 698-702.</p> <p>Chrispeels, M. J. and Jones, R. L. (1980/81). Isr. J. Bot. 29, 222-245.</p> <p>Gould, S. E. B., and Rees, D. A. (1964). J. Sci. Food Agric. 16, 702-709.</p>
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	(CLONE_ID 16461) - Signal recognition particle RP54 (CLONE_ID 22158)	
Modulate floral organ number	Transcriptional control ANT (AP2-domain) DNA binding protein SUP (Zinc finger)	Elliot et al. (1996). Plant Cell 8, 155-168. Sakai et al. (2000). Plant Cell 12, 1607-1618. Jacobsen and Meyerowitz (1997). Science 277, 1100- 1103.
Floral organ size	Transcriptional control ANT (AP2-domain) DNA binding protein	Mizukami et al. (2000). PNAS 97, 942-947. Krizek (1999). Developmental Genetics 25, 224-236.
Female organ number/Floral meristem size	Membrane receptor kinase signal transduction CLV1 (LRR domain and kinase domain) receptor CLV2 (LRR domain) receptor CLV3 (Receptor ligand)	Clark and Meyerowitz (1997). Cell 89, 575-585 Jeong et al. (1999). Plant Cell 11, 1925-1934. Fletcher et al. (1999). Science 283, 1911-1914.
Female reproduction	DNA binding protein	

	AG (MADS domain) DNA binding protein	Yanofsky et al. (1990). Nature 346, 35-39.
Female reproduction	Signal transduction CTR1 (Raf kinase)	Kieber et al. (1993). Cell 72, 427-441.
Male organ number	DNA methylation MET1 (DNA methyltransferase)	Jacobsen and Meyerowitz (1997). Science 277, 1100- 1103.
Seed size control	DNA binding protein AP2 (AP2 domain) RAP2 (AP2 domain)	Jofuku et al. (1994). Plant Cell 6, 1211-1225. US Patent #6,093,874; #5,994,622
Seed size control	Polycomb group protein complex FIE, FIS2, MEA	Luo et al. (2000). PNAS 97, 10637-10642.
Seed size control	DNA methylation MET1	Scott et al. (2000). Development 127, 2493- 2502. Vinkenoog et al. (2000). Plant Cell 12, 2271-2282. Luo et al. (2000). PNAS 97, 10637-10642.
Embryo development/Embryo viability	CAAT box binding complex LEC1/HAP3 HAP2, HAP5	Lotan et al. (1998). Cell 93, 1195. US Patent #6,235,975

Embryo development/Seed dormancy	DNA binding proteins ABI4 (AP2 domain) FUS3 (B3 domain) VP1 (B3 domain)	Finkelstein et al. (1998). Plant Cell 10, 1043-1054. Luerssen et al. (1998). Plant J. 15, 755-764.
Embryo development	Signal transduction ABI1, ABI2 [Serine/threonine protein phosphatase 2C (PP2C)]	Leung et al. (1994). Science 264, 1448-1452. Leung et al. (1997). Plant Cell 9, 759-771.
Endosperm development	Chromatin level control of gene activity Polycomb complex; FIE, MEA, FIS2	Ohad et al. (1996). PNAS 93, 5319-5324. US Patent #6,229,064 Kiyosue et al. (1999). PNAS 96, 4186-4191. Grossniklaus et al. (1998). Science 280, 446-450. Chaudhury et al. (1997) PNAS 94, 4223-4228.
Integument development/Seed coat development	DNA binding AP2, ANT (AP2 domain) BEL1 (Homeodomain)	Jofuku et al. (1994). Plant Cell 6, 1211-1225. Klucher et al. Plant Cell 8, 137-153. Reiser et al. (1995). Cell 83, 735-742.

Anthocyanin production	Secondary transporter TT12 (MATE; multidrug and toxic compound extrusion)	Debeaujon et al. (2001). Plant Cell 13, 853-872.
Anthocyanin production	DNA binding protein TT8 (Basic helix-loop-helix domain)	Nesi et al. (2000). Plant Cell 12, 1863-1878.
Fruit development	Chromatin level control of gene activity Polycomb complex; FIE, MEA, FIS2	Ohad et al. (1996). PNAS 93, 5319-5324. Kiyosue et al. (1999). PNAS 96, 4186-4191. Grossniklaus et al. (1998). Science 280, 446-450. Chaudhury et al. (1997) PNAS 94, 4223-4228.
Fruit size control	Signal transduction FW2.2 (c-Ras P21)	Frary et al. (2000). Science 289, 85-88.
Fruit development/Pod shattering	Transcriptional control SHP1, SHP2, FUL (MADS domain) DNA binding proteins	Liljegren et al. (2000). Nature 404, 766-770. Ferrandiz et al. (2000). Science 289, 436-438..
Transcription and Posttranscription	Transcription - SRF-domain AGL11 (CLONE_ID 32791) - AP2-domain containing protein (CLONE_ID 332) - Myb-DNA binding protein	Delseny, M. et al. (1977). Planta 135, 125-128. Lalonde, L. and Bewley, J. D. (1986). J. Exp. Bot. 37, 754-764. Walling, L. et al. (1986). PNAS 83, 2123-2125. Okamuro, J. K. and

	<p>(CLONE_ID 94597)</p> <p>Transcription factors</p> <p>Signal transduction mechanisms</p> <ul style="list-style-type: none"> - Protein-kinases - Phosphatases - meiosis proteins - Chromatin remodeling proteins - Chaperones - Chalcone synthase - Putative Ser/Thr protein kinase (CLONE_ID 31383) - ER6-like protein (implicated in ethylene signal transduction) (CLONE_ID 7474) <p>Translation, ribosomal structure and biogenesis</p> <ul style="list-style-type: none"> - Ribosomal proTein S15A (CLONE_ID 17466) - Translation initiation factor (CLONE_ID 103464) 	<p>Goldberg, R. B. (1989). In "Biochemistry of Plants, Vol 15." Academic Press, Inc.</p> <p>Wong, J. et al. (1995). Genes Dev. 9, 2696-2711.</p> <p>Dimitrov et al. (1994). J. Cell Biol. 126, 591-601.</p> <p>Landsberger, N. and Wolffe, A. P. (1997). EMBO J. 16, 4361-4373.</p> <p>Bogdanove, A. J. and Martin, G. G. (2000). PNAS 97, 8836-8840.</p> <p>Zhu, H. et al. Science July 26, 2001: 10.1126/science.1062191 (Reports).</p>
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	<p>Posttranslational modification, protein turnover, chaperones</p> <ul style="list-style-type: none"> - DnaJ-domain containing protein (CLONE_ID 4150) - Cyclophilin-like protein (CLONE_ID 35643) 	
Cell division and Repair	<p>Cell division and chromosome partitioning</p> <ul style="list-style-type: none"> - Protein of unknown function with tropomyosin-, myosin tail- and filament- domains (CLONE_ID 15546) - Actin-1 (CLONE_ID 25785) <p>DNA replication, recombination and repair</p> <ul style="list-style-type: none"> - Proliferating cell nuclear antigen-1 (axillary protein, DNA polymerase I delta) (CLONE_ID 28554) 	<p>Rogan, P. G. and Simon, E. W. (1975). New Phytol. 74, 273-275.</p> <p>Morahashi, Y. and Bewley, J. D. (1980). Plant Physiol 66, 70-73.</p> <p>Morahashi, Y. et al. (1981). Plant Physiol. 68, 318-323.</p> <p>Morahashi, Y. (1986). Physiol. Plant. 66, 653-658.</p> <p>Zlatanova, J. et al. (1987). Plant Mol. Biol. 10, 139- 144.</p> <p>Zlatanova, J. and Ivanov, P. (1988). Plant Sci. 58, 71-76.</p>

	<p>- AAA-type ATPase, cdc48 (CLONE_ID 100292)</p> <p>Cell envelope biogenesis, outer membrane</p> <p>- dTDP-D-glucose 4,6- dehydratase (CLONE_ID 28597)</p> <p>- Putative cinnamoyl- CoA reductase (CLONE_ID 109228)</p>	
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Other biological activities that are modulated by the reproductive genes and gene products are listed in the Reference tables. Assays for detecting such biological activities are described in the Protein Domain table, for example.

III.5.A.c. Use Of Reproduction Genes, Gene Components And Products To Modulate Transcription Levels

Reproduction genes are characteristically differentially transcribed in response to cell signals such as fluctuating hormone levels or concentrations, whether internal or external to an organism or cell. Many reproduction genes belong to networks or cascades of genes under the control of regulatory genes. Thus some reproduction genes are useful to modulate the expression of other genes. Examples of transcription profiles of reproduction genes are described in the Table below with associated biological activities. "Up-regulated" profiles are those where the mRNA transcript levels are higher in flowers, flower parts or siliques as compared to the plant as a whole. "Down-regulated" profiles represent higher transcript levels in the whole plant as compared to flowers, flower parts or siliques alone.

TRANSCRIPT LEVELS	TYPE OF GENES WITH ALTERED ACTIVITY	PHYSIOLOGICAL CONSEQUENCES OF ALTERING GENE EXPRESSION	EXAMPLES OF BIOCHEMICAL ACTIVITIES OF GENES WITH ALTERED EXPRESSION
Up Regulated Transcripts Flower Reproduction Genes	<p>Genes that control flower differentiation, number and size</p> <p>Genes that promote petal, stamen and carpel formation</p> <p>Genes controlling flower-specific metabolism such as petal pigments</p> <p>Genes that promote ovule formation</p> <p>Genes that promote fertilization, seed, embryo and endosperm formation</p>	<p>Flowers form from flower meristem</p> <p>Floral organs mature</p> <p>Flavonoid pathways induced</p>	<p>Transcription Factors</p> <p>Signal transduction</p> <p>Membrane Structure</p> <p>Protein kinases</p> <p>Phosphatases</p> <p>Meiosis proteins</p> <p>Chromatin remodeling proteins</p> <p>Chaperones</p> <p>Chalcone synthase</p> <p>Amino acid transport and metabolism</p> <p>Storage protein synthesis</p> <p>Lipid metabolic enzymes</p> <p>Carbohydrate transport and metabolism</p> <p>Starch biosynthesis</p>

TRANSCRIPT LEVELS	TYPE OF GENES WITH ALTERED ACTIVITY	PHYSIOLOGICAL CONSEQUENCES OF ALTERING GENE EXPRESSION	EXAMPLES OF BIOCHEMICAL ACTIVITIES OF GENES WITH ALTERED EXPRESSION
AP2 Reproduction Genes	<p>Genes activated by AP2 transcription factors</p> <p>Genes that induce petal and stamen formation</p>	<p>Many steps and pathways induced, developmental and metabolic</p> <p>No petals or stamens produced</p>	<p>Proteins associated with:</p> <p>Energy production and conversion</p> <p>Amino acid transport and metabolism</p> <p>Carbohydrate transport and metabolism</p> <p>Lipid metabolism</p> <p>Transcription and signal transduction</p> <p>Poor translational modification</p> <p>DNA replication</p> <p>Chromatin remodeling</p>
Down-Regulated Transcripts			

TRANSCRIPT LEVELS	TYPE OF GENES WITH ALTERED ACTIVITY	PHYSIOLOGICAL CONSEQUENCES OF ALTERING GENE EXPRESSION	EXAMPLES OF BIOCHEMICAL ACTIVITIES OF GENES WITH ALTERED EXPRESSION
Flower Reproduction Genes	Genes that repress flower development	Flowers form from flower meristem	Transcription factors Signal transduction pathways Kinases and phosphatases
	Genes that induce stem, leaf and other organ differentiation	Non-floral organs are repressed	Chromatin remodeling proteins
	Genes that negatively regulate flower specific metabolism	Flower-specific pathways are induced	
	Genes that negatively regulate ovule formation, meiosis, fertilization and seed development		
AP2 Reproduction Genes	Genes activated by AP2 transcription factors	Many steps and pathways induced, developmental and metabolic	Proteins associated with: Energy production and conversion

TRANSCRIPT LEVELS	TYPE OF GENES WITH ALTERED ACTIVITY	PHYSIOLOGICAL CONSEQUENCES OF ALTERING GENE EXPRESSION	EXAMPLES OF BIOCHEMICAL ACTIVITIES OF GENES WITH ALTERED EXPRESSION
	Genes that induce petal and stamen formation	No petals or stamens produced	Amino acid transport and metabolism Carbohydrate transport and metabolism Lipid metabolism Transcription and signal transduction Poor translational modification DNA replication Chromatin remodeling

While polynucleotides and gene products modulating reproduction can act alone, combinations of these polynucleotides also affect growth and development. Useful combinations include different polynucleotides and/or gene products of the instant invention that have similar transcription profiles or similar biological activities, and members of the same or similar biochemical pathways. In addition, the combination of a polynucleotide and/or gene product(s) capable of modulating reproduction with a hormone responsive polynucleotide, particularly one affected by gibberellic acid and/or Auxin, is also useful because of the interactions that exist between hormone-regulated pathways, and development. Here, in addition to polynucleotides

having similar transcription profiles and/or biological activities, useful combinations include polynucleotides that may have different transcription profiles but which participate in common or overlapping pathways.

USE OF PROMOTERS AND REPRODUCTION GENES

Promoter of reproduction genes are useful for transcription of desired polynucleotides, both plant and non-plant. For example, extra copies of carbohydrate transporter genes can be operably linked to a reproduction gene promoter and inserted into a plant to increase the “sink” strength of flowers or siliques. Similarly, reproduction gene promoters can be used to drive transcription of metabolic enzymes capable of altering the oil, starch, protein or fiber of a flower or silique. Alternatively, reproduction gene promoters can direct expression of non-plant genes that can, for instance confer insect resistance specifically to a flower.

III.A.7. OVULE GENES, GENE COMPONENTS AND PRODUCTS

The ovule is the primary female sexual reproductive organ of flowering plants. It contains the egg cell and, after fertilization occurs, contains the developing seed. Consequently, the ovule is at times comprised of haploid, diploid and triploid tissue. As such, ovule development requires the orchestrated transcription of numerous polynucleotides, some of which are ubiquitous, others that are ovule-specific and still others that are expressed only in the haploid, diploid or triploid cells of the ovule.

Although the morphology of the ovule is well known, little is known of these polynucleotides and polynucleotide products. Mutants allow identification of genes that participate in ovule development. As an example, the pistillata (PI) mutant replaces stamens with carpels, thereby increasing the number of ovules present in the flower. Accordingly, comparison of transcription levels between the wild-type and PI mutants allows identification of ovule-specific developmental polynucleotides.

Changes in the concentration of ovule-specific polynucleotides during development results in the modulation of many polynucleotides and polynucleotide products. Examples of such ovule-specific responsive polynucleotides and polynucleotide products are shown in the Reference, Sequence, Protein Group, Protein Group Matrix, MA_diff, and MA_clust tables. These

polynucleotides and/or products are responsible for effects on traits such as fruit production and seed yield.

While ovule-specific developmentally responsive polynucleotides and polynucleotide products can act alone, combinations of these polynucleotides also affect fruit and seed growth and development. Useful combinations include different ovule-specific developmentally responsive polynucleotides and/or polynucleotide products that have similar transcription profiles or similar biological activities, and members of the same or similar biochemical pathways. In addition, the combination of an ovule-specific developmentally responsive polynucleotide and/or polynucleotide product with an environmentally responsive polynucleotide is also useful because of the interactions that exist between development, hormone-regulated pathways, stress pathways and nutritional pathways. Here, in addition to polynucleotides having similar transcription profiles and/or biological activities, useful combinations include polynucleotides that may have different transcription profiles but which participate in a common pathway. The MA_diff Table(s) reports the transcript levels of the experiment (see EXPT ID: 108595). For transcripts that had higher levels in the samples than the control, a "+" is shown. A "-" is shown for when transcript levels were reduced in root tips as compared to the control. For more experimental detail see the Example section below.

Ovule genes are those sequences that showed differential expression as compared to controls, namely those sequences identified in the MA_diff tables with a "+" or "-" indication.

Ovule Genes Identified By Cluster Analyses Of Differential Expression

Ovule Genes Identified By Correlation To Genes That Are Differentially Expressed

As described above, the transcription profiles of genes that act together are well correlated. Applicants not only have identified the genes that are differentially expressed in the microarray experiments, but also have identified the genes that act in concert with them. The MA_clust table indicates groups of genes that have well correlated transcription profiles and therefore participate in the same pathway or network.

A pathway or network of Ovule genes is any group in the MA_clust that comprises a cDNA ID that also appears in Expt ID 108595 of the MA_diff table(s).

Ovule Genes Identified By Correlation To Genes That Cause Physiological

Consequences

Additionally, the differential expression data and the phenotypic observations can be merged to identify pathways or networks of Ovule genes. A group in the MA_clust is considered a Ovule pathway or network if the group comprises a cDNA ID that also appears in Knock-in or Knock-out tables that causes one or more of the phenotypes described in section above.

Ovule Genes Identified By Amino Acid Sequence Similarity

Ovule genes from other plant species typically encode polypeptides that share amino acid similarity to the sequences encoded by corn and Arabidopsis Ovule genes. Groups of Ovule genes are identified in the Protein Group table. In this table, any protein group that comprises a peptide ID that corresponds to a cDNA ID member of a Ovule pathway or network is a group of proteins that also exhibits Ovule functions/utilities.

Such ovule-specific developmentally responsive polynucleotides and polynucleotide products can function to either increase or dampen the above phenotypes or activities either in response to transcript changes during ovule development or in the absence of ovule-specific polynucleotide fluctuations. More specifically, ovule-specific developmentally responsive polynucleotides and polynucleotide products are useful to or modulate one or more of the phenotypes, including egg cell, maturation (for development of parthenogenic embryos), metabolism, polar nuclei, fusion (for development of parthenogenic endosperm), central cell, maturation, metabolism (for alteration of endosperm metabolism), synergids, maturation, programmed cell death, nucellus, maturation, integuments, maturation, funiculus, extension (for increased seed), cuticle, maturation, tensile properties (for increased seed size), ovule, modulation of ovule senescence, and shaping (for increased seed number).

To produce the desired phenotype(s) above, one or more of the ovule-specific developmentally responsive polynucleotides and polynucleotide products can be tested by screening for the desired trait. Specifically, the polynucleotide, mRNA levels, or protein levels can be altered in a plant utilizing the procedures described herein and the phenotypes can be

assayed. As an example, a plant can be transformed according to Bechtold and Pelletier (1998, Methods. Mol. Biol. 82:259-266) and visually inspected for the desired phenotype or metabolically and/or functionally assayed according to Weigel et al. (2000, Plant Physiol 122: 1003-14) and Winkler et al. (1998, Plant Physiol 118: 743-50).

Alternatively, the activities of one or more of the ovule-specific developmentally responsive polynucleotides and polynucleotide products can be modulated to change biochemical or metabolic activities and/or pathways such as those noted below. Such biological activities can be measured according to the citations included in the Table below:

GENERAL CATEGORY	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	ASSAY
Cell Growth and Differentiation	-Programmed Cell Death - DNA Methylation and Imprinting	Pennell and Lamb (1997) Plant Cell 9, 1157-1168 Adams et al. (2000) Development 127: 2493-502
Organ Growth and Development	-Ovule Growth and Development -Ethylene Response -Megagametophyte Development -Seed Growth and Development -Fertilization Independent	De Martinis and Mariani (1999) Plant Cell 11: 1061-72 Christensen et al. (1997) Sexual Plant Reproduc 10: 49-64 Scott et al. (1998) Development 125: 3329-41 Ohad et al. (1996)

GENERAL CATEGORY	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	ASSAY
	Seed Development	PNAS USA 93: 5319-24 Chaudhury et al. (1997) PNAS USA 94: 4223-28
Signal Transduction	-Ethylene Metabolism - Protein Remodeling -Sucrose Mobilization and Partitioning -Pollen Tube Adhesion -Jasmonic Acid Biosynthesis -	DeMartinis and Mariani (1999) Plant Cell 11: 1061-1072 Winkler et al. (1998) Plant Physiol 118: 743- 750
Senescence and Cell Death	-Apomixis	
Environmental Responses	-Wound and Defense Response Gene Expression -Stress Response	Epple and Bohlmann (1997) Plant Cell 9: 509- 20 He et al. (1998) Plant J. 14: 55-63

	Repressor of Abscissic acid Deprivation Pathways	Negative Regulation of Abscissic acid Pathways	
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USE OF PROMOTERS OF OVULE GENES

Promoters of Ovule genes are useful for transcription of any desired polynucleotide or plant or non-plant origin. Further, any desired sequence can be transcribed in a similar temporal, tissue, or environmentally specific patterns as the Ovule genes where the desired sequence is operably linked to a promoter of a Ovule gene. The protein product of such a polynucleotide is usually synthesized in the same cells, in response to the same stimuli as the protein product of the gene from which the promoter was derived. Such promoter are also useful to produce antisense mRNAs to down-regulate the product of proteins, or to produce sense mRNAs to down-regulate mRNAs via sense suppression.

III.A.8. SEED AND FRUIT DEVELOPMENT GENES, GENE COMPONENTS AND PRODUCTS

The ovule is the primary female sexual reproductive organ of flowering plants. At maturity it contains the egg cell and one large central cell containing two polar nuclei encased by two integuments that, after fertilization, develops into the embryo, endosperm, and seed coat of the mature seed, respectively. As the ovule develops into the seed, the ovary matures into the fruit or silique. As such, seed and fruit development requires the orchestrated transcription of numerous polynucleotides, some of which are ubiquitous, others that are embryo-specific and still others that are expressed only in the endosperm, seed coat, or fruit. Such genes are termed fruit development responsive genes.

Changes in the concentration of fruit-development responsive polynucleotides during development results in the modulation of many polynucleotides and polynucleotide products. Examples of such fruit development responsive polynucleotides and polynucleotide products relative to leaves and floral stem are shown in the Reference, Sequence, Protein Group, Protein Group Matrix, MA_diff, MA_clust, Knock-in and Knock-out tables. The polynucleotides were

discovered by isolating fruits at developmental stages from *Arabidopsis* wild-type ecotype "Wassilewskija", and measuring the mRNAs expressed in them relative to those in a leaf and floral stem sample. These polynucleotides and/or products are responsible for effects on traits such as seed size, seed yield, seed composition, seed dormancy, fruit ripening, fruit production, and pod shattering.

While fruit development responsive polynucleotides and polynucleotide products can act alone, combinations of these polynucleotides also affect fruit and seed growth and development. Useful combinations include different polynucleotides and/or polynucleotide products that have similar transcription profiles or similar biological activities, and members of the same or functionally similar biochemical pathways. In particular, modulation of transcription factors and/or signal transduction pathways are likely to be useful for manipulating whole pathways and hence phenotypes. In addition, the combination of ovule-developmentally responsive polynucleotides and/or polynucleotide products with environmentally responsive polynucleotides is also useful because of the interactions that exist between development, hormone-regulated pathways, stress and pathogen induced pathways and nutritional pathways. Here, useful combinations include polynucleotides that may have different transcription profiles, and participate in common or overlapping pathways but combine to produce a specific, phenotypic change.

Such fruit development responsive polynucleotides and polynucleotide products can function to either increase or dampen the above phenotypes or activities either in response to transcript changes in fruit development or in the absence of fruit development polynucleotide fluctuations.

The MA_diff Table(s) reports the transcript levels of the experiment (see EXPT ID: 108436, 108437, 108438). For transcripts that had higher levels in the samples than the control, a "+" is shown. A "-" is shown for when transcript levels were reduced in root tips as compared to the control. For more experimental detail see the Example section below.

Fruit genes are those sequences that showed differential expression as compared to controls, namely those sequences identified in the MA_diff tables with a "+" or "-" indication.

Fruit Genes Identified By Cluster Analyses Of Differential Expression

Fruit Genes Identified By Correlation To Genes That Are Differentially Expressed

As described above, the transcription profiles of genes that act together are well correlated. Applicants not only have identified the genes that are differentially expressed in the microarray experiments, but also have identified the genes that act in concert with them. The MA_clust table indicates groups of genes that have well correlated transcription profiles and therefore participate in the same pathway or network.

A pathway or network of Fruit genes is any group in the MA_clust that comprises a cDNA ID that also appears in Expt ID 108436, 108437, 108438 of the MA_diff table(s).

Fruit Genes Identified By Correlation To Genes That Cause Physiological Consequences

Additionally, the differential expression data and the phenotypic observations can be merged to identify pathways or networks of Fruit genes. A group in the MA_clust is considered a Fruit pathway or network if the group comprises a cDNA ID that also appears in Knock-in or Knock-out tables that causes one or more of the phenotypes described in section above.

Fruit Genes Identified By Amino Acid Sequence Similarity

Fruit genes from other plant species typically encode polypeptides that share amino acid similarity to the sequences encoded by corn and Arabidopsis Fruit genes. Groups of Fruit genes are identified in the Protein Group table. In this table, any protein group that comprises a peptide ID that corresponds to a cDNA ID member of a Fruit pathway or network is a group of proteins that also exhibits Fruit functions/utilities.

USE OF FRUIT DEVELOPMENT RESPONSIVE GENES TO MODULATE PHENOTYPES

Manipulation of the polynucleotides in the mature ovule, developing embryo, endosperm, seed coat and fruit enables many features of seed and fruit to be improved including the following:

- Female fertility, megasporogenesis, embryo and endosperm development, ovule size, endosperm size, embryo size, seed size, seed yield, seed protein, seed oil, seed starch, seed cell number, cell size, seed coat development, organ size, dormancy and acquisition of desiccation tolerance, seed storage and longevity, seed germination, apomixis, production of seedless fruit and vegetables and hybrid seed production.

To improve any of the phenotype(s) above, activities of one or more of the fruit development responsive polynucleotides and polynucleotide products can be modulated and the plants can be tested by screening for the desired trait. Specifically, the polynucleotide, mRNA levels, or protein levels can be altered in a plant utilizing the procedures described herein and the phenotypes can be assayed. As an example, a plant can be transformed according to Bechtold and Pelletier (1998, *Methods. Mol. Biol.* 82:259-266) and visually inspected for the desired phenotype or metabolically and/or functionally assayed.

USE OF FRUIT DEVELOPMENT RESPONSIVE GENES TO MODULATE BIOCHEMICAL ACTIVITIES

The activities of one or more of the fruit-expressed polynucleotides and polynucleotide products can be modulated to change biochemical or metabolic activities and/or pathways such as those noted below. Such biological changes can be achieved and measured according to citations such as the following:

1. Winkler et al. (1998). *Plant Physiol.* 118, 743-750
2. Weigel et al. (2000). *Plant Physiol.* 122, 1003-1014
3. Cosgrove (1997). *Plant Cell* 9, 1031-1041
4. Jacobs (1997). *Plant Cell* 9, 1021-1029
5. Reismeier et al. (1994). *EMBO J.* 13, 1-7
6. Carland et al. (1999). *Plant Cell* 11, 2123-2138
7. Cheng et al. (1996). *Plant Cell* 8, 971-983
8. Weber et al. (1995). *Plant Cell* 7, 1835-1846
9. Leyser and Furrer (1992). *Development* 116, 397-403
10. Hayashi et al. (1998). *Plant Cell* 10, 183-196.
11. Pyke (1999). *Plant Cell* 11, 549-556
12. Lotan et al. (1998). *Cell* 93, 1195-1205
13. Lending and Larkins (1989). *Plant Cell* 1, 1011-1023
14. Hong et al. (1996). *Development* 122, 2051-2058.
15. Fernandez et al. (2000). *Science* 289, 436-438

16. D'Aoust et al. (1999). Plant Cell 11, 2407-2418
17. Bewley (1997). Plant Cell 9, 1055-1066
18. Heath et al. (1986). Planta 169, 304-312
19. Browse et al. (1986). Anal. Biochem. 152, 141-145
20. D'Aoust et al. (1999). Plant Cell 11, 2407-2418

Other biological activities that can be modulated by the fruit-specific developmentally responsive polynucleotides and polynucleotide products are listed in Reference Tables. Assays for detecting such biological activities are described in the table as well as in the Protein Domain tables.

	BIOLOGICAL FUNCTION	UTILITY	CITATION	ASSAY	CITATION
Ovule Growth, Ovule Development and Seed Growth and Development	Ethylene and ethylene signal transduction pathway Examples: AP2 domain DNA binding proteins; EREBP, EBF Example: Leucine-rich receptor kinase; ETR- like Example: Raf kinase; CTR	Manipulate female fertility. Manipulate megasporo- genesis. Manipulate female gametophyte development. Manipulate fertilization independent endosperm development. Manipulate fertilization independent	De Martinis and Mariani (1999). Plant Cell 11, 1061- 1072. Silencing gene expression of the ethylene- forming enzyme results in a reversible inhibition of ovule development in transgenic tobacco plants. Christensen et al. (1997).	Analyze ovule and seed development by light microscopy or by confocal microscopy. Test for fertilization independent endosperm development. Test for fertilization independent embryo	Winkler et al. (1998). Plant Physiol. 118, 743-750. Systematic reverse genetics of transfer- DNA-tagged lines of Arabidopsis. Weigel et al. (2000). Plant Physiol 122, 1003-1014. Activation tagging in Arabidopsis.

	kinase; CTR	independent embryo development. Manipulate fertilization independent seed development. Manipulate ovule size. Manipulate endosperm size. Manipulate embryo size. Manipulate seed size. Manipulate seed yield. Manipulate seed protein. Manipulate seed oil. Manipulate starch production.	Sexual Plant Reproduc. 10, 49-64. Megagametogenesis in Arabidopsis wild type and the Gf mutant. Christiansen and Drews, unpublished	development. Test for fertilization independent seed production. Analyze seed size. Analyze seed yield. Analyze seed composition. Analyze fruit size.	Ohad et al. (1996). PNAS USA 93, 5319-5324. A mutation that allows endosperm development without fertilization Chaudhury et al. (1997). PNAS USA 94, 4223-4228. Fertilization-independent seed development in Arabidopsis thaliana De Martinis and Mariani (1999). Plant Cell 11, 1061-1072. Silencing gene expression of the ethylene-
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		<p>Manipulate cell number.</p> <p>Manipulate cell size.</p> <p>Produce seedless fruit and vegetables</p> <p>Manipulate fruit size.</p>			<p>forming enzyme results in a reversible inhibition of ovule development in transgenic tobacco plants.</p> <p>Christensen et al. (1997). Sexual Plant Reproduc. 10, 49-64.</p> <p>Megagametogenesis in Arabidopsis wild type and the Gf mutant.</p> <p>Scott et al. (1998). Development 125, 3329-3341. Parent-of-origin effects on seed development in Arabidopsis</p>
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					<p>thaliana</p> <p>Heath et al. (1986). Planta 169, 304-312.</p> <p>Browse et al. (1986). Anal. Biochem. 152, 141-145.</p> <p>D'Aoust et al. (1999). Plant Cell 11, 2407-2418.</p>
	<p>2. <i>Growth and developmental control genes</i></p> <p>-----</p> <p><i>Upregulated genes</i></p> <p>Example: DNA binding proteins; tiny-like, AGL1, FBP2, AGL9, AP3, CPC-like myb.</p>	<p>Manipulate female fertility.</p> <p>Manipulate megasporogenesis.</p> <p>Manipulate female gametophyte development.</p> <p>Manipulate fertilization independent endosperm develop-</p>	<p>Wilson et al. (1996). Plant Cell 8, 659-671. A dissociation insertion causes a semidominant mutation that increases expression of TINY, an Arabidopsis gene related to APETALA2.</p>	<p>Analyze ovule and seed development by light microscopy or by confocal microscopy.</p> <p>Test for fertilization independent endosperm development.</p> <p>Test for fertilization independent embryo</p>	<p>Winkler et al. (1998). Plant Physiol. 118, 743-750.</p> <p>Systematic reverse genetics of transfer-DNA-tagged lines of Arabidopsis.</p> <p>Weigel et al. (2000). Plant Physiol 122, 1003-1014.</p> <p>Activation</p>

	ment.	Zhao et al	embryo	Activation
Example:	Manipulate	(1999).	development.	tagging in
Protein	fertilization	Developmenta	Test for	Arabidopsis.
kinase;	independent	l Genetics 25,	fertilization	Ohad et al.
ASK1.	embryo	209-223. The	independent	(1996). PNAS
Example:	develop-	ASK1 gene	seed	USA 93,
Auxin	ment.	regulates	production.	5319-5324. A
conjugating	Manipulate	development	Analyze seed	mutation that
enzyme;	fertilization	and interacts	size.	allows
indole-3-	independent	with the UFO	Analyze seed	endosperm
acetate beta-	seed	gene to	yield.	development
glucosyltransf	development.	control floral	Analyze seed	without
erase.	Manipulate	organ identity	composition.	fertilization
Example: S/T	ovule size.	in	Analyze fruit	Chaudhury et
protein	Manipulate	Arabidopsis.	size.	al. (1997).
kinase;	endosperm	Flanagan et	Analyze	PNAS USA
APK1.	size.	al. (1996).	seedling size.	94, 4223-
Example:	Manipulate	Plant J. 10,	Analyze	4228.
Leucine-rich	embryo size.	343-53.	seedling	Fertilization-
receptor	Manipulate	Specific	viability.	independent
kinase;	organ size	expression of	Screen for	seed
CLV1, ER,	and number.	the AGL1	changes in	development
BRI, Cf-2-	Manipulate	MADS-box	shatter time.	in
like.	seed size.	gene suggests	Screen for	Arabidopsis
-----	Manipulate	regulatory	changes in	thaliana
<i>Downregulate</i>	seed yield.	functions in	germination	
<i>d genes</i>	Manipulate	Arabidopsis	frequency.	De Martinis
Example:	seedling size	gynoecium		and Mariani
		and ovule		(1999). Plant
		development.		

	<p>Cyclin-dependent kinase; cdc2.</p> <p>seedling size through seed size.</p> <p>Manipulate seedling vigor through seed size.</p> <p>Manipulate seed protein.</p> <p>Manipulate seed oil.</p> <p>Manipulate starch production.</p> <p>Manipulate integument development.</p> <p>Manipulate seedcoat development.</p> <p>Manipulate cell size.</p> <p>Manipulate cell number.</p> <p>Manipulate homeotic gene expression.</p>	<p>development.</p> <p>Angenent et al. (1994).</p> <p>Plant J 1994. 5, 33-44. Co-suppression of the petunia homeotic gene fbp2 affects the identity of the generative meristem.</p> <p>AGL9 web page.</p> <p>Wada et al. (1997)</p> <p>Science 277, 1113-6.</p> <p>Epidermal cell differentiation in Arabidopsis determined by a Myb homolog CPC.</p> <p>Szerszen et al. (1994).</p> <p>Science 16.</p>	<p>Screen for seed longevity and viability.</p>	<p>Cell 11, 1061-1072. Silencing gene expression of the ethylene-forming enzyme results in a reversible inhibition of ovule development in transgenic tobacco plants.</p> <p>Christensen et al. (1997).</p> <p>Sexual Plant Reproduc. 10, 49-64.</p> <p>Megagametogenesis in Arabidopsis wild type and the Gf mutant.</p> <p>Scott et al. (1998).</p> <p>Development 125, 3329-3341. Parent-</p>
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		expression. Manipulate organ size. Manipulate meristem size. Produce seedless fruit and vegetables Manipulate fruit size. Manipulate time of seed dispersal. Manipulate seed viability upon storage. Manipulate germination frequency.	Science 16, 1699-1701. iaglu, a gene from Zea mays involved in conjugation of growth hormone indole-3- acetic acid. Ito et al. (1997). Plant Cell Physiol. 38, 248-258. A serine/threoni ne protein kinase gene isolated by an in vivo binding procedure using the Arabidopsis floral homeotic gene product, AGAMOUS.		of-origin effects on seed development in Arabidopsis thaliana. Heath et al. (1986). Planta 169, 304-312. Browse et al. (1986). Anal. Biochem. 152, 141-145. D'Aoust et al. (1999). Plant Cell 11, 2407- 2418.
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			<p>Clark et al. (1997). Cell 89, 575-585. The CLAVATA1 gene encodes a putative receptor kinase that controls shoot and floral meristem size in Arabidopsis.</p> <p>Torii et al. (1996). Plant Cell 8, 735- 746. The Arabidopsis ERECTA gene encodes a putative receptor protein kinase with extracellular leucine-rich repeats.</p> <p>Li and Chory</p>		
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			(1997). Cell 90, 929-38. A putative leucine-rich repeat receptor kinase involved in brassinosteroid signal transduction.		
	<p>3. <i>Cell senescence and cell death</i></p> <p>Example: Cystatin</p> <p>Example: WIPK</p>	<p>Manipulate female fertility.</p> <p>Manipulate seed set.</p> <p>Manipulate seed yield.</p> <p>Manipulate seed size.</p> <p>Manipulate fruit set.</p> <p>Promote apomixis.</p> <p>Produce seedless fruit and vegetables.</p>	<p>Solomon et al. (1999). Plant Cell 11, 431-444. The involvement of cysteine proteases and protease inhibitor genes in the regulation of programmed cell death in plants.</p> <p>Zhang et al. (2000). Plant J. 23, 339-347. Multiple levels of tobacco</p>	<p>Analyze ovule and seed development by light microscopy or by confocal microscopy.</p> <p>Analyze seed set.</p> <p>Analyze seed size.</p> <p>Analyze seed yield.</p> <p>Analyze fruit set.</p> <p>Screen for fertilization independent</p>	<p>Winkler et al. (1998). Plant Physiol. 118, 743-750. Systematic reverse genetics of transfer-DNA-tagged lines of Arabidopsis.</p> <p>Weigel et al. (2000). Plant Physiol 122, 1003-1014. Activation tagging in Arabidopsis.</p>

			of tobacco WIPK activation during the induction of cell death by fungal elicitors.	independent seed development.	Ohad et al. (1996). PNAS USA 93, 5319-5324. A mutation that allows endosperm development without fertilization
	4. <i>Protein remodelin g</i> Example: DNA-J protein/chape rones	Manipulate female fertility. Manipulate female gametophyte development. Promote apomixis. Manipulate endosperm development. Manipulate embryo development. Manipulate seed size.	Christensen et al. (1997). Sexual Plant Reproduc. 10, 49-64. Megagametoge nesis in Arabidopsis wild type and the Gf mutant. Cory Christiansen and Gary Drews, unpublished	Test for altered female fertility, seed set, seed yield. Analyze ovule development by light microscopy or by confocal microscopy. Analyze seed size. Analyze seed yield. Analyze seed composition.	Winkler et al. (1998). Plant Physiol. 118, 743-750. Systematic reverse genetics of transfer- DNA-tagged lines of Arabidopsis. Weigel et al. (2000). Plant Physiol 122, 1003-1014. Activation tagging in Arabidopsis.

		Manipulate seed yield.			Christensen et al. (1997).
		Manipulate seed protein.			Sexual Plant Reproduc. 10, 49-64.
		Manipulate seed oil.			Megagametogenesis in Arabidopsis wild type and the Gf mutant.
		Manipulate starch.			Ohad et al. (1996). PNAS USA 93, 5319-5324. A mutation that allows endosperm development without fertilization
		Produce seedless fruit and vegetables.			Scott et al. (1998). Development 125, 3329-3341. Parent-of-origin effects on seed development

					<p>in Arabidopsis thaliana.</p> <p>Heath et al. (1986). Planta 169, 304-312.</p> <p>Browse et al. (1986). Anal. Biochem. 152, 141-145.</p> <p>D'Aoust et al. (1999). Plant Cell 11, 2407-2418.</p>
	<p>5. <u>Sucrose mobilization and partitioning</u></p> <p>Example: <u>Invertase inhibitor</u></p> <p>Example: bZIP transcription factor (translation of bZIP protein is inhibited by sucrose levels greater than</p>	<p>Manipulate female fertility.</p> <p>Manipulate ovule development.</p> <p>Manipulate seed development.</p> <p>Manipulate endosperm development.</p> <p>Manipulate</p>	<p>Mapping of tomato genes associated with sugar metabolism.</p> <p>Tomato Genetics Co- op Report 48, 22-23 (1998)</p> <p>Ikeda et al. (1999). Plant Physiol 121, 813-820.</p> <p>Sucrose and</p>	<p>Analyze ovule and seed development by light microscopy or by confocal microscopy.</p> <p>Determine female fertility.</p> <p>Analyze seed mass.</p> <p>Analyze seed</p>	<p>Winkler et al. (1998). Plant Physiol. 118, 743-750.</p> <p>Systematic reverse genetics of transfer-DNA- tagged lines of Arabidopsis.</p> <p>Weigel et al. (2000). Plant Physiol 122, 1003-1014.</p>

	greater than 25 mM) Example: Lipoxygenase ---- <i>Downregulate d gene</i> Example: SNF1-related protein kinase	embryo development. Manipulate seed size. Manipulate seed yield. Manipulate seed protein. Manipulate seed oil. Manipulate starch. Manipulate cell size. Manipulate cell number. Manipulate organ size. Manipulate meristem size. Manipulate seedling size through seed size. Manipulate seedling	Sucrose and Cytokinin Modulation of WPK4, a Gene Encoding a SNF1-Related Protein Kinase from Wheat. Rook et al. (1998). Plant J. 15, 253- 263. Sucrose- specific signaling represses translation of the Arabidopsis ATB2 bZIP transcription factor gene. Rook et al. (1998). Plant Mol Biol 37,171-178. The light- regulated Arabidopsis	yield. Analyze seed composition. Analyze organ size. Analyze seedling size. Analyze seedling viability.	1003-1014. Activation tagging in Arabidopsis. Christensen et al. (1997). Sexual Plant Reproduc. 10, 49-64. Megagametog enesis in Arabidopsis wild type and the Gf mutant. Ohad et al. (1996). PNAS USA 93, 5319-5324. A mutation that allows endosperm development without fertilization Scott et al. (1998). Development 125, 3329-
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		<p>viability through seed size.</p> <p>Produce seedless fruit and vegetables.</p> <p>Translational control of gene expression in ovule and seed by sucrose.</p> <p>Manipulate assimilate partitioning in ovule and seed development.</p>	<p>Arabidopsis bZIP transcription factor gene ATB2 encodes a protein with an unusually long leucine zipper domain.</p> <p>Bunker et al. (1995). Plant Cell 7, 1319-1331. Sink limitation induces the expression of multiple soybean vegetative lipoxygenase mRNAs while the endogenous jasmonic acid level remains low.</p> <p>Lowry et al.</p>		<p>3341. Parent-of-origin effects on seed development in Arabidopsis thaliana.</p> <p>6. Heath et al. (1986). Planta 169, 304-312.</p> <p>7. Browse et al. (1986). Anal. Biochem. 152, 141-145.</p> <p>8. D'Aoust et al. (1999). Plant Cell 11, 2407-2418.</p>
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			(1998). Plant Physiol. 116, 923-933. Specific soybean lipoxygenases localize to discrete subcellular compartments and their mRNAs are differentially regulated by source-sink status.		
	6. <i>Jasmonic acid biosynthesis is and signal transduction on pathway</i> Example: Biosynthetic enzyme; FMN	Targeted death of cells belonging to the female gametophyte, ovule or integuments. Delay senescence of unfertilized female gametophyte,	Sanders et al. (2000). Plant Cell 12, 1041- 1062. The Arabidopsis DELAYED DEHISCENCE E1 gene encodes an enzyme in the jasmonic acid synthesis	Test for altered female fertility. Analyze male fertility. Screen for enhanced expression of pathogen defense response genes.	Winkler et al. (1998). Plant Physiol. 118, 743-750. Systematic reverse genetics of transfer- DNA-tagged lines of Arabidopsis Weigel et al.

	<p>oxidoreductase 12-oxophyto-dienoate reductase, OPR1, OPR1-like.</p> <p>Example: Signal transduction pathway kinase WIPK.</p>	<p>ovule or integuments.</p> <p>Manipulate female fertility</p> <p>Coordinate female with male reproduction.</p> <p>Manipulate male fertility.</p> <p>Enhanced defense response in ovules and seed</p>	<p>pathway.</p> <p>Vijayan et al. (1998). A role for jasmonate in pathogen defense of Arabidopsis. PNAS USA 95, 7209-7214.</p> <p>Seo et al. (1999). Plant Cell 11, 289-298.</p> <p>Jasmonate-based wound signal transduction requires activation of WIPK, a tobacco mitogen-activated protein kinase.</p>	<p>genes.</p>	<p>(2000). Plant Physiol 122, 1003-1014.</p> <p>Activation tagging in Arabidopsis.</p>
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<i>Environmental responses</i>	<p><i>1. Wound and defense response gene expression</i></p> <p>Example: Leucine rich receptor S/T kinase; Xa21-like and TMK-like.</p> <p>Example: Cell wall-associated protein kinase WAK1.</p> <p>Example: Thionins.</p>	<p>Pathogen resistant ovules.</p> <p>Pathogen resistant seeds.</p> <p>Pathogen resistant fruit.</p>	<p>Song et al. (1995). Science 270, 1804-1806. A receptor kinase-like protein encoded by the rice disease resistance gene, Xa21.</p> <p>Seo et al. (1995). Science 270, 1988-1992. Tobacco MAP kinase: a possible mediator in wound signal transduction pathways.</p> <p>He et al. (1998). Plant J. 14, 55-63. Requirement for the induced expression of a cell wall associated</p>	<p>Resistance to <i>Xanthomonas</i> sp.</p> <p>Resistance to known arabidopsis pathogens in ovules, seed and fruit.</p>	<p>Winkler et al. (1998). Plant Physiol. 118, 743-750. Systematic reverse genetics of transfer-DNA-tagged lines of Arabidopsis.</p> <p>Weigel et al. (2000). Plant Physiol 122, 1003-1014. Activation tagging in Arabidopsis.</p> <p>Epple and Bohlmann (1997). Plant Cell 9, 509-520. Overexpression of an endogenous thionin enhances resistance of</p>
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		<p>receptor kinase for survival during the pathogen response.</p> <p>He et al. (1999). Plant Mol. Biol. 39, 1189-1196. A cluster of five cell wall- associated receptor kinase genes, Wak1-5, are expressed in specific organs of Arabidopsis.</p> <p>Epple and Bohlmann (1997). Plant Cell 9, 509- 520.</p> <p>Overexpressi on of an endogenous thionin enhances</p>		<p>Arabidopsis against Fusarium oxysporum.</p> <p>He et al. (1998). Plant J. 14, 55-63.</p> <p>Requirement for the induced expression of a cell wall associated receptor kinase for survival during the pathogen response.</p>
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			<p>resistance of Arabidopsis against Fusarium oxysporum.</p> <p>Ichimura et al. (1998). DNA Res. 5,341-5348.</p> <p>Molecular cloning and characterization of three cDNAs encoding putative mitogen-activated protein kinase kinases (MAPKKs) in Arabidopsis thaliana.</p>		
	<p>2. <i>Stress response to cold, drought, salinity, seed maturation, embryo development,</i></p>	<p>Manipulate drought resistance.</p> <p>Manipulate desiccation tolerance in flowers,</p>	<p>Close, T.J. (1996). Physiol.Plant 97, 795-803.</p> <p>Dehydrins: emergence of a biochemical</p>	<p>Test for enhanced sensitivity to drought, dessication, cold, salinity, in ovules,</p>	<p>Winkler et al. (1998). Plant Physiol. 118, 743-750.</p> <p>Systematic reverse genetics of</p>

	<p><i>ABA.</i></p> <p>Example: Dehydrins</p> <p>Example: NPK1-like protein kinase</p> <p>Example: DNA binding protein genes: CBF-like, DREB2A, RAP2.1.</p>	<p>ovules and seeds.</p> <p>Manipulate cold tolerance in flowers, ovules, and seeds.</p> <p>Manipulate seed dormancy.</p> <p>Manipulate germination frequency.</p> <p>Manipulate seed storage and viability.</p>	<p>role of a family of plant dehydration proteins.</p> <p>Kovtun et al. (2000). PNAS USA 97, 2940-2945.</p> <p>Functional analysis of oxidative stress- activated mitogen- activated protein kinase cascade in plants.</p>	<p>developing seed and seedlings.</p> <p>Test for enhanced tolerance to drought, dessication, cold, salinity, in ovules, developing seed and seed.</p> <p>Test for changes in seed viability upon storage.</p> <p>Test for changes in germination frequencies.</p>	<p>transfer- DNA-tagged lines of Arabidopsis.</p> <p>Weigel et al. (2000). Plant Physiol 122, 1003-1014.</p> <p>Activation tagging in Arabidopsis.</p>
	<p><i>3. Response to starvation, wounding, and pathogen attack by tryptophan synthesis.</i></p> <p>Example: DNA binding</p>	<p>Altered response to starvation.</p> <p>Altered response to wounding.</p> <p>Altered response to pathogen</p>	<p>Bender and Fink (1998). A myb homologue, ATR1, activates tryptophan gene expression in</p>	<p>Test for enhanced sensitivity to starvation, wounding, and pathogen attack.</p> <p>Test for enhanced</p>	<p>Winkler et al. (1998). Plant Physiol. 118, 743-750.</p> <p>Systematic reverse genetics of transfer- DNA-tagged</p>

	<p>DNA binding protein; ATR1-like myb.</p> <p>Example: Auxin conjugating enzyme; indole-3-acetate beta-glucosyltransferase.</p>	<p>pathogen attack.</p>	<p>arabidopsis. PNAS USA 95, 5655-5660.</p>	<p>enhanced tolerance to starvation, wounding, and pathogen attack.</p>	<p>lines of Arabidopsis.</p> <p>Weigel et al. (2000). Plant Physiol 122, 1003-1014. Activation tagging in Arabidopsis.</p>
<p><i>Cell metabolism</i></p>	<p><i>Stearoyl-acyl carrier protein desaturase</i></p> <p>Example: C18 fatty acid desaturation</p>	<p>Production of oils high in saturated fatty acids</p> <p>Manipulate membrane composition</p>	<p>Merlo et al. (1998). Plant Cell 10, 1603-1621.</p>	<p>Analyze seed size.</p> <p>Analyze seed yield.</p> <p>Analyze seed composition.</p> <p>Analyze seed oil by gas chromatography.</p>	<p>Winkler et al. (1998). Plant Physiol. 118, 743-750.</p> <p>Systematic reverse genetics of transfer-DNA-tagged lines of Arabidopsis.</p> <p>Weigel et al. (2000). Plant Physiol 122, 1003-1014. Activation tagging in</p>

					<p>Arabidopsis.</p> <p>Browse et al. (1986). Anal. Biochem. 152, 141-145.</p>
	<p>2. <i>Manipulate nitrogen economy</i></p> <p>Example: Asparaginase</p>	<p>Manipulate asparagine degradation in ovules and seeds.</p> <p>Manipulate endosperm production.</p> <p>Manipulate embryo development.</p> <p>Manipulate ovule size.</p> <p>Manipulate seed size.</p>	<p>Mathews and Van Holde</p>	<p>Analyze seed size.</p> <p>Analyze seed yield.</p> <p>Analyze seed composition.</p>	<p>Winkler et al. (1998). Plant Physiol. 118, 743-750.</p> <p>Systematic reverse genetics of transfer-DNA-tagged lines of Arabidopsis.</p> <p>Weigel et al. (2000). Plant Physiol 122, 1003-1014.</p> <p>Activation tagging in Arabidopsis.</p> <p>Heath et al. (1986). Planta 169,</p>

					304-312. Browse et al. (1986). Anal. Biochem. 152, 141-145. D'Aoust et al. (1999). Plant Cell 11, 2407-2418.
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Fruit development responsive polynucleotides are characteristically differentially transcribed in response to fluctuating developmental-specific polynucleotide levels or other signals, whether internal or external to a cell. MA_diff reports the changes in transcript levels of various fruit development responsive polynucleotides in fruits.

These data can be used to identify a number of types of fruit development responsive polynucleotides. Profiles of some of these different fruit development responsive polynucleotides are shown in the table below with examples of the kinds of associated biological activities. Because development is a continuous process and many cell types are being examined together, the expression profiles of genes overlap between stages of development in the chart below.

Transcript Levels	Developmental Process	Metabolic Pathways	Examples of Biochemical Activity
(0-5 mm)>>(5-10 mm) \cong (>10 mm)	Ovule Elongation	- Hormone Production, Transport, Perception, Signalling, Response (e.g., Gibberellin, Ethylene, Auxin)	- Transcription Factors
(0-5 mm)>>(5-10 mm) > (>10 mm)	Tissue Specialization - Vascular system	- Cell wall Biosynthesis	- Transporters
(0-5 mm)>(5-10 mm) \cong (>10 mm)	- Meristem - Endosperm - Seed coat - Fruit	- Lipid Biosynthesis - Specific Gene Transcription Initiation	- Kinases - Changes in cytoskeletal protein activity modulating cell

Transcript Levels	Developmental Process	Metabolic Pathways	Examples of Biochemical Activity
		<ul style="list-style-type: none"> - Sucrose Mobilization and Partitioning - Sucrose Signaling - Lipoxygenase Localization - Repressors of Metabolic Pathways - Protein Remodeling 	<ul style="list-style-type: none"> - structure - Stability factors for protein translation - Changes in cell wall/membrane structure - Chromatin structure and/or DNA topology - Biosynthetic enzymes
<p>(5-10 mm) >>(0-5 mm) > (>10 mm)</p> <p>(5-10 mm) >(0-5 mm) \cong (>10 mm)</p> <p>(5-10 mm) >>(0-5 mm) \cong (>10 mm)</p>	<p>Tissue Specialization</p> <ul style="list-style-type: none"> - Vascular System <p>Organelle</p> <p>Differentiation</p> <p>Cotyledon Elongation (cell division)</p> <p>Vacuome</p> <p>Development</p> <p>Lipid Deposition</p>	<ul style="list-style-type: none"> - Cell Wall Biosynthesis - Specific Gene Transcription Initiation - Sucrose Mobilization and Partitioning - Sucrose Signaling - Repressors of Metabolic Pathways - Auxin Perception, Response and Signaling - Protein Remodeling - Lipid Biosynthesis and Storage 	<ul style="list-style-type: none"> - Transcription Factors - Transporters - Kinases - Chaperones - Changes in cytoskeletal protein activity modulating cell structure - Stability of factors for protein translation - Changes in cell wall/membrane structure - Chromatin structure and/or DNA topology - Biosynthetic enzymes
<p>(>10 mm) >(0-5 mm) \cong (5-10 mm)</p>	<p>Cotyledon Elongation (expansion)</p> <p>Lipid Deposition</p> <p>Protein Deposition</p> <p>Desiccation</p>	<ul style="list-style-type: none"> - Cell Elongation - Specific Gene Transcription Initiation - Sucrose Mobilization and Partitioning - Sucrose Signaling - Lipoxygenase Localization 	<ul style="list-style-type: none"> - Transcription Factors - Transporters - Kinases - Chaperones for protein translation - Changes in cell

Transcript Levels	Developmental Process	Metabolic Pathways	Examples of Biochemical Activity
		<ul style="list-style-type: none"> - Repressors of metabolic pathways - Hormone Perception, Response and Signaling (e.g. abscissic acid) - Protein Remodeling - Protein synthesis and Storage - Lipid Synthesis and Storage - Acquisition of Dessication Tolerance - Senescence 	<ul style="list-style-type: none"> wall/membrane structure - Chromatin structure and/or DNA topology - Biosynthetic enzymes - Metabolic enzymes
<p>(0-5 mm) < (5-10 mm) \cong (>10 mm)</p> <p>(0-5 mm) << (5-10 mm) \cong (>10 mm)</p> <p>(0-5 mm) << (5-10 mm) < (>10 mm)</p> <p>(0-5 mm) << (>10 mm) < (5-10 mm)</p>	<p>Ovule Elongation</p> <p>-Repressors of Ethylene production</p> <p>Tissue specialization</p> <p>- Vascular System</p> <p>- Meristem</p> <p>- Cotyledon</p> <p>- Seed Coat</p>	<ul style="list-style-type: none"> - Cell elongation - Negative regulation of ethylene pathways - Maintenance of Ethylene response - Changes in pathways and processes operation in cells 	<ul style="list-style-type: none"> - Transcription Factors - Transporters - Kinases - Chaperones - Stability of factors - Biosynthetic enzymes - Metabolic enzymes
(5-10 mm) < (0-5 mm) \cong (>10 mm)	<p>Organelle differentiation</p> <p>Cotyledon elongation (division)</p> <p>Vacuome development</p> <p>Lipid development</p> <p>Desiccation</p>	<ul style="list-style-type: none"> - Negative regulation of hormone pathways - Maintenance of hormone response - Changes in pathways and processes operation in cells - Dehydration and acquisition of desiccation tolerance - Senescence 	<ul style="list-style-type: none"> - Transcription Factors - Transporters - Kinases - Chaperones
(>10 mm) < (0-5 mm) \cong (5-10 mm)	<p>Cotyledon Elongation (expansion)</p> <p>Lipid deposition</p> <p>Protein deposition</p> <p>Desiccation</p>	<ul style="list-style-type: none"> - Cell elongation - Negative regulation of hormone pathways - Maintenance of hormone response - Changes in pathways and processes operation in cells 	<ul style="list-style-type: none"> - Transcription Factors - Transporters - Kinases - Chaperones - Metabolic enzymes

Transcript Levels	Developmental Process	Metabolic Pathways	Examples of Biochemical Activity
		- Dehydration and acquisition of desiccation tolerance - Senescence	- Biosynthetic enzymes
(0-5 mm) \cong (5-10 mm) \cong (>10 mm)	All stages	- Ribosome/polysome production and maintenance - Housekeeping genes	- Transcription Factors - Transporters - Kinases - Chaperones

III.B. DEVELOPMENT GENES, GENE COMPONENTS AND PRODUCTS

III.B.1. IMBIBITION AND GERMINATION RESPONSIVE GENES, GENE COMPONENTS AND PRODUCTS

Seeds are a vital component of the world's diet. Cereal grains alone, which comprise ~90% of all cultivated seeds, contribute up to half of the global per capita energy intake. The primary organ system for seed production in flowering plants is the ovule. At maturity, the ovule consists of a haploid female gametophyte or embryo sac surrounded by several layers of maternal tissue including the nucleus and the integuments. The embryo sac typically contains seven cells including the egg cell, two synergids, a large central cell containing two polar nuclei, and three antipodal cells. That pollination results in the fertilization of both egg and central cell. The fertilized egg develops into the embryo. The fertilized central cell develops into the endosperm. And the integuments mature into the seed coat. As the ovule develops into the seed, the ovary matures into the fruit or silique. Late in development, the developing seed ends a period of extensive biosynthetic and cellular activity and begins to desiccate to complete its development and enter a dormant, metabolically quiescent state. Seed dormancy is generally an undesirable characteristic in agricultural crops, where rapid germination and growth are required. However, some degree of dormancy is advantageous, at least during seed development. This is particularly true for cereal crops because it prevents germination of grains while still on the ear of the parent plant (preharvest sprouting), a phenomenon that results in major losses to the agricultural industry. Extensive domestication and breeding of crop species have ostensibly reduced the level of dormancy mechanisms present in the seeds of their wild ancestors, although

under some adverse environmental conditions, dormancy may reappear. By contrast, weed seeds frequently mature with inherent dormancy mechanisms that allow some seeds to persist in the soil for many years before completing germination.

Germination commences with imbibition, the uptake of water by the dry seed, and the activation of the quiescent embryo and endosperm. The result is a burst of intense metabolic activity. At the cellular level, the genome is transformed from an inactive state to one of intense transcriptional activity. Stored lipids, carbohydrates and proteins are catabolized fueling seedling growth and development. DNA and organelles are repaired, replicated and begin functioning. Cell expansion and cell division are triggered. The shoot and root apical meristem are activated and begin growth and organogenesis. Schematic 4 summarizes some of the metabolic and cellular processes that occur during imbibition. Germination is complete when a part of the embryo, the radicle, extends to penetrate the structures that surround it. In Arabidopsis, seed germination takes place within twenty-four (24) hours after imbibition. As such, germination requires the rapid and orchestrated transcription of numerous polynucleotides. Germination is followed by expansion of the hypocotyl and opening of the cotyledons. Meristem development continues to promote root growth and shoot growth, which is followed by early leaf formation.

Genes with activities relevant to imbibition-germination and early seedling growth are described in the two sections A and B below.

III.B.1.a. Identification Of Imbibition And Germination Genes

Imbibition and germination includes those events that commence with the uptake of water by the quiescent dry seed and terminate with the expansion and elongation of the shoots and roots. The germination period exists from imbibition to when part of the embryo, usually the radicle, extends to penetrate the seed coat that surrounds it. Imbibition and germination genes identified herein are defined as genes, gene components and products capable of modulating one or more processes of imbibition and germination described above. They are useful to modulate many plant traits from early vigor to yield to stress tolerance. Examples of such germination genes and gene products are shown in the Reference and Sequence Tables. The functions of many of the genes were deduced from comparisons with known proteins and are also given in the REF Tables.

Imbibition and Germination Genes Identified by Phenotypic Observations

Imbibition and germination genes are active, potentially active or more active during growth and development of a dry seed into a seedling. These genes herein were discovered and characterized from a much larger set of genes in experiments designed to find genes that cause poor germination.

In these experiments, imbibition and germination genes were identified by either 1) ectopic expression of a cDNA in a plant or (2) mutagenesis of the plant genome. The seeds were then imbibed and cultivated under standardized conditions and any phenotypic differences in the modified plants compared with the parental "wild-type" seedlings were recorded. The genes causing the changes were deduced from the cDNA inserted or gene mutated. The phenotypic differences observed were poor germination and aberrant seedlings.

Imbibition and Germination Genes Identified by Differential Expression

Germination genes were also identified by measuring the relative levels of mRNA products of genes in different stages of germination of a seed versus the plant as a whole. Specifically, mRNA was isolated from whole imbibed seeds of Arabidopsis plants 1, 2, 3 or 4 days after imbibition and compared to mRNA isolated from dry seed-utilizing microarray procedures. The MA_diff Table reports the transcript levels of the experiment. For transcript levels that were higher in the imbibed seed than in dry seed a "+" is shown. A "-" is shown when the transcript levels in dry seed were greater than those in imbibed seed. For more experimental detail, see the examples below:

Germination associated genes can be identified by comparing expression profiles of imbibed gibberellin treated and untreated ga1 mutant seed. Germination associated genes can also be identified by comparing expression profiles in late maturation seed from wild-type and mutants that are defective for the establishment of dormancy and can germinate precociously (e.g. aba1, aba2, abi4 in arabidopsis and vp1, vp5 in maize) or are defective for the specification of cotyledon identity and dessication tolerance (e.g. lec1, lec2, and fus3).

The MA_diff Table(s) reports the transcript levels of the experiment (see EXPT ID: 108461, 108462, 108463, 108464, 108528, 108529, 108530, 108531, 108545, 108546, 108547,

108518, 108529, 108543, 108544). For transcripts that had higher levels in the samples than the control, a "+" is shown. A "-" is shown for when transcript levels were reduced in root tips as compared to the control. For more experimental detail see the Example section below.

Imbibed & Germinating Seeds genes are those sequences that showed differential expression as compared to controls, namely those sequences identified in the MA_diff tables with a "+" or "-" indication.

Imbibed & Germinating Seeds Genes Identified By Cluster Analyses Of Differential Expression

Imbibed & Germinating Seeds Genes Identified By Correlation To Genes That Are Differentially Expressed

As described above, the transcription profiles of genes that act together are well correlated. Applicants not only have identified the genes that are differentially expressed in the microarray experiments, but also have identified the genes that act in concert with them. The MA_clust table indicates groups of genes that have well correlated transcription profiles and therefore participate in the same pathway or network.

A pathway or network of Imbibed & Germinating Seeds genes is any group in the MA_clust that comprises a cDNA ID that also appears in Expt ID 108461, 108462, 108463, 108464, 108528, 108529, 108530, 108531, 108545, 108546, 108547, 108518, 108529, 108543, 108544 of the MA_diff table(s).

Imbibed & Germinating Seeds Genes Identified By Correlation To Genes That Cause Physiological Consequences

Additionally, the differential expression data and the phenotypic observations can be merged to identify pathways or networks of Imbibed & Germinating Seeds genes. A group in the MA_clust is considered a Imbibed & Germinating Seeds pathway or network if the group comprises a cDNA ID that also appears in Knock-in or Knock-out tables that causes one or more of the phenotypes described in section above.

Imbibed & Germinating Seeds Genes Identified By Amino Acid Sequence Similarity

Imbibed & Germinating Seeds genes from other plant species typically encode polypeptides that share amino acid similarity to the sequences encoded by corn and Arabidopsis Imbibed & Germinating Seeds genes. Groups of Imbibed & Germinating Seeds genes are identified in the Protein Group table. In this table, any protein group that comprises a peptide ID that corresponds to a cDNA ID member of a Imbibed & Germinating Seeds pathway or network is a group of proteins that also exhibits Imbibed & Germinating Seeds functions/utilities.

III.B.1.b. Use Of Imbibition And Germination Genes, Gene
Components And Products To Modulate Phenotypes

Imbibition and germination genes and gene products can be divided into those that act during primary events, secondary events, and/or termination. The genes and gene products of the instant invention are useful to modulate any one or more of the phenotypes described below:

I. Primary events

A. Dormancy

Imbibition and germination genes and gene products of the invention can act to modulate different types of dormancy including:

1. Primary dormancy – dormancy is established during seed development
2. Seed coat-imposed dormancy – dormancy is imposed by blocking water uptake, mechanical restraint of embryo, blocking the exit of inhibitors
3. Embryo dormancy – cotyledon mediated inhibition of embryonic axis growth
4. Secondary dormancy – dormancy is induced when dispersed, mature seeds are exposed to unfavorable conditions for germination (e.g. anoxia, unsuitable temperature or illumination).
5. Hormone-induced

B. Dormancy-breaking signal perception and transduction

Germination genes and gene products include those that are able to modulate the response to dormancy releasing signals such as fruit ripening and seed development; imbibition; temperature (low and high, range 0-23°); light, particularly for coat imposed dormancy (white light, intermittent illumination, orange and red region of the spectrum (longer than 700 or 730 nm), and phytochrome); coat softening; chemicals (respiratory inhibitors, sulfhydryl compounds, oxidants, nitrogenous compounds, growth regulators – ga, ba, ethylene, and various, ethanol, methylene blue, ethyl ether, fusicoccin); oxygen and carbon dioxide; and stress.

II. Secondary Events

During the secondary events of germination, dormancy-maintaining metabolism is repressed, dormancy-breaking metabolism is induced and structures surrounding the embryo weaken (where present). Germination genes and gene products are useful to modulate processes of the secondary events including water uptake, such as cell expansion and change in osmotic state (ion exchange); and respiration – (oxygen consumption). the genes and genes products of the invention can regulate the following pathways which resume during the first respiratory burst of germination including glycolysis, pentose phosphate, citric acid, and tricarboxylic acid cycle.

A. Mitochondrial development

Tissues of the mature dry seed contain mitochondria, and although these organelles are poorly differentiated as a consequence of the drying, they contain sufficient Kreb's cycle enzymes and terminal oxidases to provide adequate amount of ATP to support metabolism for several hours after imbibition. During germination of embryos, there appears to be two distinct patterns of mitochondrial development. In starch-storing seeds, repair and activation of preexisting organelles predominate, whereas oil-storing seeds typically produce new mitochondria. Germination genes and gene products of the invention are useful to modulate the repair, activation and biogenesis pathways of mitochondria, including membrane formation and repair, DNA repair and synthesis, protein synthesis, and coordinated regulation of mitochondrial and nuclear genomes

B. Metabolism

In addition to respiration and organelle activity, enzyme activity, DNA repair, RNA synthesis and protein synthesis are fundamental cellular activities intimately involved in the completion of germination and the preparation for subsequent growth. Imbibition and germination genes and gene products of the invention can participate in or modulate these activities, including ABA response, GA response, ATP synthesis and adenylate energy charge during germination, and the synthesis and utilization of reducing power: pyridine nucleotides (NADH and NADPH)

III. Termination

The last stage of seed germination is characterized by the emergence of the radicle or root apex through the seed coat. Typically, the cell walls loosen and the radicle extends from the embryo during late germination. Germination genes and gene products are useful to modulate the mobilization of stored reserves, DNA synthesis and cell division that are typical of this stage of germination.

To regulate any of the phenotype(s) above, activities of one or more of the late germination genes or gene products can be modulated and tested by screening for the desired trait. Specifically, the gene, mRNA levels, or protein levels can be altered in a plant utilizing the procedures described herein and the phenotypes can be assayed. As an example, a plant can be transformed according to Bechtold and Pelletier (1998, Methods. Mol. Biol. 82:259-266) and/or screened for variants as in Winkler et al. (1998) Plant Physiol 118: 743-50 and visually inspected for the desired phenotype or metabolically and/or functionally assayed according to Dolan et al. (1993, Development 119: 71-84), Dolan et al. (1997, Development 124: 1789-98), Crawford and Glass (1998, Trends Plant Science 3: 389-95), Wang et al. (1998, PNAS USA 95: 15134-39), Gaxiola et al. (1998, PNAS USA 95: 4046-50), Apse et al. (1999, Science 285: 1256-58), Fisher and Long (1992, Nature 357: 655-60), Schneider et al. (1998, Genes Devel 12: 2013-21) and Hirsch (1999, Curr Opin Plant Biol. 2: 320-326).

III.B.1.c. Use Of Imbibition And Germination Genes, Gene Components And Product To Modulate Biochemical Activities

The roles of the biochemical changes associated with imbibition and germination can be appreciated from a summary of the processes occurring.

Physiology

Water plays an important role throughout the plant life cycle. The most dramatic example of this is in seed germination. Although germination is triggered by water, the germination response is also positively regulated by the plant growth regulators the gibberellins and negatively affected by the growth regulator abscisic acid. Genes that are activated by water and genes that are activated by gibberellins can be identified through expression profiling experiments using arabidopsis mutants defective for gibberellin biosynthesis or perception (ga1, gai), abscisic acid biosynthesis or perception (aba1, abi3, and abi4) in the presence or absence of exogenous gibberellins. These genes can be used to promote seedling growth and development and other phases of plant development.

Transcriptional Control of Gene Activity

At the end of seed development, dessication and dormancy have imposed a global state of repression on gene activity throughout the seed. Reactivation of the genome requires water and gibberellins. One function of the genes that are activated early by imbibition is the rapid and dramatic reversal of gene repression. For example, expression-profiling experiments revealed that several thousand genes are hyperactivated in arabidopsis upon imbibition. These include genes involved in metabolic pathways, genes that promote cell growth and division, and transcriptional control genes. Thus one class of genes expressed early in imbibition includes those that promote high levels of gene expression. Other early genes are responsible for regulating specific metabolic, cell, and developmental processes. The strategy for distinguishing these functions was outlined in the Introduction.

Mobilization of Storage Reserves

In contrast to the synthesis and accumulation of reserves during seed development an important function of genes expressed during imbibition and germination is the control of the mobilization and catabolism of seed storage reserves in the endosperm (in grasses and cereals) and the embryo. The mobilization of seed storage reserves is triggered by imbibition and may occur over several days. There are three classes of high molecular weight seed storage reserves: carbohydrates, triacylglycerols, and storage proteins. Upon imbibition seed storage reserves are converted into forms that can be transported and metabolized. Genes encoding enzymes for storage reserve catabolism are expressed shortly after imbibition. Starch for example is converted to sucrose. Triacylglycerols are converted into acetyl-CoA. Storage proteins are converted into amino acids or deaminated to provide carbon skeletons for oxidation.

Carbohydrate Catabolism

Starch is the most common storage carbohydrate in seeds. The primary components of starch are amylose and amylopectin.

Mobilization

There are two pathways for starch catabolism – hydrolytic and phosphorolytic. The product of these pathways is the monosaccharide glucose. Examples of the enzymes responsible for hydrolytic catabolism of starch are: amylase, glucosidase, amylase, dextrinase, isoamylase. The enzyme responsible for phosphorolytic activity is starch phosphorylase.

Transport

The mobilization of starch involves the synthesis of sucrose from glucose, which can then be transported to sites for growth in the root and shoot. In some seeds, maltose may be a major form of transported carbohydrate. The production of sucrose-6-P from glucose involves the following enzymes: UDP-glucose pyrophosphorylase, sucrose-6-P synthetase, and sucrose phosphatase.

Sucrose Catabolism

In target tissues sucrose is hydrolyzed by fructofuransidase (invertase) and/or sucrose synthetase. The synthesis of glucose from glucose-1-P involves sucrose synthetase.

Cell Biology

The lumen of the endoplasmic reticulum (ER) is target for other hydrolase activities including mannosidase, glucosaminidase, acid phosphatase, phosphodiesterase, and phospholipase D.

Triacylglycerol (TAG) Catabolism

Triacylglycerols are the major storage lipids of seeds. The products of TAG catabolism in imbibed and germinating seed are glycerol and free fatty acids. Most of the glycerol is converted to sucrose for export. Free fatty acids are catabolized through oxidation through the glyoxylate cycle and gluconeogenesis.

Mobilization

Hydrolysis of triacylglycerols is by lipases yielding glycerol and free fatty acids. Free fatty acids are oxidized to acetyl-CoA and propionyl-CoA via oxidation requiring ATP and coenzyme A. Catabolism of unsaturated fatty acids also requires cis, trans-isomerases, epimerases, and hydratases. Acetyl-CoA is oxidized through the citric acid cycle to CO₂ and H₂O. More importantly, acetyl-CoA can be utilized via the glyoxylate cycle and gluconeogenesis for glucose synthesis. Free fatty acids are also broken down via oxidation. Glycerol is converted via phosphorylation and oxidation to DHAP and G3P, which are used to synthesize glucose or oxidized via the citric acid cycle. Examples of other induced enzymes include isocitrate lyase and malate synthetase

Transport

Most of the glycerol, acetyl-CoA, and propionyl-CoA are converted to sucrose for transport. This requires the enzymes glycerol kinase and glycerol phosphate oxidoreductase.

Cell Biology

Glyoxysome biogenesis is required to support fatty acid catabolism and gluconeogenesis. Upon exposure to light there is a loss of glyoxysomes due to their conversion to peroxisomes.

STORAGE PROTEIN CATABOLISM

Mobilization

The hydrolysis of storage proteins to amino acids is performed by a diverse group of proteinases and peptidases. The peptidases include endopeptidases, aminopeptidases, and carboxypeptidases. They include the A and B class proteinases. The liberated amino acids are available for protein synthesis, for deamination and reutilization of ammonia via glutamine and asparagine synthesis, and to provide carbon skeletons for respiration. Several enzymes including, deaminase, asparagine synthetase, glutamine synthetase and glutamate dehydrogenase are important players in the mobilization and utilization of stored nitrogen in imbibed seed.

Transport

The major transported form of amino acid in germinated seeds is asparagine. In some species glutamine and/or homoserine are the major form of transported amino acid. Aspartate, glutamate, alanine, glycine, and serine can be converted to sucrose and transported as sucrose. Other amino acids are transported unchanged.

Cell Biology

Proteinases are sequestered in lumen of endoplasmic reticulum (ER) which then fuses with protein bodies.

While catabolism is high in the storage tissues of imbibed seed the products of catabolism are transported to sites of growth including the shoot and root apices fueling respiration, biosynthesis, cell division and differentiation.

Development

Imbibition triggers several key processes for seedling development. One is the activation of the shoot and root apical meristems. The shoot apical meristem is responsible for two primary growth activities. One is the production of the protoderm, procambium and ground meristem.

The protoderm gives rise to the epidermal system of the plant, the procambium to the primary vascular tissues, and the ground meristem to the ground tissues including the cortex and pith. The second is the production of leaf primordia, which arise on the flanks of the apex. Thus, activation of the shoot apical meristem results in shoot growth and organogenesis.

The root apical meristem, by contrast is responsible for vegetative root development. The first primary growth activity of the root apical meristem is the production of the protoderm, procambium and ground meristem. The second primary growth activity is the production of the cells that give rise to the root cap.

Genes that govern shoot apical meristem activation and development can be identified in arabidopsis by gene profiling experiments comparing gene expression in wild-type imbibed seed and partial loss-of-function *stm* (shootmeristemless) mutants (see SAM). Genes governing root meristem activity can be identified by gene profiling experiments comparing gene expression in wild-type imbibed seed and *rml* (rootmeristemless) mutants.

Genes identified in this way are useful to promote or retard meristem growth, modify and strengthen shoot and root development, promote leaf development as described below.

Changes in the concentration of imbibition-germination activated polynucleotides result in the modulation of many other polynucleotides and polynucleotide products. Examples of such activated responsive polynucleotides and polynucleotide products relative to leaves and floral stem and to fruits at different development stages are shown in the Reference and Sequence Tables. These polynucleotides and/or products are responsible for effects on traits such as seedling growth, seedling viability, and seedling vigor. The polynucleotides were discovered by isolating seeds from Arabidopsis wild-type ecotype "Wassilewskija" imbibed for 24 hours, and measuring the mRNAs expressed in them relative to those in a leaf and floral stem sample and to those in fruits at different developmental stages.

While imbibition-germination activated polynucleotides and polynucleotide products can act alone, combinations of these polynucleotides also affect germination. Useful combinations include different polynucleotides and/or polynucleotide products that have similar transcription profiles or similar biological activities, and members of the same or functionally similar biochemical pathways. In addition, the combination of imbibition germination activated polynucleotides and/or polynucleotide products with environmentally responsive polynucleotides

is also useful because of the interactions that exist between development, hormone-regulated pathways, stress and pathogen induced pathways and nutritional pathways. Here, useful combinations include polynucleotides that may have different transcription profiles, and participate in common or overlapping pathways but combine to produce a specific, phenotypic change.

Such imbibition and germination activated polynucleotides and polynucleotide products can function to either increase or dampen the above phenotypes or activities either in response to transcript changes in fruit development or in the absence of fruit-specific polynucleotide fluctuations.

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS ALTERED	CITATIONS INCLUDING ASSAYS
Growth, Differentiation and Development	Farnesylation Mediated Seed Dormancy	Pei et al (1998) Science 282: 287-290; Cutler et al. (1996) Science 273: 1239
Metabolic activity	Nitrogen metabolism	Goupil et al (1998) J Exptl Botany 49:1855-62
Metabolic activity	-H ⁺ export and membrane hyperpolarization	Cerana et al. (1983)
Metabolic activity	Chloroplast functioning	Benkova et al (1999) Plant Physiol 121: 245-252
Growth, Differentiation and development	Regulation of Morphogenesis	Riou-Khamlichi et al. (1999) Science 283: 1541-44
Metabolic activity	Cell Death	Lohman et al. (1994) Physiol Plant 92: 322-328
Growth and development	Promotion of cell division Shoot formation in absence of exogenous cytokinin	Kakimoto (1996) Science 274: 982-985
Metabolic activity	Membrane repair	Heath et al. (1986) Planta 169: 304-12 Browse et al. (1986) Anal Biochem 152: 141-5 D'Aoust et al (1999) Plant Cell 11: 2407-18
Metabolism	Organic molecule export	Moody et al. (1988) Phytochemistry 27: 2857-61

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS ALTERED	CITATIONS INCLUDING ASSAYS
Metabolic activity	Nutrient Uptake	Uozumio et al. (2000) Plant Physiol 122: 1249-59
Metabolic activity	Ion export	Uozumi et al. (2000) Plant Physiol 122: 1249-59 Frachisse et al. (2000) Plant J 21: 361-71
Growth, Differentiation and development	Division and/or elongation	Zhang and Forde (1998) Science 279: 407-409. Coruzzi et al. U.S. Pat. No. 5,955,651
Metabolic activity	Regulation of Molecular chaperones	Wisniewski et al. (1999) Physiolgia Plantarum 105: 600-608
Metabolic activity	Reactivation of Aggregation and Protein Folding	Lee and Vierling (2000) Plant Physiol. 122: 189-197
Metabolic activity	Maintenance of Native Conformation (cytosolic proteins)	Queitsch et al. (2000) The Plant Cell 12: 479-92
Metabolic activity	Regulation of Translational Efficiency	Wells et al. (1998) Genes and Development 12: 3236-51
Metabolic activity	DNA Repair	Bewley (1997) Plant Cell 9: 1055-66
Metabolic activity	Protein Synthesis using stored or newly synthesized mRNAs	Heath et al. (1986) Planta 169: 304-12
Metabolic activity	Mitochondrial repair and	MacKenzie and McIntosh

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS ALTERED	CITATIONS INCLUDING ASSAYS
	synthesis	(1999) Plant Cell 11: 571-86
Metabolic activity	Commencement of respiration	Debeaujon et al. (2000) Plant Physiol 122: 403-4132
	Water Uptake	Debeaujon et al. (2000) Plant Physiol 122: 403-4132

Other biological activities that are modulated by the imbibition-activated polynucleotides and polynucleotide products are listed in the Reference Tables. Assays for detecting such biological activities are described in the Table below as well as in the Domain section of the Reference Table.

III.B.1.d. Use Of Imbibition And Germination Genes To Modulate The Transcription Levels Of Other Genes

The expression of many genes is “upregulated” or “downregulated” during imbibition and germination because some imbibition and germination genes are integrated into complex networks that regulate transcription of many other genes. Some imbibition and germination genes are therefore useful for regulating other genes and hence complex phenotypes.

Imbibition-activated polynucleotides may also be differentially transcribed in response to fluctuating developmental-specific polynucleotide levels or concentrations, whether internal or external to a cell, at different times during the plant life cycle to promote associated biological activities. These activities are, by necessity, a small subset of the genes involved in the development process. Furthermore, because development is a continuous process with few clear demarcations between stages, the associated metabolic and biochemical pathways overlap. Some of the changes in gene transcription are summarized in the Table below:

DEVELOPMENTAL PROCESS REGULATED BY IMBIBITION- GERMINATION GENES	PHYSIOLOGICAL/METABO LIC CONSEQUENCES OF MODIFYING GENE PRODUCT LEVELS	EXAMPLES OF BIOCHEMICAL REGULATORY ACTIVITIES ASSOCIATED WITH IMBIBITION AND GERMINATION
<p>Tissue Specialization</p> <ul style="list-style-type: none"> - Cotyledon Expansion - Endosperm (???) - Activation of the Shoot Apical Meristem - Activation of the Root Apical Meristem - Radicle Growth - Vascular System Development 	<ul style="list-style-type: none"> - Lipid Catabolism - Lipoxygenase Localization - Starch Catabolism - Seed Protein Catabolism - Growth Regulator Production, Transport, Perception, Signaling, Response (e.g., Gibberellins, Ethylene, Auxin) - Global Gene Activation - Transcription Initiation - Sucrose Synthesis and Partitioning - Sucrose catabolism - Sucrose Signaling - Cell Wall Biosynthesis - Activators of Metabolic Pathways 	<ul style="list-style-type: none"> - Transcription Factors - Transporters - Kinases - Changes in cytoskeletal protein activity modulating cell structure - Stability of factors for protein translation - Changes in cell wall/membrane structure - Chromatin structure and/or DNA topology - Biosynthetic enzymes - Metabolic enzymes

<p>Organelle Differentiation and Development</p>	<ul style="list-style-type: none"> - Protein Remodeling - Cell Wall Biosynthesis - Membrane Repair and Synthesis - Specific Gene Transcription Initiation - Sucrose Mobilization and Partitioning - Sucrose Signaling - Activators of Metabolic Pathways - Auxin Perception, Response and Signaling - Protein Remodeling - Lipid Mobilization, Metabolism and Biosynthesis - Protein Transport, Metabolism, and Biosynthesis 	<ul style="list-style-type: none"> - Transcription Factors - Transporters - Kinases - Chaperones - Changes in cytoskeletal protein activity modulating cell structure - Stability of factors for protein translation - Changes in cell wall/membrane structure - Chromatin structure and/or DNA topology - Biosynthetic enzymes - Metabolic enzymes
<p>DNA Repair</p>	<ul style="list-style-type: none"> - Cell Division - Cell Cycle Control - DNA Replication - Specific Gene Transcription Initiation - Protein Remodeling - Protein Synthesis - Repressors of Senescence 	<ul style="list-style-type: none"> - Transcription Factors - Transporters - Kinases - Chaperones for protein translation - Changes in cell wall/membrane structure - Chromatin structure and/or DNA topology - Biosynthetic enzymes

Cellular Metabolism	<ul style="list-style-type: none"> - Lipid Catabolism <ul style="list-style-type: none"> - oxidation - Glyoxylate cycle - Citric acid cycle - Gluconeogenesis - Sucrose Synthesis and Partitioning - Starch Catabolism - Seed Protein Catabolism <ul style="list-style-type: none"> - Asparagine Synthesis and Transport - Sucrose catabolism - Sucrose Signaling - Ribosome/polysome production and maintenance - Housekeeping genes - Respiration - Photosynthesis 	<ul style="list-style-type: none"> - Transcription Factors - Transporters - Kinases - Chaperones - Translation Initiation Factors - Biosynthetic Enzymes - Metabolic Enzymes
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Changes in the processes of germination are the result of modulation of the activities of one or more of these many germination genes and gene products. These genes and/or products are responsible for effects on traits such as fast germination, plant vigor and seed yield, especially when plants are growing in the presence of biotic or abiotic stresses or when they are growing in barren conditions or soils depleted of certain minerals.

Germination genes and gene products can act alone or in combination as described in the introduction. Of particular interest are combination of these genes and gene products with those that modulate stress tolerance and/or metabolism. Stress tolerance and metabolism genes and gene products are described in more detail in the sections below.

USE OF PROMOTERS OF IMBIBITION AND GERMINATION GENES

These promoters can be used to control expression of any polynucleotide, plant or non-plant, in a plant host. Selected promoters when operably linked to a coding sequence can direct synthesis of the protein in specific cell types or to loss of a protein product, for example when the coding sequence is in the antisense configuration. They are thus useful in controlling changes in imbibition and germination phenotypes or enabling novel proteins to be made in germinating seeds.

III.B.2. EARLY SEEDLING-PHASE SPECIFIC RESPONSIVE GENES, GENE COMPONENTS AND PRODUCTS

One of the more active stages of the plant life cycle is a few days after germination is complete, also referred to as the early seedling phase. During this period the plant begins development and growth of the first leaves, roots, and other organs not found in the embryo. Generally this stage begins when germination ends. The first sign that germination has been completed is usually that there is an increase in length and fresh weight of the radicle.

III.B.2.a. Identification Of Early Seedling Phase Genes, Gene Components And Products

These genes defined and identified herein are capable of modulating one or more processes of development and growth of many plant organs as described below. These genes and gene products can regulate a number of plant traits to modulate yield. Examples of such early seedling phase genes and gene products are shown in the Reference and Sequence, Knock-in, Knock-out and MA-diff Tables. The functions of the protein of some of these genes are also given in these Tables.

Early Seedling Genes Identified by Phenotypic Observations

Some early seedling genes were discovered and characterized from a much larger set of genes by experiments designed to find genes that cause phenotypic changes in germinating seeds as the transitioned into seedlings.

In these experiments, leaf genes were identified by either (1) ectopic expression of a cDNA in a plant or (2) mutagenesis of the plant genome. The plants were then cultivated and

one or more of the following leaf phenotypes, which varied from the parental “wild-type”, were observed:

- Abnormal growth
- Abnormal cotyledons or root growth
 - Reduced growth
 - Abnormal first leaf
 - Abnormal hypocotyl
 - Abnormal pigmentation

The genes identified by these phenotypes are given in the Knock-in and Knock-out Tables.

Early Seedling Phase Genes Identified By Differential Expression

Such genes are active or potentially active to a greater extent in developing and rapidly growing cells, tissues and organs, as exemplified by development and growth of a seedling 3 or 4 days after planting a seed. These genes herein were also discovered and characterized from a much larger set of genes in experiments designed to find genes. Early seedling phase genes were identified by measuring the relative levels of mRNA products in a seedling 3 or 4 days after planting a seed versus a sterilized seed. Specifically, mRNA was isolated from aerial portion of a seedling 3 or 4 days after planting a seed and compared to mRNA isolated from a sterilized seed utilizing microarray procedures. The MA_diff Table(s) reports the transcript levels of the experiment (see EXPT ID: Sqn (relating to SMD 7133, SMD 7137)). For transcripts that had higher levels in the samples than the control, a “+” is shown. A “-” is shown for when transcript levels were reduced in root tips as compared to the control. For more experimental detail see the Example section below.

Early Seedling Phase genes are those sequences that showed differential expression as compared to controls, namely those sequences identified in the MA_diff tables with a “+” or “-” indication.

Early Seedling Phase Genes Identified By Cluster Analyses Of Differential Expression

Early Seedling Phase Genes Identified By Correlation To Genes That Are Differentially Expressed

As described above, the transcription profiles of genes that act together are well correlated. Applicants not only have identified the genes that are differentially expressed in the microarray experiments, but also have identified the genes that act in concert with them. The MA_clust table indicates groups of genes that have well correlated transcription profiles and therefore participate in the same pathway or network.

A pathway or network of Early Seedling Phase genes is any group in the MA_clust that comprises a cDNA ID that also appears in Expt ID Sqn (relating to SMD 7133, SMD 7137) of the MA_diff table(s).

Early Seedling Phase Genes Identified By Correlation To Genes That Cause Physiological Consequences

Additionally, the differential expression data and the phenotypic observations can be merged to identify pathways or networks of Early Seedling Phase genes. A group in the MA_clust is considered a Early Seedling Phase pathway or network if the group comprises a cDNA ID that also appears in Knock-in or Knock-out tables that causes one or more of the phenotypes described in section above.

Early Seedling Phase Genes Identified By Amino Acid Sequence Similarity

Early Seedling Phase genes from other plant species typically encode polypeptides that share amino acid similarity to the sequences encoded by corn and Arabidopsis Early Seedling Phase genes. Groups of Early Seedling Phase genes are identified in the Protein Group table. In this table, any protein group that comprises a peptide ID that corresponds to a cDNA ID member of a Early Seedling Phase pathway or network is a group of proteins that also exhibits Early Seedling Phase functions/utilities.

Of particular interest are early seedling phase genes that are differentially expressed 3 or 4 days after planting a seed but not differentially expressed germinating seeds and/or mature leaves.

Examples of phenotypes, biochemical activities, and transcription profiles that can be modulated by these genes and gene products are described above and below.

III.B.2.b. Use Of Early Seedling Genes, Gene Components And
Products To Modulate Phenotypes

Rapid, efficient establishment of a seedling is very important in commercial agriculture and horticulture. It is also vital that resources are approximately partitioned between shoot and root to facilitate adaptive growth. Phototropism and geotropism need to be established. All these require post-germination process to be sustained to ensure that vigorous seedlings are produced. Early seedling phase genes, gene components and products are useful to manipulate these and other processes.

I. Development

The early seedling phase genes, gene components and products of the instant invention are useful to modulate one or more processes of the stages of leaf morphogenesis including: stage 1- organogenesis that gives rise to the leaf primordium; stage 2- delimiting basic morphological domains; and stage 3- a coordinated processes of cell division, expansion, and differentiation. Early seedling phase genes include those genes that terminate as well as initiate leaf development. Modulating any or all of the processes leads to beneficial effects at specific locations .

Gene Sequences Affecting Types of Leaves - Applicants provide with these genes; gene components and gene products the means to modulate one or more of the types of leaves, and stem, including cotyledons and major leaves.

Gene sequences affecting cell properties - These genes, gene components and gene products are useful to modulate changes in cell size, cell division, rate and direction, cell elongation, cell differentiation, xylem and phloem cell numbers, cell wall composition, and all cell types.

Gene Sequences Affecting Leaf Architecture – Modifying leaf architecture is useful to modulate change in overall leaf architecture including venation, such as improvements in photosynthetic efficiency, stress tolerance efficiency of solute and nutrient movement to and from the leaf which are accomplished by increases or decreases in vein placement and number of cells in the vein and shape, such as elongated versus rounded and symmetry (around either

abaxial-adaxial (dorsiventral) axis or apical-basal (proximodistal) axis, margin-blade-midrib (lateral) axis).

Genes Sequences Influencing Leaf Responses - Shoot apical meristem cells differentiate to become leaf primordia that eventually develop into leaves. The genes, gene components and gene products of this invention are useful to modulate any one or all of these growth and development processes, by affecting timing and rate or planes of cell divisions for example, in response to the internal plant stimuli and/or programs such as embryogenesis, germination, hormones (like Auxin), phototropism, coordination of leaf growth and development with that of other organs (like roots and stems), and stress-related program.

II. Interaction with the Environment

Successful seedling establishment demands successful interaction with the environment in the soil. Early vegetation genes orchestrate and respond to interactions with the environment. Thus early seedling phase genes are useful for improving interactions between a plant and the environment including pigment accumulation, oxygen gain/loss control, carbon dioxide gain/loss control, water gain/loss control, nutrient transport, light harvesting, chloroplast biogenesis, circadian rhythm control, light/dark adaptation, defense systems against biotic and abiotic stresses, metabolite accumulation, and secondary metabolite production

III. Organizing Tissues for Photosynthesis and Metabolism

Following germination and utilization of seed reserves, plant tissues prepare for photosynthesis and seedling metabolism. Leaf meristems, and root meristems participate in these changes before cell differentiation. Many of the uses for plants depend on the success of leaves as the powerhouses for plant growth, their ability to withstand stresses and their chemical composition. Leaves are organs with many different cell types and structures. Most genes of a plant are active in leaves and therefore leaves have very diverse of pathways and physiological processes. Examples of such pathways and processes that are modulated by early seedling phase genes, gene components and products include photosynthesis, sugar metabolism, starch synthesis, starch degradation, nitrate and ammonia metabolism, amino acid biosynthesis, transport, protein biosynthesis, DNA replication, repair, lipid biosynthesis and breakdown,

protein biosynthesis, storage and breakdown, nucleotide transport and metabolism, cell envelope biogenesis, membrane formation, mitochondrial and chloroplast biogenesis, transcription and rna metabolism, vitamin biosynthesis, steroid and terpenoid biosynthesis, devise secondary metabolite synthesis, co-enzyme metabolism, flavonoid biosynthesis and degradation, synthesis of waxes, glyoxylate metabolism, and hormone perception and response pathways.

USE OF PLANTS THAT ARE MODIFIED AS DESCRIBED ABOVE

Altering leaf genes or gene products in a plant modifies one or more the following plant traits, to make the plants more useful for specific purposes in agriculture, horticulture and for the production of valuable molecules. The useful plants have at least one of the following characteristics: More seedling vigor; a higher yield of early leaves and their molecular constituents due to different number, size, weight, harvest index, composition including and amounts and types of carbohydrates, proteins, oils, waxes, etc., photosynthetic efficiency, e.g. reduced photorespiration, absorption of water and nutrients to enhance yields, including under stresses such as high light, herbicides, and heat, pathways to accumulate new valuable molecules; more optimal leaf shape and architecture in early seedling— enhancing photosynthesis and enhancing appeal in ornamental species including size, number, or pigment; a better overall plant architecture – enhancing photosynthesis and enhancing appeal in ornamental species; reduced negative effects of high planting density, by altering leaf placement to be more vertical instead of parallel to the ground; for instance better stress tolerance, including drought resistance, by decreasing water loss, and pathogen resistance; better overall yield and vigor - Plant yield of biomass and of constituent molecules and plant vigor are modulated to create benefits by genetically changing the growth rate of seedling, coleoptile elongation, and young leaves.

To change any of the phenotype(s) above, activities of one or more of the early seedling phase genes or gene products are modulated in an organism and the consequence evaluated by screening for the desired trait. Specifically, the gene, mRNA levels, or protein levels are altered in a plant utilizing the procedures described herein and the phenotypes can be assayed. As an example, a plant can be transformed according to Bechtold and Pelletier (Methods. Mol. Biol.

82:259-266 (1998)) with leaf gene constructs and/or screened for variants as in Winkler et al., Plant Physiol. 118: 743-50 (1998) and visually inspected for the desired phenotype and metabolically and/or functionally assayed for altered levels of relevant molecules.

**III.B.2.c. Use Of Early Seedling Phase Genes, Gene Components
And Products To Modulate Biochemical Activities**

Seedlings are complex and their structure, function and properties result from the integration of many processes and biochemical activities. Some of these are known from the published literature and some can be deduced from the genes and their products described in this application. Early seedling phase genes, and gene components are used singly or in combination to modify these processes and biochemical activities and hence modify the phenotypic and trait characteristics described above. Examples of the processes and metabolic activities are given in the Table below. The resulting changes are measured according to the citations included in the Table.

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
Metabolism – anabolic and catabolic	G. Farnesyl ation	Pei et al., <u>Science</u> 282: 287-290 (1998); Cutler et al., <u>Science</u> 273: 1239 (1996)
	H. Cell Wall Biosynt hesis	Goupil et al., <u>J Exptl. Botany</u> 49:1855-62 (1998) Walch-Liu et al., <u>J Exppt. Botany</u>
	I. Nitrogen Metabol ism	51, 227-237 (2000)
	J. Seconda	

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
	ry Metabol ite Biosynt hesis and Degrada tion	
Water Conservation And Resistance To Drought And Other Related Stresses	A. Production of polyols B. Regulation of salt concentration C. ABA response(s)	Allen et al., <u>Plant Cell</u> 11: 1785- 1798 (1999) Li et al., <u>Science</u> 287: 300-303 (2000) Burnett et al., <u>J Exptl. Botany</u> 51: 197-205 (2000) Raschke, In: <u>Stomatal Function</u> , Zeiger et al. Eds., 253-279 (1987)
Transport Anion and Cation Fluxes	(i) Ca ²⁺ Accumu lation (a) K ⁺ Fluxes (b) Na ⁺ Fluxes 1. Receptor – ligand binding	Lacombe et al., <u>Plant Cell</u> 12: 837- 51 (2000); Wang et al., <u>Plant Physiol.</u> 118:1421-1429 (1998); Shi et al., <u>Plant Cell</u> 11: 2393- 2406 (1999) Gaymard et al., <u>Cell</u> 94:647-655

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
	2. Anion and Cation fluxes	(1998) Jonak et al., <u>Proc. Natl. Acad. Sci.</u> <u>93</u> : 11274-79 (1996); Sheen, <u>Proc. Natl. Acad. Sci.</u> <u>95</u> : 975-80 (1998); Allen et al., <u>Plant Cell</u> <u>11</u> : 1785-98 (1999)
Carbon Fixation	3. Calvin Cycle 5. Photorespiration 6. Oxygen evolution 7. RuBisCO 4. Chlorophyll metabolism (ii) Chloroplast Biogenesis and Metabolism 5. Fatty Acid and Lipid Biosynthesis	Wingler et al., <u>Philo Trans R Soc Lond B Biol Sci</u> <u>355</u> , 1517-1529 (2000); Palecanda et al., <u>Plant Mol Biol</u> <u>46</u> , 89-97 (2001); Baker et al., <u>J Exp Bot</u> <u>52</u> , 615- 621 (2001) Chen et al., <u>Acta Biochim Pol</u> <u>41</u> , 447-457 (1999) Imlau et al., <u>PlantCell</u> <u>II</u> , 309-322 (1999)

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
	<p>(iii) Glyoxylate metabolism</p> <p>(iv) Sugar Transport</p> <p>(v) Starch Biosynthesis and Degradation</p>	
Hormone Perception and Growth	<p>(vi) Hormone Receptors and Downstream Pathways for</p> <p>(a) ethylene</p> <p>(b) jasmonic acid</p> <p>(c) brassinosteroid</p>	<p>Tieman et al., <u>Plant J</u> 26, 47-58 (2001)</p> <p>Hilpert et al., <u>Plant J</u> 26, 435-446 (2001)</p> <p>Wenzel et al., <u>Plant Phys</u> 124, 813-822 (2000)</p> <p>Dengler and Kang, <u>Curr Opin Plant Biol</u> 4, 50-56 (2001)</p>

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
	(d) gibberellin (e) Auxin (f) cytokinin - Activation Of Specific Kinases And Phosphatases	Tantikanjana et al., <u>Genes Dev</u> 15 , 1577-1580 (2001)
See Imbibition, Shoot Apical Meristem, Root and Leaf sections for more details		

Other biological activities that are modulated by the leaf genes and gene products are listed in the Reference tables. Assays for detecting such biological activities are described in the Protein Domain table, for example.

III.B.2.d. Use Of Early Seedling Phase Genes, Gene Components And Products To Modulate Transcription Levels

The expression of many genes is “up regulated” or down regulated” in plants because some genes and their products are integrated into complex networks that regulate transcription of many other genes. Some early seedling phase genes, gene components and products are therefore useful for modifying the transcription of other genes and hence complex phenotypes, as described above. Profiles of leaf gene activities are described in the Table below with associated biological activities. “Up-regulated” profiles are those where the mRNA transcript levels are higher in young seedlings as compared to the sterilized seeds. “Down-regulated” profiles represent higher transcript levels in the plantlet as compared to sterilized seed only.

III.B.3. SIZE AND STATURE GENES, GENE COMPONENTS AND PRODUCTS

Great agronomic value can result from modulating the size of a plant as a whole or of any of its organs. For example, the green revolution came about as a result of creating dwarf wheat plants, which produced a higher seed yield than taller plants because they could withstand higher levels and inputs of fertilizer and water. Size and stature genes elucidated here are capable of modifying the growth of either an organism as a whole or of localized organs or cells. Manipulation of such genes, gene components and products can enhance many traits of economic interest from increased seed and fruit size to increased lodging resistance. Many kinds of genes control the height attained by a plant and the size of the organs. For genes additional to the ones in this section other sections of the Application should be consulted.

III.B.3.a. Identification Of Size And Stature Genes, Gene Components And Products

Size and stature genes identified herein are defined as genes, gene components and products capable of modulating one or more processes in growth and development, to produce changes in size of one or more organs. Examples of such stature genes and gene products are shown in the Reference, Sequence, Protein Group, Protein Group Matrix, Knock-in, Knock-out, MA-diff and MA-clust. The biochemical functions of the protein products of many of these genes determined from comparisons with known proteins are also given in the Reference tables.

SIZE AND STATURE GENES, GENE COMPONENTS AND PRODUCTS IDENTIFIED BY PHENOTYPIC OBSERVATIONS

Mutant plants exhibiting increased or decreased stature in comparison to parental wild-type plants were used to identify size and stature genes. In these experiments, size and stature genes were identified by either (1) the ectopic expression of a cDNA in a plant or (2) mutagenesis of the plant genome. The plants were then cultivated and stature genes were identified from plants that were smaller than the parental "wild-type". The phenotypes and gene mutations associated with them are given in Tables

Examples of phenotypes, biochemical activities, or transcript profiles that are modulated using these genes are described above and below.

USE OF SIZE AND STATURE GENES, GENE COMPONENTS AND PRODUCTS
TO MODULATE PHENOTYPES

Typically, these genes can cause or regulate cell division, rate and time; and also cell size and shape. Many produce their effects via meristems. These genes can be divided into three classes. One class of genes acts during cytokinesis and/or karyokinesis, such as mitosis and/or meiosis. A second class is involved in cell growth; examples include genes regulating metabolism and nutrient uptake pathways. Another class includes genes that control pathways that regulate or constrain cell division and growth. Examples of these pathways include those specifying hormone biosynthesis, hormone sensing and pathways activated by hormones.

Size and stature genes and gene components are useful to selectively alter the size of organs and stems and so make plants specifically improved for agriculture, horticulture and other industries. There are a huge number of utilities. For example, reductions in height of specific ornamentals, crops and tree species can be beneficial, while increasing height of others may be beneficial.

Increasing the length of the floral stems of cut flowers in some species would be useful, while increasing leaf size in others would be economically attractive. Enhancing the size of specific plant parts, such as seeds, to enhance yields by stimulating hormone (Brassinolide) synthesis specifically in these cells would be beneficial. Another application would be to stimulate early flowering by altering levels of gibberellic acid in specific cells. Changes in organ size and biomass also results in changes in the mass of constituent molecules. This makes the utilities of size and stature genes useful for the production of valuable molecules in parts of plants, for extraction by the chemical and pharmaceutical industries.

Examples of phenotypes that can be modulated by the genes and gene components include cell size, cell shape, cell division, rate and direction, cell elongation, cell differentiation, stomata number, and trichome number. The genes of the invention are useful to regulate the development and growth of roots (primary, lateral, root hairs, root cap, apical meristem,

epidermis, cortex, and stele); stem (phloem, xylem, nodes, internodes, and shoot apical meristem); leaves (cauline, rosette, and petioles); flowers (receptacle, sepals, petals, and tepals, including color, shape, size, number, and petal drop, androecium, stamen, anther, pollen, sterility, size, shape, weight, color, filament, gynoecium, carpel, ovary, style, stigma, ovule, size, shape, and number, pedicel and peduncle, flowering time, and fertilization); seeds (placenta, embryo, cotyledon, endosperm, suspensor, and seed coat (testa)); and fruits (pericarp – thickness, texture, exocarp, mesocarp, and endocarp. Traits can be modulated with the genes and gene products of this invention to affect the traits of a plant as a whole include architecture (such as branching, ornamental architecture, shade avoidance, planting density effects, and wind resistance) and vigor (such as increased biomass and drought tolerance).

To regulate any of the phenotype(s) above, activities of one or more of the sizing genes or gene products are modulated in an organism and tested by screening for the desired trait. Specifically, the gene, mRNA levels, or protein levels can be altered in a plant utilizing the procedures described herein and the phenotypes can be assayed. As an example, a plant can be transformed according to Bechtold and Pelletier (Methods. Mol. Biol. 82:259-266 (1998)) and/or screened for variants as in Winkler et al., (Plant Physiol. 118: 743-50 1998) and visually inspected for the desired phenotype or metabolically and/or functionally assayed.

III.B.3.b. Use Of Size And Stature Genes, Gene Components And Products To Modulate Biochemical Activities

Many metabolic and developmental processes can be modulated by size and stature genes and gene components to achieve the phenotypic characteristics exemplified above. Some of these are listed below. Such biological activities can be measured according to the citations included in the Table below:

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
Growth and Development	Gibberellic Acid Biosynthesis Gibberellic Acid Receptor and Downstream Pathways	Swain SM, Tseng Ts, Olszewski NE. Altered expression of spindly affects gibberellin response and plant

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
	<p>Brassinolide Biosynthesis Brassinolide Receptors, Degradation of Brassinolide Pathways affected by Brassinolide</p>	<p>development. Plant Physiol 2001 Jul;126(3):1174-85</p> <p>Hooley, R. Gibberellins: perception, transduction, and responses. Plant Mol. Biol. 1994 26:1529-1555.</p> <p>Hooley, R. Gibberellins: perception, transduction, and responses. Plant Mol. Biol. 1994 26:1529-1555.</p> <p>Perata, P, Matsukura, C, Vernieri, P, Yamaguchi, J, Sugar repression of a gibberellin-dependent signaling pathway in barley embryos. Plant Cell 1997 9:2197-2208.</p> <p>Noguchi T, Fujioka S, Choe S, Takatsuto S, Tax FE, Yoshida S, Feldmann KA. Biosynthetic pathways of brassinolide in Arabidopsis. Plant Physiol 2000 Sep;124(1):201-9</p> <p>Wang ZY, Seto H, Fujioka S, Yoshida S, Chory J. BRI1 is a critical component of a plasma-membrane receptor for plant steroids. Nature 2001 Mar 15;410(6826):380-3</p> <p>Neff MM, Nguyen SM, Malancharuvil EJ, Fujioka S, Noguchi T, Seto H, Tsubuki M, Honda T, Takatsuto S, Yoshida S, Chory J. BAS1: A gene regulating brassinosteroid levels and light responsiveness</p>

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
		<p>in Arabidopsis. Proc Natl Acad Sci U S A 1999 Dec 21;96(26):15316-23</p> <p>Kang JG, Yun J, Kim DH, Chung KS, Fujioka S, Kim JI, Dae HW, Yoshida S, Takatsuto S, Song PS, Park CM. Light and brassinosteroid signals are integrated via a dark-induced small G protein in etiolated seedling growth. Cell 2001 Jun 1;105(5):625-36</p> <p>Mok DW, Mok MC. Cytokinin metabolism and action. Annu Rev Plant Physiol Plant Mol Biol 2001;52:89-118</p> <p>Schmulling T. CREAm of cytokinin signalling: receptor identified. Trends Plant Sci 2001 Jul;6(7):281-4</p> <p>Mok DW, Mok MC. Cytokinin metabolism and action. Annu Rev Plant Physiol Plant Mol Biol 2001;52:89-118</p> <p>Seyedi M, Selstam E, Timko MP, Sundqvist C. The cytokinin 2-isopentenyladenine causes partial reversion to skotomorphogenesis and induces formation of prolamellar bodies and protochlorophyllide657 in the lip1 mutant of pea. Physiol Plant 2001 Jun;112(2):261-272</p> <p>Zhao Y, Christensen SK, Fankhauser C, Cashman JR,</p>
	<p>Cytokinin biosynthesis Cytokinin receptor Degradation of Cytokinin Pathways affected by Cytokinin</p>	
	<p>Auxin Biosynthesis Auxin Receptor</p>	

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
	Auxin Degradation Pathways affected by Auxins Auxin transport	<p>Cohen JD, Weigel D, Chory J. A role for flavin monooxygenase-like enzymes in Auxin biosynthesis. Science 2001 Jan 12;291(5502):306-9</p> <p>Abel S, Ballas N, Wong LM, Theologis A. DNA elements responsive to Auxin. Bioessays 1996 Aug;18(8):647-54</p> <p>del Pozo JC, Estelle M. Function of the ubiquitin-proteasome pathway in Auxin response. Trends Plant Sci 1999 Mar;4(3):107-112.</p> <p>Rahman A, Amakawa T, Goto N, Tsurumi S. Auxin is a positive regulator for ethylene-mediated response in the growth of Arabidopsis roots. Plant Cell Physiol 2001 Mar; 42(3):301-7</p> <p>Zhao Y, Christensen SK, Fankhauser C, Cashman JR, Cohen JD, Weigel D, Chory J. A role for flavin monooxygenase-like enzymes in Auxin biosynthesis. Science 2001 Jan 12;291(5502):306-9</p> <p>Abel S, Ballas N, Wong LM, Theologis A. DNA elements responsive to Auxin. Bioessays 1996 Aug;18(8):647-54</p> <p>del Pozo JC, Estelle M. Function of the ubiquitin-proteasome pathway in Auxin response. Trends Plant Sci 1999 Mar;4(3):107-112.</p>

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
		<p>Rahman A, Amakawa T, Goto N, Tsurumi S. Auxin is a positive regulator for ethylene-mediated response in the growth of Arabidopsis roots. Plant Cell Physiol 2001 Mar; 42(3):301-7</p> <p>Gil P, Dewey E, Friml J, Zhao Y, Snowden KC, Putterill J, Palme K, Estelle M, Chory J. BIG: a calossin-like protein required for polar Auxin transport in Arabidopsis. Genes Dev. 2001 Aug 1;15(15):1985-97</p> <p>Estelle M., Polar Auxin transport. New support for an old model. Plant Cell 1998 Nov;10(11):1775-8</p> <p>Cosgrove DJ., Loosening of plant cell walls by expansins. Nature 2000 Sep 21;407(6802):321-6</p>
	Cell wall growth	

Other biological activities that are modulated by the stature genes and gene products are listed in the Reference tables. Assays for detecting such biological activities are described in the Protein Domain table, for example.

Changes in the size, vigor, or yield of a plant are the result of modulation of the activities of one or more of these many size and stature genes and gene products. While size and stature polynucleotides and gene products can act alone, combinations of these polynucleotides and also with others that also affect growth and development are especially useful.

USE OF PROMOTERS OF "SIZE AND STATURE" GENES

Promoters of “size and stature” genes are useful for controlling the transcription of any desired polynucleotides, both plant and non-plant. They can be discovered from the “size and stature” genes in the Reference Tables, and their patterns of activity from the MA Tables. When operably linked to any polynucleotide encoding a protein, and inserted into a plant, the protein will be synthesized in those cells in which the promoter is active. Many “size and stature” genes will function in meristems, so the promoters will be useful for expressing proteins in meristems. The promoters can be used to cause loss of, as well as synthesis of, specific proteins via antisense and sense suppression approaches.

III.B.4. SHOOT-APICAL MERISTEM GENES, GENE COMPONENTS AND PRODUCTS

New organs, stems, leaves, branches and inflorescences develop from the stem apical meristem (SAM). The growth structure and architecture of the plant therefore depends on the behavior of SAMs. Shoot apical meristems (SAMs) are comprised of a number of morphologically undifferentiated, dividing cells located at the tips of shoots. SAM genes elucidated here are capable of modifying the activity of SAMs and thereby many traits of economic interest from ornamental leaf shape to organ number to responses to plant density.

III.B.4.a. Identification Of Sam Genes, Gene Components And Products

SAM genes identified herein are defined as genes, gene components and products capable of modulating one or more processes or functions of SAMs as described below. Regulation of SAM genes and gene products are useful to control many plant traits including architecture, yield and vigor. Examples of such SAM genes and gene products are shown in the Reference, Sequence, Protein Group, Protein Group Matrix, phenotype and MA-diff Tables. The functions of many of the protein products of these genes are also given in the Reference tables.

Sam Genes, Gene Components And Products Identified By Phenotypic Observations

SAM genes were discovered and characterized from a much larger set of genes by experiments designed to find genes that cause phenotypic changes in leaf morphology, such as

cotyledon or leaf fusion. In these experiments, SAM genes were identified by either (1) ectopic expression of a cDNA in a plant or (2) mutagenesis of the plant genome. The plants were then cultivated and one or more of the following phenotypes, which varied from the parental "wild-type", was observed:

- I. Cotyledon
 - Fused
- II. Leaves
 - Fused
 - Leaf placement on stems
- III. Branching
 - Number
- IV. Flowers
 - Petals fused
 - Altered bolting
 - Early bolting
 - Late bolting
 - Strong bolting
 - Weak bolting
 - Abnormal branching

For more experimental detail see the Example section below. The genes identified by these results of the phenotypes that are shown in Knock-in and Knock-out Tables.

Sam Genes, Gene Components And Products Identified By Differential Expression

SAM genes were also identified in experiments designed to find genes whose mRNA products are associated specifically or preferentially with SAMs. The concentration of mRNA products in the arabidopsis plant with the SHOOTMERISTEMLESS (STM) gene knocked-out was measured relative to the concentration in the parental, non-mutant plant. The Arabidopsis STM gene is required for embryonic SAM formation. The STM gene encodes a Knotted1 (Kn1) type of homeodomain protein. Homeodomain proteins regulate transcription of many genes in many

species and have been shown to play a role in the regulation of translation as well. Seedlings homozygous for recessive loss-of-function alleles germinate with roots, a hypocotyl, and cotyledons, but no SAM is formed. The MA_diff Table(s) reports the transcript levels of the experiment (see EXPT ID: 108478, 108479, 108480, 108481, 108598, 108535, 108536, 108435). For transcripts that had higher levels in the samples than the control, a "+" is shown. A "-" is shown for when transcript levels were reduced in root tips as compared to the control. For more experimental detail see the Example section below.

Meristem genes are those sequences that showed differential expression as compared to controls, namely those sequences identified in the MA_diff tables with a "+" or "-" indication.

Meristem Genes Identified By Cluster Analyses Of Differential Expression

Meristem Genes Identified By Correlation To Genes That Are Differentially Expressed

As described above, the transcription profiles of genes that act together are well correlated. Applicants not only have identified the genes that are differentially expressed in the microarray experiments, but also have identified the genes that act in concert with them. The MA_clust table indicates groups of genes that have well correlated transcription profiles and therefore participate in the same pathway or network.

A pathway or network of Meristem genes is any group in the MA_clust that comprises a cDNA ID that also appears in Expt ID 108478, 108479, 108480, 108481, 108598, 108535, 108536, 108435 of the MA_diff table(s).

Meristem Genes Identified By Correlation To Genes That Cause Physiological Consequences

Additionally, the differential expression data and the phenotypic observations can be merged to identify pathways or networks of Meristem genes. A group in the MA_clust is considered a Meristem pathway or network if the group comprises a cDNA ID that also appears in Knock-in or Knock-out tables that causes one or more of the phenotypes described in section above.

Meristem Genes Identified By Amino Acid Sequence Similarity

Meristem genes from other plant species typically encode polypeptides that share amino acid similarity to the sequences encoded by corn and Arabidopsis Meristem genes. Groups of Meristem genes are identified in the Protein Group table. In this table, any protein group that comprises a peptide ID that corresponds to a cDNA ID member of a Meristem pathway or network is a group of proteins that also exhibits Meristem functions/utilities.

Examples of phenotypes, biochemical activities, and transcription profiles that can be modulated by SAM genes and gene products are described above and below.

III.B.4.b. Use Of Sam Genes, Gene Components And Products To Modulate Phenotypes

With the SAM genes and gene products of the invention, Applicants provide the means to modulate one or more of the following types of SAMs:

1. Embryonic meristem
2. Vegetative lateral SAMs
3. Inflorescence lateral SAMs
4. Floral meristems
5. Adventitious SAM

The SAM genes of the instant invention are useful for modulating one or more processes of SAM structure and/or function including (I) cell size and division; (II) cell differentiation and organ primordia.

I. Cell Size and Division

A. Cell Properties

SAM genes and gene products can be used to modulate changes in cell size, cell division, rate and direction, and cell division symmetry.

A key attribute of the SAM is its capacity for self-renewal. The self-renewing initial cell population resides in the central zone of the SAM. A small number of slowly dividing initial cells (typically 2 to 4 per layer) act as a self-replenishing population, whereas some of their descendants, pushed out onto the flanks of the SAM, differentiate into leaves. Other descendants, displaced below the SAM, differentiate into stem. The immediate descendants of the initial cells divide

further, amplifying the cell population before being incorporated into leaf or stem primordia.

The genes and gene components of this invention are useful for modulating any one or all of these cell division processes generally, as in timing and rate, for example. In addition, the polynucleotides and polypeptides of the invention can control the response of these processes to the internal plant programs associated with embryogenesis, hormone responses like cytokinin (inhibitory for root development, see section on cytokinin-responsive genes), coordination of growth and development with that of other plant organs (such as leaves, flowers, seeds, and fruits.

SAM genes can also be used to control the response of these processes to changes in the environment, including heat, cold, drought, high light and nutrition.

B. Sam Cell Patterns And Organization

Although SAMs appear as small regions of morphological undifferentiated dividing cells, a group of morphologically undifferentiated dividing cells does not necessarily constitute a SAM. Rather, evidence indicates that SAMs are highly organized or patterned regions of the plant in which many important events in early organogenesis occur. Thus, the term "SAM" is used to denote a highly organized structure and site of pattern formation. The invention also permits engineering of specific as well as overall features of SAM architecture including zones (central, peripheral, and rib), layers (l1, l2, and l3) and symmetry.

II Cell Differentiation And Organ Primordia

The apical meristem in many species first undergoes a vegetative phase whereby cells set aside from the apex become leaf primordia with an axillary vegetative meristem. Upon floral induction, the apical meristem is converted to an inflorescence meristem. The inflorescence meristem arises in the axils of modified leaves and is indeterminate, producing whorls or rings of floral organ primordia. In species which produce terminal flowers, the apical meristem is determinate and eventually adopts a third identity, that of a floral meristem. Examples of the plant properties that the genes and gene products of the invention can be used to modulate include indeterminacy (inhibiting or increasing differentiation and enhancing plant growth and yield), symmetry (symmetry of organs developed, and symmetry of arrangement of organs, such as leaves,

petals, flowers, etc.), leaf fate and timing internode length modulation, such as longer internodes to increase shade avoidance and shorter internodes to favor leaf development), and floral fate and timing of flowering.

USES OF PLANTS MODIFIED AS DESCRIBED ABOVE USING SAM GENES, GENE COMPONENTS AND PRODUCTS

Because SAMs determine the architecture of the plant, modified plants will be useful in many agricultural, horticultural, forestry and other industrial sectors. Plants with a different shape, numbers of flowers and seed and fruits will have altered yields of plant parts. For example, plants with more branches can produce more flowers, seed or fruits. Trees without lateral branches will produce long lengths of clean timber. Plants with greater yields of specific plant parts will be useful sources of constituent chemicals. Such plants will have, for example, more prolific leaf development, better optimized stem and shoot development, adventitious shoots, more flowers, seeds, and fruits, enhanced vigor (including growth rate of whole plant, including height, flowering time, etc., seedling, coleoptile elongation, young leaves, flowers, seeds, and fruit. higher yields based on biomass (fresh and dry weight during any time in plant life, including maturation and senescence), number of flowers, seed yield (number, size, weight, harvest index, content and composition, e.g. amino acid, jasmonate, oil, protein and starch) and fruit yield (number, size, weight, harvest index, content and composition, e.g. amino acid, jasmonate, oil, protein and starch).

To regulate any of the phenotype(s) above, activities of one or more of the SAM genes or gene products can be modulated and tested by screening for the desired trait. Specifically, the gene, mRNA levels, or protein levels can be altered in a plant utilizing the procedures described herein and the phenotypes can be assayed. As an example, a plant can be transformed according to Bechtold and Pelletier (1998, *Methods. Mol. Biol.* 82:259-266) and/or screened for variants as in Winkler et al. (1998) *Plant Physiol* 118: 743-50 and visually inspected for the desired phenotype or metabolically and/or functionally assayed according to Dolan et al. (1993, *Development* 119: 71-84), Dolan et al. (1997, *Development* 124: 1789-98), Crawford and Glass (1998, *Trends Plant Science* 3: 389-95), Wang et al. (1998, *PNAS USA* 95: 15134-39), Gaxiola et al. (1998, *PNAS USA* 95: 4046-50), Apse et al. (1999, *Science* 285: 1256-58), Fisher and

Long (1992, Nature 357: 655-60), Schneider et al. (1998, Genes Devel 12: 2013-21) and Hirsch (1999, Curr Opin Plant Biol. 2: 320-326).

III.B.4.c. Use Of Sam Genes And Gene Components To Modulate
Biochemical Activities

SAM genes and gene components are useful for modulating biochemical or metabolic activities and/or pathways such as those noted below. Such biological activities can be measured according to the citations included in the Table below:

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
Growth , Differentiation And Development	Leaf shape and inflorescence and flower morphology systems Activities of SAM transcriptional regulatory proteins.	Chuck, G. et al., 1996 Plant Cell 8: 1227-1289. Schneeberger et al., 1998 Development 125: 2857-2865.
	Meristem size and organ number determinants - Regulated by Receptor Kinases - Receptor kinase location and activity.	- Kayes, J.M. and Clark, S.E. 1998 Development 125: 3843- 3851. - Jeong, S. et al., 1999 Plant Cell 11: 1925-1934.
	Meristem proliferation activities	Tantikanjana, T. Genes and Development. June 15, 2001. 15(12):1577-1588.
- Internode elongation	Hormone signaling pathways	Yamamuro, C. et al., 2000 Plant Cell. 12: 1591-1605.
Hormone	Levels of growth hormones	Kusaba, S. et al; 1998 Plant

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
Perception	including gibberellic acid, Auxin and cytokinin.	Physiology 116(2):471-476.
	Gibberellic acid biosynthesis GA biosynthetic enzyme GA-20 oxidase is a required step in GA biosynthesis. GA-20 oxidase is Regulated by some SAM gene products.	Modulation of GA perception and function can be assayed as described in Sakamoto, T. et al. 2001 Genes and Development 15: 581-590.
	Over expression of SAM genes can lead to reduced internode elongation, reduced cell elongation and reduced cell expansion.	Sakamoto, T. et al. 2001. Genes and Development 15: 581-590.
	Cytokinin Receptor activity	Inoue, T. et al., Nature 409:1060-1063.
	SAM gene products can affect the activity of Auxin dependent postranscriptional gene protein expression.	Sieberer, T. et al., 2000 Current Biology 10:1595-1598. del Pozo, J. C.; Estelle, M. PNAS (USA) 1999. 96(26):15342-15347.
	SAM gene products can affect Auxin Perception/metabolism in the meristem to produce useful changes in plant architecture.	Tantikanjana, T. Genes and Development. June 15, 2001. 15(12):1577-1588.
Leaf senescence	SAM gene products can increase	Ori, N. et al; Plant Cell. June,

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
	and decrease leaf senescence rate. This can be done by modulating cytokinin hormone levels.	1999. 11(6):1073-1080.
	Cytokinin effect on cell division and expansion.	Beemster, Gerrit T. S.; Baskin, Tobias I. 2000 Plant Physiology 124:1718-1727.
Adventitious shoot formation	Alter growth hormone status.	Kusaba, S. et al; 1998 Plant Physiology 116(2):471-476
	Ectopic expression of SAM genes in leaf or other non SAM organs or tissue can produce shoots	Chuck, G. 1996 Plant Cell 8: 1227-1289.
	Pathways comprising isopentenyl transferase (ipt)	

Other biological activities that can be modulated by the SAM genes and gene products are listed in the Reference tables. Assays for detecting such biological activities are described in the Protein Domain table.

III.B.4.d. Use Of Sam Genes, Gene Components And Products To Modulate Transcription Levels Of Other Genes

The expression of many genes is “upregulated” or “downregulated” in the SAM mutants because some of the SAM genes are integrated into complex networks that regulate the transcription of many other genes. Some SAM genes and gene components are therefore useful for modifying

the transcription of other genes and hence complex phenotypes as described above. Profiles of genes altered by SAM mutations and genes are described in the Table below with associated biological activities. “Up-regulated” profiles are for genes whose mRNA levels are higher in the *stm* plants as compared to parental wild-type plants; and vice-versa for “down-regulated” profiles.

TRANSCRIPT LEVELS	TYPE OF GENES WHOSE TRANSCRIPTS ARE CHANGED	PHYSIOLOGICAL CONSEQUENCES OF MODIFYING SAM GENE PRODUCT LEVELS	EXAMPLES OF BIOCHEMICAL ACTIVITIES WHOSE TRANSCRIPTS ARE CHANGED
Up Regulated Transcripts	Genes repressed by SAMs directly or indirectly	<ul style="list-style-type: none"> • Altered Auxin/cytokinin hormone ratio and perception. • Increased/decreased cell expansion – promoting effects of brassinosteroids and gibberellic acids, due to altered levels of biosynthetic pathway enzymes and or the amount of functional hormone receptor. • Increased or decreased rate of cell division. • Altered planes of cell division • Increased or 	<ul style="list-style-type: none"> • Transporters • Metabolic Enzymes • Cell Membrane Structure • Kinases, Phosphatases, G-Proteins • Transcription Activators/Repressors • Transcription coactivators/corepressor s • Chromatin Structure And/Or Localized DNA Topology Proteins • Cell Wall Proteins • Translational activators/repressors • Cell wall proteins involved in cell rigidity e.g. extensin, glycine

TRANSCRIPT LEVELS	TYPE OF GENES WHOSE TRANSCRIPTS ARE CHANGED	PHYSIOLOGICAL CONSEQUENCES OF MODIFYING SAM GENE PRODUCT LEVELS	EXAMPLES OF BIOCHEMICAL ACTIVITIES WHOSE TRANSCRIPTS ARE CHANGED
		<p>decreased rate and extent of cell expansion.</p> <ul style="list-style-type: none"> • Increased or decreased rigidity of cell walls. 	<p>rich proteins.</p> <ul style="list-style-type: none"> • Cell cycle regulatory proteins such as cyclins and cyclin dependent protein kinases (CDKs).
Down-Regulated Transcripts	Genes involved in SAM cells and genes whose expression is induced by SAMs	<ul style="list-style-type: none"> • Altered pattern of organs emerging from the meristem • Increased or decreased the number of cells partitioned into a lateral organ. • Altered apical dominance due to suppression of lateral bud growth. • Altered apical dominance due to releasing of axillary meristems from repression. • Increased/or decreased production 	<ul style="list-style-type: none"> • Auxin transporter proteins • Auxin receptor proteins • Cytokinin receptor proteins • Gibberellic acid receptor proteins • Brassinolide receptor proteins • Hormone biosynthesis proteins • Hormone degradation proteins • Hormone conjugation proteins • Ubiquitin conjugating enzymes. • Receptor kinase signal

TRANSCRIPT LEVELS	TYPE OF GENES WHOSE TRANSCRIPTS ARE CHANGED	PHYSIOLOGICAL CONSEQUENCES OF MODIFYING SAM GENE PRODUCT LEVELS	EXAMPLES OF BIOCHEMICAL ACTIVITIES WHOSE TRANSCRIPTS ARE CHANGED
		<p>of adventitious meristems.</p> <ul style="list-style-type: none"> • Increased potential to form somatic embryos. • Altered cell signaling pathways • Altered hormone levels 	transduction

SAM genes and gene products can be modulated alone or in combination as described in the introduction. Of particular interest are combination of these genes and gene products with those that modulate hormone responsive pathways. Hormone responsive genes and gene products are described in more detail in the sections below.

USE OF SAM GENE PROMOTERS TO MODIFY SAMs

Promoters of SAM genes, as described in the Reference tables, for example, can be used to modulate transcription of coding sequences in SAM cells to influence growth, differentiation or patterning of development or any of the phenotypes or biological activities above. For example, any desired sequence can be transcribed in similar temporal, tissue, or environmentally specific patterns as a SAM gene when the desired sequence is operably linked to the promoter of the SAM gene.

A specific instance is linking of a SAM gene promoter normally active in floral meristem primordia, to a phytotoxic protein coding sequence to inhibit apical meristem switching into an inflorescence and/or floral meristem, thereby preventing flowering.

SAM gene promoters can also be used to induce transcription of antisense RNA copies of a

gene or an RNA variant to achieve reduced synthesis of a specific protein in specific SAM cells.

This provides an alternative way to the example above, to prevent flowering.

TRANSCRIPT LEVELS	TYPE OF GENES WHOSE TRANSCRIPTS ARE CHANGED	PHYSIOLOGICAL CONSEQUENCES OF MODIFYING GENE PRODUCT LEVELS	EXAMPLES OF BIOCHEMICAL ACTIVITIES OF GENE PRODUCTS WITH MODIFIED LEVELS
Up regulated Transcripts	<p>Genes involved in leaf, stem and root cell differentiation, cell division, cell expansion</p> <p>Genes involved in positive regulation of root, stem and leaf genes</p> <p>Repressors of root and other organ cell types e.g. flowers</p>	<ul style="list-style-type: none"> • Leaf cells proliferate and differentiate; • Leaf structures form and expand 	<ul style="list-style-type: none"> • Transcription factors, signal transduction proteins, kinase and phosphatases • Chromatin remodeling • Hormone biosynthesis enzymes • Receptors
	Genes involved in photosynthesis	<ul style="list-style-type: none"> • Photosynthesis and plastid differentiation • Calvin cycle activated • Chloroplast biogenesis and plastid differentiation activated 	<ul style="list-style-type: none"> • Light harvesting coupled to ATP production • Chlorophyll biosynthesis • Ribulose Bisphosphate carboxylase • Chloroplast membranes synthesis • Chloroplast ribosome biogenesis
	Other genes involved in metabolism	<ul style="list-style-type: none"> • Starch biosynthesis • Lipid biosynthesis • Nitrogen metabolism – 	<ul style="list-style-type: none"> • Starch synthase • Nitrate reductase • Terpenoid biosynthesis • Transcription factors

TRANSCRIPT LEVELS	TYPE OF GENES WHOSE TRANSCRIPTS ARE CHANGED	PHYSIOLOGICAL CONSEQUENCES OF MODIFYING GENE PRODUCT LEVELS	EXAMPLES OF BIOCHEMICAL ACTIVITIES OF GENE PRODUCTS WITH MODIFIED LEVELS
		NO ₃ reduced and amino acids made <ul style="list-style-type: none"> Secondary metabolites produced 	<ul style="list-style-type: none"> Transporters Kinases Phosphatases and signal transduction protein Chromatin structure modulators
Down regulated genes	Genes involved in negative regulation of root, stem and leaf genes Genes involved in other organs e.g. flowers	<ul style="list-style-type: none"> Leaf genes activated and leaf functions induced Other organs not induced Leaf, stem and root metabolic pathways induced 	<ul style="list-style-type: none"> Transcription factors Signal transduction proteins – kinases and phosphatases Metabolic enzymes Chromatin remodeling proteins

While early seedling phase polynucleotides and gene products are used singly, combinations of these polynucleotides are often better to optimize new growth and development patterns. Useful combinations include different leaf polynucleotides and/or gene products with a hormone responsive polynucleotide. These combinations are useful because of the interactions that exist between hormone-regulated pathways, nutritional pathways and development.

USE OF EARLY SEEDLING PHASE GENE PROMOTERS

Promoters of early seedling phase genes are useful for transcription of desired polynucleotides, both plant and non-plant. If the gene is expressed only in the post-germination seedling, or in certain kinds of leaf cells, the promoter is used to drive the synthesis of proteins specifically in those cells. For example, extra copies of carbohydrate transporter cDNAs

operably linked to a early seedling phase gene promoter and inserted into a plant increase the “sink” strength of leaves. Similarly, early seedling phase promoters are used to drive transcription of metabolic enzymes that alter the oil, starch, protein, or fiber contents of the seedling. Alternatively, the promoters direct expression of non-plant genes that can, for instance, confer resistance to specific pathogen. Additionally the promoters are used to synthesize an antisense mRNA copy of a gene to inactivate the normal gene expression into protein. The promoters are used to drive synthesis of sense RNAs to inactivate protein production via RNA interference.

III.B.5. VEGETATIVE-PHASE SPECIFIC RESPONSIVE GENES, GENE COMPONENTS AND PRODUCTS

Often growth and yield are limited by the ability of a plant to tolerate stress conditions, including water loss. To combat such conditions, plant cells deploy a battery of responses that are controlled by a phase shift, from so called juvenile to adult. These changes at distinct times involve, for example, cotyledons and leaves, guard cells in stomata, and biochemical activities involved with sugar and nitrogen metabolism. These responses depend on the functioning of an internal clock, that becomes entrained to plant development, and a series of downstream signaling events leading to transcription-independent and transcription-dependent stress responses. These responses involve changes in gene expression.

Manipulation of the activation of one or more genes controlling the phase changes is useful to modulate the biological processes and/or phenotypes listed below. Phase responsive genes and gene products can act alone or in combination. Useful combinations include phase responsive genes and/or gene products with similar transcription profiles, similar biological activities, or members of the same or functionally related biochemical pathways. Whole pathways or segments of pathways are controlled by transcription factor proteins and proteins controlling the activity of signal transduction pathways. Therefore, manipulation of such protein levels is especially useful for altering phenotypes and biochemical activities of plants.

Phase responsive genes and gene products can function to either increase or dampen the above phenotypes or activities. Characterization of phase responsive genes was carried out using microarray technology. Microarray technology allows monitoring of gene expression levels for

thousands of genes in a single experiment. This is achieved by hybridizing labeled fluorescent cDNA pools to glass slides that contain spots of DNA (Schena et al. (1995) Science 270: 467-70). The US Arabidopsis Functional Genomics Consortium (AFGC) has recently made public the results from such microarray experiments conducted with AFGC chips containing about 10,000 non-redundant ESTs, selected from about 37,000 randomly sequenced ESTs generated from mRNA of different tissues and developmental stages.

The sequences of the ESTs showing at least two-fold increases or decreases in a mutant of *Arabidopsis thaliana*, squint, that appears not to undergo phase changes and appears adult-like throughout its growth cycle, compared with wild type were identified, compared to the Ceres full length cDNA and genomic sequence databanks, and equivalent Ceres clones identified. The MA_diff tables reports the results of this analysis, indicating those Ceres clones which are up or down regulated over controls, thereby indicating the Ceres clones which represent phase responsive genes. The MA_diff Table(s) reports the transcript levels of the experiment (see EXPT ID: Sqn (relating to SMD 7133, SMD 7137)). For transcripts that had higher levels in the samples than the control, a "+" is shown. A "-" is shown for when transcript levels were reduced in root tips as compared to the control. For more experimental detail see the Example section below.

Phase responsive genes are those sequences that showed differential expression as compared to controls, namely those sequences identified in the MA_diff tables with a "+" or "-" indication.

Phase Responsive Genes Identified By Cluster Analyses Of Differential Expression

Phase Responsive Genes Identified By Correlation To Genes That Are Differentially Expressed

As described above, the transcription profiles of genes that act together are well correlated. Applicants not only have identified the genes that are differentially expressed in the microarray experiments, but also have identified the genes that act in concert with them. The MA_clust table indicates groups of genes that have well correlated transcription profiles and therefore participate in the same pathway or network.

A pathway or network of phase responsive genes is any group in the MA_clust that comprises a cDNA ID that also appears in Expt ID Sqn (relating to SMD 7133, SMD 7137) of the MA_diff table(s).

Phase Responsive Genes Identified By Correlation To Genes That Cause Physiological Consequences

Additionally, the differential expression data and the phenotypic observations can be merged to identify pathways or networks of phase responsive genes. A group in the MA_clust is considered a phase responsive pathway or network if the group comprises a cDNA ID that also appears in Knock-in or Knock-out tables that causes one or more of the phenotypes described in section above.

Phase Responsive Genes Identified By Amino Acid Sequence Similarity

Phase responsive genes from other plant species typically encode polypeptides that share amino acid similarity to the sequences encoded by corn and Arabidopsis phase responsive genes. Groups of phase responsive genes are identified in the Protein Grouping table. In this table, any protein group that comprises a peptide ID that corresponds to a cDNA ID member of a phase responsive pathway or network is a group of proteins that also exhibits Phase responsive functions/utilities.

Further, promoters of phase responsive genes, as described in Reference tables, for example, are useful to modulate transcription that is induced by phase or any of the following phenotypes or biological activities below. Further, any desired sequence can be transcribed in similar temporal, tissue, or environmentally specific patterns as the phase responsive genes when the desired sequence is operably linked to a promoter of a phase responsive gene.

III.B.5.a. Use Of Phase Responsive Genes To Modulate

Phenotypes Phase responsive genes and gene products are useful to or modulate one or more phenotype including timing phenotypes, dormancy, germination, cotyledon opening, first leaves, juvenile to adult transition, bolting, flowering, pollination, fertilization, seed development, seed set, fruit drop, senescence, epinasty, biomass, fresh and dry weight during

any time in plant life, such as maturation, number of flowers, seeds, branches, and/or leaves, seed yield, including number, size, weight, and/or harvest index, fruit yield, including number, size, weight, and/or harvest index, plant development, time to fruit maturity, cell wall strengthening and reinforcement, stress tolerance, drought tolerance, flooding tolerance, and UV tolerance.

To regulate any of the phenotype(s) above, activities of one or more of the phase responsive genes or gene products can be modulated and the plants can be tested by screening for the desired trait. Specifically, the gene, mRNA levels, or protein levels can be altered in a plant utilizing the procedures described herein and the phenotypes can be screened for variants as in Anderson et al. (1997) *Plant Cell* 9: 1727-1743; Heintzen et al. (1997) *Proc. Natl. Acad. Sci. USA* 94: 8515-20; Schaffer et al. (1998) *Cell* 93:1219-1229; Somers et al. (1998) *Development* 125: 485-494; Somers et al. (1998) *Science* 282: 1488-1490; Wang and Tobin (1998) *Cell* 93: 1207-1217; Zhong et al. (1998) *Plant Cell* 10: 2005-2017; Sugano et al. (1998) *Proc. Natl. Acad. Sci. USA* 95: 11020-11025; Dowson-Day and Millar (1999) *Plant J* 17: 63-71; Green and Tobin (1999) *Proc. Natl. Acad. Sci. USA* 96: 4176-419; Staiger and Apel (1999) *Mol. Gen. Genet.* 261: 811-819; Strayer and Kay (1999) *Curr. Opin. Plant Biol.* 2:114-120; Strayer et. al. (2000) *Science* 289:768-771; Kreps et al. (2000) *J Biol Rhythms* (2000) 15:208-217; Nelson et al. (2000) *Cell* 101:331-340; Somers et al. (2000) *Cell* 101:319-329.

III.B.5.b. Use Of Phase Responsive Genes To Modulate Biochemical Activities

The activities of one or more of the phase responsive genes can be modulated to change biochemical or metabolic activities and/or pathways such as those noted below. Such biological activities are documented and can be measured according to the citations above and included in the table below:

Process	Biochemical Or Metabolic Activities And/Or Pathways	Citations including assays
Germination And Seedling Development	Cold, Light And Water Modulated Signal Transduction Pathways, Receptors, Kinases, PAS Domain Proteins	Bognar et al. (1999) <i>Proc. Natl. Acad. Sci. USA</i> 96:14652-14657; Sugano et al (1999) <i>Proc. Natl. Acad. Sci. USA</i> 96:12362-12366; Dowson-Day and Millar (1999) <i>Plant J</i> 17: 63-71; Somers et al. (2000) <i>Cell</i> 101:319-329; Zhong et al. (1998) <i>Plant Cell</i> 10: 2005-2017
Growth Transitions And Flowering	Cold And Light Modulated Signal Transduction Pathways, Receptors, Kinases, PAS Domain Proteins	Nelson et al. (2000) <i>Cell</i> 101:331-340; Fowler et al. (1999) <i>EMBO J.</i> 18:4679-4688
Tuber Formation	Cold And Light Modulated Signal Transduction Pathways	Yanovsky et al. (2000) <i>Plant J.</i> 23: 223-232
<u>METABOLISM</u>		
Lipid Metabolism	Membrane Lipid Synthesis Including Omega-3 Fatty Acid Desaturase, Lipases, Lipid Transfer Proteins	Bradley and Reddy (1997) <i>J. Bacteriol.</i> 179: 4407-4410; Martin, M et al. 1999 <i>Europe J. Biochem</i> 262: 283-290

Process	Biochemical Or Metabolic Activities And/Or Pathways	Citations including assays
Sugar Metabolism	Glycosylhydrolases, Glycosyltransferases, Amylases, Sucrose Synthase, CAB, Rubisco, Light Signal Transduction	Liu et al. (1996) <i>Plant Physiol.</i> 112:43-51; Millar and Kay (1996) <i>Proc Natl Acad Sci U S A</i> 93:15491-15496; Wang et al. (1997) <i>Plant Cell</i> 9:491-507; Shinohara et al (1999) <i>J. Biol. Chem.</i> 273: 446-452
Nitrogen Metabolism	Aminotransferases, Arginase, Proteases And Vegetative Storage Proteins, Aromatic Amino Acid Synthesis	Bradley and Reddy (1997) <i>J. Bacteriol.</i> 179: 4407-4410
Photorespiration	Mitochondrial, Chloroplast And Peroxisomal Photorespiratory Enzymes, Serine Hydroxymethyl Transferases, Catalase	Zhong and McClung (1996) <i>Mol. Gen. Genet.</i> 251:196-203; McClung (1997) <i>Free. Radic. Biol. Med.</i> 23:489-496; McClung et al. (2000) <i>Plant Physiol.</i> 123:381-392
Responses To Environmental Stress	Expression Of Genes Involved In Responses To Drought, Salt, UV	McClung (1997) <i>Free Radic Biol Med</i> 23:489-496; Shi et al. (2000) <i>Proc. Natl. Acad. Sci. USA</i> 97:6896-6901

Other biological activities that can be modulated by the phase responsive genes and their products are listed in the Reference tables. Assays for detecting such biological activities are described in the Protein Domain table.

Phase responsive genes are characteristically differentially transcribed in response to maturity of the cell, organ or tissue which depends on a timing mechanism, which is internal to an organism or cell. The Intensity Table reports the changes in transcript levels of various phase responsive genes in a plant.

The data from this experiment reveal a number of types of phase responsive genes and gene products. Profiles of some classes of phase responsive genes are shown in the table below with examples of which associated biological activities are modulated when the activities of one or more such genes vary in plants.

Transcript Levels	Type Of Genes	Physiological Consequences	Examples Of Biochemical Activity
Up Regulated Transcripts	<p>Responders To mutation that confers adult like phase</p> <p>Genes induced in adult-like phase</p>	<ul style="list-style-type: none"> • Adult phase adoption • Metabolisms Affected By phase change • Synthesis Of Secondary Metabolites And/Or Proteins • Modulation Of Phase Response Transduction Pathways • Specific Gene Transcription Initiation 	<ul style="list-style-type: none"> • Metabolic Enzymes • Change In Cell Membrane Structure And Potential • Kinases And Phosphatases • Transcription Activators • Change In Chromatin Structure And/Or Localized DNA Topology
Down-Regulated Transcripts	<p>Responders To mutation that confers adult phase</p> <p>Genes repressed in adult-like phase</p> <p>Genes With Discontinued Expression Or Unstable mRNA in adult-like phase</p>	<ul style="list-style-type: none"> • Negative Regulation of adult phase pathways • Changes In Pathways And Processes Operating In Cells • Changes In Metabolic pathways other than phase specific pathways 	<ul style="list-style-type: none"> • Transcription Factors • Change In Protein Structure By Phosphorylation (Kinases) Or Dephosphorylation (Phosphatases) • Change In Chromatin Structure And/Or DNA Topology • Stability Factors For Protein Synthesis And Degradation • Metabolic Enzymes

USE OF PROMOTERS OF PHASE RESPONSIVE GENES

Promoters of phase responsive genes are useful for transcription of any desired polynucleotide or plant or non-plant origin. Further, any desired sequence can be transcribed in a similar temporal, tissue, or environmentally specific patterns as the phase responsive genes where the desired sequence is operably linked to a promoter of a phase responsive gene. The protein product of such a polynucleotide is usually synthesized in the same cells, in response to the same stimuli as the protein product of the gene from which the promoter was derived. Such promoter are also useful to produce antisense mRNAs to down-regulate the product of proteins, or to produce sense mRNAs to down-regulate mRNAs via sense suppression.

III.C. HORMONE RESPONSIVE GENES, GENE COMPONENTS AND PRODUCTS

III.C.1. ABSCISSIC ACID RESPONSIVE GENES, GENE COMPONENTS AND PRODUCTS

Plant hormones are naturally occurring substances, effective in very small amounts, which act as signals to stimulate or inhibit growth or regulate developmental processes in plants. Abscissic acid (ABA) is a ubiquitous hormone in vascular plants that has been detected in every major organ or living tissue from the root to the apical bud. The major physiological responses affected by ABA are dormancy, stress stomatal closure, water uptake, abscission and senescence. In contrast to Auxins, cytokinins and gibberellins, which are principally growth promoters, ABA primarily acts as an inhibitor of growth and metabolic processes.

Changes in ABA concentration internally or in the surrounding environment in contact with a plant results in modulation of many genes and gene products. Examples of such ABA responsive genes and gene products are shown in the Reference, Sequence, Protein Group, Protein Group Matrix tables, MA_diff, and MA_clust tables. These genes and/or products are responsible for effects on traits such as plant vigor and seed yield. They were discovered and characterized from a much larger set of genes by experiments designed to find genes whose mRNA products changed in concentration in response to application of ABA to plants.

While ABA responsive polynucleotides and gene products can act alone, combinations of these polynucleotides also affect growth and development. Useful combinations include different ABA responsive polynucleotides and/or gene products that have similar transcription profiles or similar biological activities, and members of the same or similar biochemical pathways. Whole pathways or segments of pathways are controlled by transcription factor proteins and proteins controlling the activity of signal transduction pathways. Therefore, manipulation of such protein levels is especially useful for altering phenotypes and biochemical activities of plants. In addition, the combination of an ABA responsive polynucleotide and/or gene product with another environmentally responsive polynucleotide is also useful because of the interactions that exist between hormone-regulated pathways, stress and defence induced pathways, nutritional pathways and development. Here, in addition to polynucleotides having similar transcription profiles and/or biological activities, useful combinations include polynucleotides that may have different transcription profiles but which participate in common or overlapping pathways.

Such ABA responsive genes and gene products can function to either increase or dampen the above phenotypes or activities either in response to changes in ABA concentration or in the absence of ABA fluctuations. The MA_diff Table(s) reports the transcript levels of the experiment (see EXPT ID: 108560, 108561, 108513, 108597). For transcripts that had higher levels in the samples than the control, a "+" is shown. A "-" is shown for when transcript levels were reduced in root tips as compared to the control. For more experimental detail see the Example section below.

ABA genes are those sequences that showed differential expression as compared to controls, namely those sequences identified in the MA_diff tables with a "+" or "-" indication.

ABA Genes Identified By Cluster Analyses Of Differential Expression

ABA Genes Identified By Correlation To Genes That Are Differentially Expressed

As described above, the transcription profiles of genes that act together are well correlated. Applicants not only have identified the genes that are differentially expressed in the microarray experiments, but also have identified the genes that act in concert with them. The

MA_clust table indicates groups of genes that have well correlated transcription profiles and therefore participate in the same pathway or network.

A pathway or network of ABA genes is any group in the MA_clust that comprises a cDNA ID that also appears in Expt ID 108560, 108561, 108513, 108597 of the MA_diff table(s).

ABA Genes Identified By Correlation To Genes That Cause Physiological Consequences

Additionally, the differential expression data and the phenotypic observations can be merged to identify pathways or networks of ABA genes. A group in the MA_clust is considered a ABA pathway or network if the group comprises a cDNA ID that also appears in Knock-in or Knock-out tables that causes one or more of the phenotypes described in section above.

ABA Genes Identified By Amino Acid Sequence Similarity

ABA genes from other plant species typically encode polypeptides that share amino acid similarity to the sequences encoded by corn and Arabidopsis ABA genes. Groups of ABA genes are identified in the Protein Group table. In this table, any protein group that comprises a peptide ID that corresponds to a cDNA ID member of a ABA pathway or network is a group of proteins that also exhibits ABA functions/utilities.

Further, promoters of ABA responsive genes, as described in the Reference tables, for example, are useful to modulate transcription that is induced by ABA or any of the following phenotypes or biological activities below.

III.C.1.a. Use Of Abscissic Acid Responsive Genes To Modulate Phenotypes

ABA responsive genes and gene products are useful to or modulate one or more of the following phenotypes including development such as cell growth (promotion of leaf cell elongation), fruit development (fruit drop and inhibition of parthenocarp and ovary growth), seed development (maturation of zygotic and somatic embryos, embryo development, seed development and maturation, acquisition of desiccation tolerance, dormancy including control rate and timing of germination, prolongation of seed storage and viability, and inhibition of

hydrolytic enzyme synthesis); growth of roots such as inhibition of root elongation under low water potential), stems, buds (such as promotion of dormancy and lateral/axillary bud formation), leaves, and inhibition of aba-induced growth and elongation; biomass (such as fresh and dry weight during any time in plant life, such as maturation), number, size, and weight of flowers and seeds); senescence (including abscission, leaf fall, and flower longevity); differentiation (including plastid/chloroplast differentiation and regulation of sterility); and stress responses (such as mediation of response to desiccation, drought, salt and cold).

To regulate any of the phenotype(s) above, activities of one or more of the ABA responsive genes or gene products can be modulated in an organism and tested by screening for the desired trait. Specifically, the gene, mRNA levels, or protein levels can be altered in a plant utilizing the procedures described herein and the phenotypes can be assayed. As an example, a plant can be transformed according to Bechtold and Pelletier (1998, Methods. Mol. Biol. 82:259-266) and/or screened for variants as in Winkler et al. (1998) Plant Physiol 118: 743-50 and visually inspected for the desired phenotype or metabolically and/or functionally assayed according to Koorneef and Karssen (1994, Seed dormancy and germination, In: Arabidopsis, Cold Spring Harbor Lab. Press, pp 314-334), Cramer et al (1998, J. Exptl. Botany 49:191-198), and White and Rivin (2000, Plant Physiol 122: 1089-97). Phillips et al. (1997) EMBO J 16: 4489-96; Nambara et al (1995) Development 121: 629-636; Hays et al (1999) Plant Physiol. 119: 1065-72; Filonova et al (2000) J Exptl Botany 51: 249-64; White et al (2000) Plant Physiol. 122: 1081-88; and Visser et al. (1998) Plant Mol Biol 37: 131-40; Rohde et al. (2000) Plant Cell 12:35-52; and Cramer et al. (1998) J. experimental Botany. 49: 191-198.

III.C.1.b. Use Of Abscissic Acid Responsive Genes To Modulate Biochemical Activities

The activities of one or more of the ABA responsive genes can be modulated to change biochemical or metabolic activities and/or pathways such as those noted below. Such biological activities can be measured according to the citations included in the Table below:

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
Growth , Differentiation And Development	<ul style="list-style-type: none"> Farnesylation Nitrogen Metabolism 	<p>Pei Et Al (1998) Science 282: 287-290; Cutler Et Al. (1996) Science 273: 1239</p> <p>Goupil Et Al (1998) J Exptl Botany 49:1855-62</p>
Water Conservation And Resistance To Drought And Other Related Stresses	<ul style="list-style-type: none"> Stomatal Development And Physiology Stress Response Pathways Inhibition Of Ethylene Production Under Low Water Potential Proline And Other Osmolite Synthesis And Degradation 	<p>Allen Et Al. (1999) Plant Cell 11: 1785-1798</p> <p>Li Et Al. 2000 Science 287: 300-303</p> <p>Burnett Et Al 2000. J. Exptl Botany 51: 197-205</p> <p>Raschke (1987) In: Stomatal Function Zeiger Et Al. Eds., 253-279</p> <p>Bush And Pages (1998) Plant Mol. Biol. 37: 425-35</p> <p>Spollen Et Al (2000) Plant Physiol. 122:967-976</p> <p>Hare Et Al. (1998) Plant, Cell And Environment 21:535-553; Hare Et Al. (1999) J. Exptl. Botany 50:413-434</p>
	<ul style="list-style-type: none"> Plasmalemma And Tonoplast Ion Channel Changes Ca²⁺ Accumulation 	<p>Macrobbie (1998) Philos Trans R Soc Lond B Biol Sci 353: 1475-88; Li Et Al (2000) Science 287:300-303;</p> <p>Barkla Et Al. (1999) Plant Physiol. 120:811-819</p> <p>Lacombe Et Al. (2000) Plant Cell 12: 837-51; Wang Et Al. (1998) Plant</p>

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
	<ul style="list-style-type: none"> • K⁺ Efflux • Activation Of Kinases And Phosphatases 	Physiol 118:1421-1429; Shi Et Al. (1999) Plant Cell 11: 2393-2406 Gaymard Et Al. (1998) Cell 94:647-655 Jonak Et Al. (1996) Proc. Natl. Acad. Sci 93: 11274-79; Sheen (1998) Proc. Natl. Acad. Sci. 95: 975-80; Allen Et Al. (1999) Plant Cell 11: 1785-98

Other biological activities that can be modulated by the ABA responsive genes and gene products are listed in the Reference tables. Assays for detecting such biological activities are described in the Protein Domain table.

ABA responsive genes are characteristically differentially transcribed in response to fluctuating ABA levels or concentrations, whether internal or external to an organism or cell. The MA_diff reports the changes in transcript levels of various ABA responsive genes in entire seedlings at 1 and 6 hours after a plant was sprayed with a Hoagland's solution enriched with ABA as compared to seedlings sprayed with Hoagland's solution only.

The data from this time course can be used to identify a number of types of ABA responsive genes and gene products, including "early responders," and "delayed ABA responders", "early responder repressors" and "delayed repressors". Profiles of these different ABA responsive genes are shown in the Table below together with examples of the kinds of associated biological activities.

TRANSCRIPT LEVELS	TYPE OF GENES	PHYSIOLOGICAL CONSEQUENCES	EXAMPLES OF BIOCHEMICAL ACTIVITY
Up Regulated	Early Responders	ABA Perception	Transcription Factors

TRANSCRIPT LEVELS	TYPE OF GENES	PHYSIOLOGICAL CONSEQUENCES	EXAMPLES OF BIOCHEMICAL ACTIVITY
Transcripts (Level At 1 Hr \approx 6 Hr) or (Level At 1 Hr > 6 Hr)	To ABA	ABA Uptake Modulation Of ABA Response Transduction Pathways Specific Gene Transcription Initiation	Transporters Change In Cell Membrane Structure Kinases And Phosphatases Transcription Activators Change In Chromatin Structure And/Or Localized DNA Topology
Up Regulated Transcripts (Level At 1 Hr < 6 Hr)	Delayed Responders	Maintenance Of Response To ABA Maintenance Of Seed Dormancy, Stress Stomatal Closure, Water Uptake Control, Abscission And Senescence Control Pathways	Transcription Factors Specific Factors (Initiation And Elongation) For Protein Synthesis Maintenance Of Mrna Stability Maintenance Of Protein Stability Maintenance Of Protein-Protein Interaction
Down-Regulated Transcripts (Level At 1 Hr \approx 6 Hr) or (Level At 6 Hr > 1 Hr)	Early Responder Repressors Of ABA State Of Metabolism Genes With	Negative Regulation Of ABA Pathways Released Changes In Pathways And Processes	Transcription Factors Change In Protein Structure By Phosphorylation (Kinases) Or Dephosphorylation (Phosphatases)

TRANSCRIPT LEVELS	TYPE OF GENES	PHYSIOLOGICAL CONSEQUENCES	EXAMPLES OF BIOCHEMICAL ACTIVITY
	Discontinued Expression Or UnsTable mRNA In Presence Of ABA	Operating In Cells	Change In Chromatin Structure And/Or DNA Topology
Down-Regulated Transcripts (Level At 1 Hr > 6 Hr)	Delayed Repressors Of ABA State Of Metabolism Genes With Discontinued Expression Or UnsTable mRNA In Presence Of ABA	Negative Regulation Of ABA Pathways Released Maintenance Of Pathways Released From Repression Changes In Pathways And Processes Operating In Cells	Transcription Factors Kinases And Phosphatases Stability Of Factors For Protein Synthesis And Degradation

USE OF PROMOTERS OF ABA RESPONSIVE GENES

Promoters of ABA responsive genes are useful for transcription of any desired polynucleotide or plant or non-plant origin. Further, any desired sequence can be transcribed in a similar temporal, tissue, or environmentally specific patterns as the ABA responsive genes where the desired sequence is operably linked to a promoter of a ABA responsive gene. The protein product of such a polynucleotide is usually synthesized in the same cells, in response to the same stimuli as the protein product of the gene from which the promoter was derived. Such promoter are also useful to produce antisense mRNAs to down-regulate the product of proteins, or to produce sense mRNAs to down-regulate mRNAs via sense suppression.

III.C.2. AUXIN RESPONSIVE GENES, GENE COMPONENTS AND PRODUCTS

Plant hormones are naturally occurring substances, effective in very small amounts that stimulate or inhibit growth or regulate developmental processes in plants. One of the plant hormones is indole-3-acetic acid (IAA), often referred to as Auxin.

Changes in Auxin concentration in the surrounding environment in contact with a plant or in a plant results in modulation of the activities of many genes and hence levels of gene products. Examples of such Auxin responsive genes and their products are shown in the Reference and Sequence Tables. These genes and/or products are responsible for effects on traits such as plant vigor and seed yield. The genes were discovered and characterized from a much larger set by experiments designed to find genes whose mRNA products changed in response to application of Auxin to plants.

Manipulation of one or more Auxin responsive gene activities are useful to modulate the biological activities and/or phenotypes listed below. Auxin response genes and gene products can act alone or in combination. Useful combinations include Auxin response genes and/or gene products with similar transcription profiles, similar biological activities, or members of the same or functionally related biochemical pathways. Whole pathways or segments of pathways are controlled by transcription factor proteins and proteins controlling the activity of signal transduction pathways. Therefore, manipulation of the levels of such proteins is especially useful for altering phenotypes and biochemical activities of plants. The MA_diff Table(s) reports the transcript levels of the experiment (see EXPT ID: 108564, 108565, 108516, 108554, 108466, 107886, 107891, SMD 3743, and NAA (relating to SMD 3749, SMD 6338, SMD 6339)). For transcripts that had higher levels in the samples than the control, a "+" is shown. A "-" is shown for when transcript levels were reduced in root tips as compared to the control. For more experimental detail see the Example section below.

NAA genes are those sequences that showed differential expression as compared to controls, namely those sequences identified in the MA_diff tables with a "+" or "-" indication.

NAA Genes Identified By Cluster Analyses Of Differential Expression

NAA Genes Identified By Correlation To Genes That Are Differentially Expressed

As described above, the transcription profiles of genes that act together are well correlated. Applicants not only have identified the genes that are differentially expressed in the microarray experiments, but also have identified the genes that act in concert with them. The MA_clust table indicates groups of genes that have well correlated transcription profiles and therefore participate in the same pathway or network.

A pathway or network of NAA genes is any group in the MA_clust that comprises a cDNA ID that also appears in Expt ID 108564, 108565, 108516, 108554, 108466, 107886, 107891, SMD 3743, and NAA (relating to SMD 3749, SMD 6338, SMD 6339) of the MA_diff table(s).

NAA Genes Identified By Correlation To Genes That Cause Physiological Consequences

Additionally, the differential expression data and the phenotypic observations can be merged to identify pathways or networks of NAA genes. A group in the MA_clust is considered a NAA pathway or network if the group comprises a cDNA ID that also appears in Knock-in or Knock-out tables that causes one or more of the phenotypes described in section above.

NAA Genes Identified By Amino Acid Sequence Similarity

NAA genes from other plant species typically encode polypeptides that share amino acid similarity to the sequences encoded by corn and Arabidopsis NAA genes. Groups of NAA genes are identified in the Protein Group table. In this table, any protein group that comprises a peptide ID that corresponds to a cDNA ID member of a NAA pathway or network is a group of proteins that also exhibits NAA functions/utilities.

Such Auxin responsive genes and gene products can function to either increase or dampen the above phenotypes or activities either in response to changes in Auxin concentration or in the absence of Auxin fluctuations. Further, promoters of Auxin responsive genes, as described in the Reference tables, for example, are useful to modulate transcription that is induced by Auxin or any of the following phenotypes or biological activities below.

III.C.2.a. Use Of Auxin Responsive Genes, Gene Components And
Products To Modulate Phenotypes

Auxin responsive genes and gene products are useful to or modulate one or more phenotypes including growth, apical dominance, vascular growth, roots, inhibition of primary root elongation, increased lateral root formation, stems, lateral buds, lateral branching, reduction of branching, for high density growth per acre, for increased wood production, lateral organ initiation and/or positioning in apical meristem, organ formation, for example, fruit number in tomatoes, leaves, height/stature, e.g., taller crops or increase wood production, regeneration and differentiation of cultured cells or plantlets, biomass, fresh and dry weight during any time in plant life, such as maturation; number of flowers; number of seeds; number of branches; number of leaves; starch content, seed yield, including number, size, weight, harvest index, starch content, fruit yield, number, size, weight, harvest index, starch content, development, orienting cell growth, establishment and maintenance of plant axis, apical dominance, cell plate placement, polarised growth, initiation and/or development, of embryos morphogenic progression, e.g., from early radial to late axialized torpedo stages, differentiation of cells into morphologically different cell layers, cotyledon separation, fruit development, abscission, leading to modulation of fruit drop, parthenocarpy, seedless crops resulting from lack of seed set, vascularization, e.g. hypocotyl and cotyledon tissues, genetic control of vascular patterning and influences its maturation; specification of the sites where vascular differentiation will occur; determination of the direction and extent of vascular tissue formation, maintenance of the continuity of vascular development with plant growth, tropic responses, gravitropic responses, e.g. affecting roots and shoots, and modulation of phototropic sensitivity, e.g. increase growth under a reduced light spectrum.

Further, any desired sequence can be transcribed in similar temporal, tissue, or environmentally specific patterns as the Auxin responsive genes when the desired sequence is operably linked to a promoter of an Auxin responsive gene.

To modulate any of the phenotype(s) above, activities of one or more of the Auxin response genes or gene products can be modulated and the plants can be tested by screening for the desired trait. Specifically, the gene, mRNA levels, or protein levels can be altered in a plant utilizing the procedures described herein and the phenotypes can be screened for variants as in Winkler et al. (1998) Plant Physiol 118: 743-50 and assayed, for example, in accordance with Bechtold and Pelletier (1998). Methods Mol. Biol. 82: 259-266; Clough and Bent (1998). 16: 735-743; Krysan et al. (1999). Plant Cell 11:2283-2290.

III.C.2.b. Use Of Auxin Responsive Genes, Gene Components And Products To Biochemical Activities:

The activities of one or more of the Auxin responsive genes can be modulated to change biochemical or metabolic activities and/or pathways such as those noted below. Such biological activities are documented and can be measured according to the citations included in the Table below:

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
Cell Growth and Differentiation	Protein Ubiquitination	Gray et al. (1999) Genes and Develop, 13:1678-1691 Bechtold and Pelletier (1998). Methods. Mol. Biol. 82:259-266
	Cell Wall loosening and Expansion	Catala et al. (2000). Plant Physiol. 122:527-534. Cosgrove, D. (1993). New Phytol. 124:1-23.

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
Auxin/Cytokinin Ratio	Changing Auxin and/or cytokinin synthesis and/or turnover	Chen et al. (1988). Plant Physiol. 86:822-825 Tam et al. (2000). Plant Physiol. 123:589-595 Bartel and Fink. (1995). Science 268:1745-1748. Prinsen et al. (1995). Quantifying phytohormones in transformed plants. In: Methods in Molecular Biology. 44:245-262.
Auxin Transport	Channeling of polar Auxin Transport	Reed et al. (1998). Plant Physiol. 118:1369-1378. Estelle, M. (1998). Plant Cell 10:1775-1778
	Auxin Efflux Between Cells	Reed et al. (1998). Plant Physiol. 118:1369-1378. Marchant et al. (1999). EMBO J. 18:2066-2073.
	Auxin Influx In and Out of a Cell	Reed et al. (1998). Plant Physiol. 118:1369-1378. Marchant et al. (1999). EMBO J. 18:2066-2073.
	Electrogenic Proton Symport of Auxin	Young et al. (1999). Biochim Biophys Acta. 1415(2):306-22
Signal Transduction	K ⁺ Accumulation	Philippart et al. (1999). Proc. Natl. Acad. Sci. 96:12186-12191

PROCESS	BIOCHEMICAL OR METABOLIC ACTIVITIES AND/OR PATHWAYS	CITATIONS INCLUDING ASSAYS
	Permeability of Cell Membranes	Marchant et al. (1999). EMBO J. 18:2066-2073.
	Guanine-Nucleotide Exchange	Steinmann et al. (1999). Science 286:316-318. Peyroche et al. (1996). Nature 384:479-481.
	Protein Phosphorylation	Christensen et al. (2000). Cell 100:469-478. Hirt (2000). Proc. Natl. Acad Sci. 97:2405-2407.
	Interaction with Ethylene mode of action	Madlung et al. (1999). Plant Physiol. 120:897-906. Xu et al. (1998). Plant Physiol. 118:867-874.
Protein Turnover	Localization of Polypeptides with the basal End of Cells	Grebe et al. (2000). Plant Cell. 12:343-356

Other biological activities that can be modulated to by the Auxin responsive genes and their products are listed in the Reference Tables. Assays for detecting such biological activities are described in the Domain section of the Reference Tables.

Auxin responsive genes are characteristically differentially transcribed in response to fluctuating Auxin levels or concentrations, whether internal or external to an organism or cell. The MA_diff(s) report(s) the changes in transcript levels of various Auxin responsive genes in the aerial parts of a seedling at 1 and 6 hours after the seedling was sprayed with a solution enriched with Auxin as compared to aerial parts of a seedling sprayed with water.

The data from this time course can be used to identify a number of types of Auxin responsive genes and gene products, including "early responders," and "delayed responders."

Profiles of these different classes of Auxin responsive genes are shown in the Table below together with examples of the kinds of associated biological activities.

TRANSCRIPT LEVEL	TYPE OF GENES	PHYSIOLOGICAL CONSEQUENCES	EXAMPLES OF BIOCHEMICAL ACTIVITY OF GENE PRODUCTS
Upregulated transcripts (level at 1 hr \leq 6 hours) (level at 1 hr>6 hours)	Early responders to Auxin	<ul style="list-style-type: none"> • Auxin perception • Auxin Uptake/transport • Modulation of Auxin response transduction pathways • Initiating transcription of specific gene(s) • Modification of cell walls • Modification of cell structures • Modification of metabolism 	<ul style="list-style-type: none"> • Transcription factors • Transporters; channeling of polar Auxin transport • Kinases and phosphatases; protein ubiquitination; guanine nucleotide exchange; changing Auxin and/or cytokinin synthesis and/or turnover; interaction with ethylene mode of action • Auxin metabolic pathways • Change in chromatin structure and/or DNA topology • Transcriptional activators • Change in activity of protein-protein interactions • Cell wall and cell growth promoting pathways • Change in activity of cytoskeletal proteins modulating cell structure • Metabolic enzymes • Coordination and control of central carbon and Auxin metabolism

TRANSCRIPT LEVEL	TYPE OF GENES	PHYSIOLOGICAL CONSEQUENCES	EXAMPLES OF BIOCHEMICAL ACTIVITY OF GENE PRODUCTS
Upregulated transcripts (level at 1 hr <6 hr)	"Delayed" Responders	<ul style="list-style-type: none"> • Completion and/or Maintenance of Auxin response • Initiating transcription of specific gene(s) • Modification of cell walls • Modification of cell structures • Modification of metabolism 	<p>Transcription factors</p> <p>Changes in membrane protein, membrane channel and/or transporter protein activity</p> <ul style="list-style-type: none"> - Change in chromatin structure and/or DNA topology - Transcriptional activators - Change in activity of protein-protein interactions - Cell wall proteins - Change(s) in activity of cytoskeletal proteins modulating cell structure - Coordination and control of central carbon and Auxin metabolism -metabolic enzymes

TRANSCRIPT LEVEL	TYPE OF GENES	PHYSIOLOGICAL CONSEQUENCES	EXAMPLES OF BIOCHEMICAL ACTIVITY OF GENE PRODUCTS
Downregulated transcripts (level at 1hour \cong 6 hours) (level at 1hour > 6 hours)	Early repressor responders to Auxin Genes for pathways diminished in presence of Auxin	<ul style="list-style-type: none"> • Repression of Auxin induced proteins released • Reorientation of metabolism in certain cells 	<ul style="list-style-type: none"> • Transcription factors • Changes in activity of cytoskeletal proteins modulating cell structure • Changes in chromatin structure and/or DNA topology • Changes in protein structure and/or function by phosphorylation (kinases) and/or dephosphorylation (phosphatases) • Stability of factors for protein translation • Changes in cell membrane structure • Changes in chromatin and/or localized DNA topology • Changes in protein-protein interaction • Metabolic enzymes

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